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SMITH et al.(10) **Pub. No.: US 2012/0087917 A1**(43) **Pub. Date: Apr. 12, 2012**(54) **LOX AND LOXL2 INHIBITORS AND USES
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on Aug. 2, 2007, provisional application No. 60/963,
214, filed on Aug. 2, 2007, provisional application No.
60/963,248, filed on Aug. 2, 2007, provisional appli-
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<i>C12N 1/19</i>	(2006.01)

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435/328; 435/252.3

(57)

ABSTRACT

The present application relates to anti-LOX and anti-LOXL2 antibodies and their use in purification, diagnostic and therapeutic methods. Antibodies include monoclonal antibodies, humanized antibodies and functional fragments thereof. Anti-LOX and anti-LOXL2 antibodies can be used to identify and treat conditions such as a fibrotic condition, angiogenesis, or to prevent a transition from an epithelial cell state to a mesenchymal cell state.

FIGURE 1**Lysyl Oxidase Enzymology**

LOX/L enzymes act via a ping-pong mechanism which
can be described by Michaelis-Menten kinetics

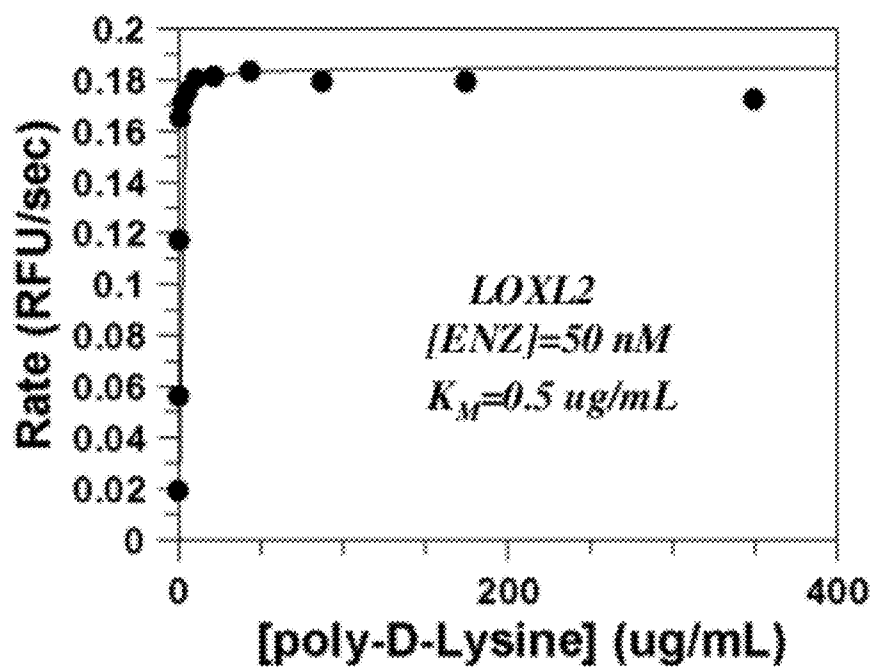


FIGURE 2

Common Modes of Enzymatic Inhibition

Competitive inhibition

- Inhibitor typically bears structural similarity to substrate
- Inhibition noticeable at low substrate concentrations but can be overcome at high substrate concentrations

Uncompetitive inhibition

- Inhibitor binds at site that becomes available after substrate is bound at the active site
- Inhibition most noticeable at high substrate concentration

Non-competitive inhibition

- Inhibitor binds at site away from substrate binding site
- Relative inhibition is the same at all substrate concentrations

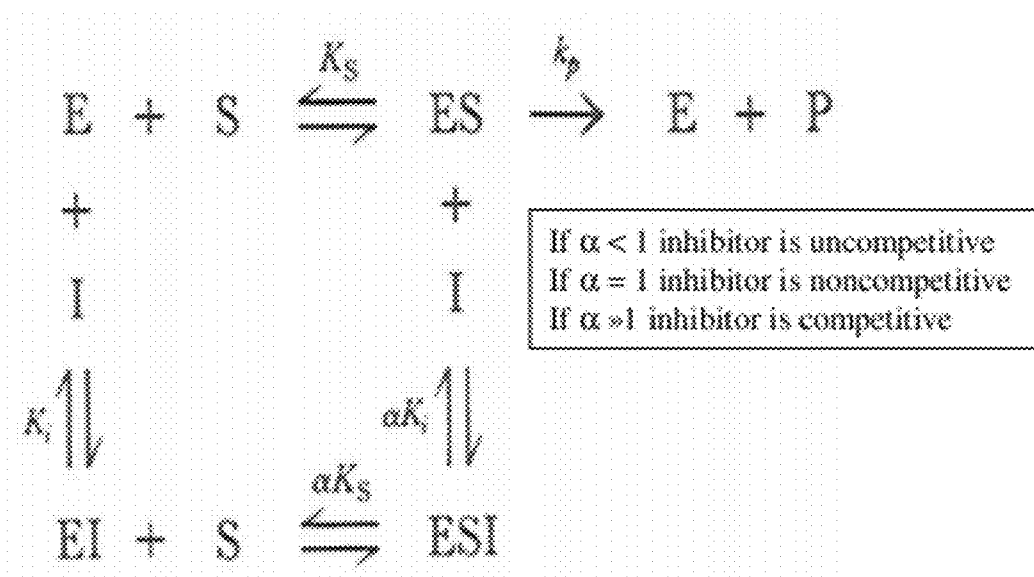


FIGURE 3
 β APN is a Competitive Inhibitor of LOXL2

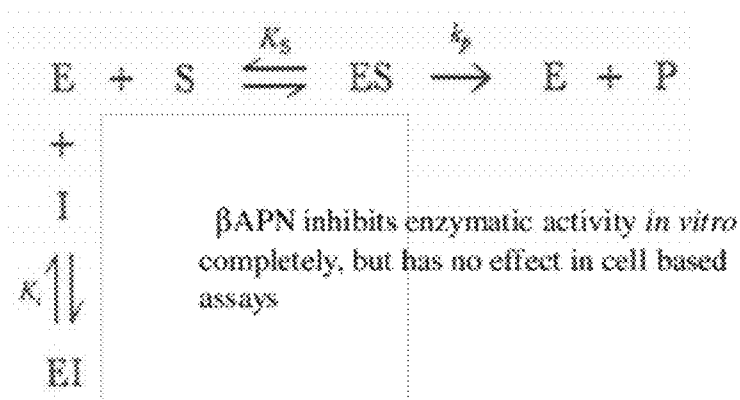
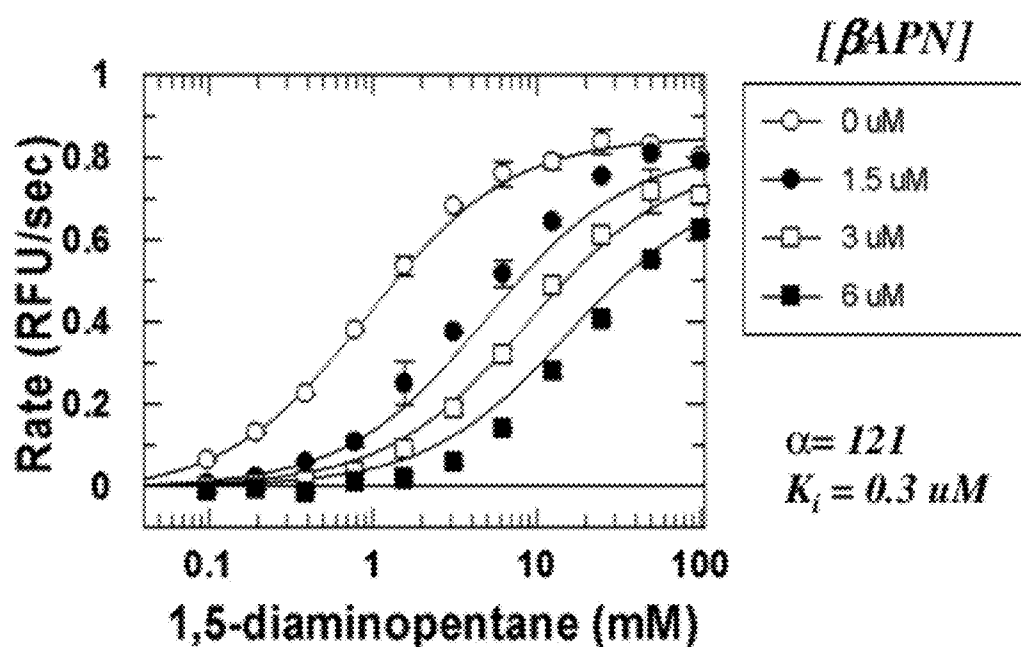


FIGURE 4
Modes of Enzymatic Inhibition: LOXL2

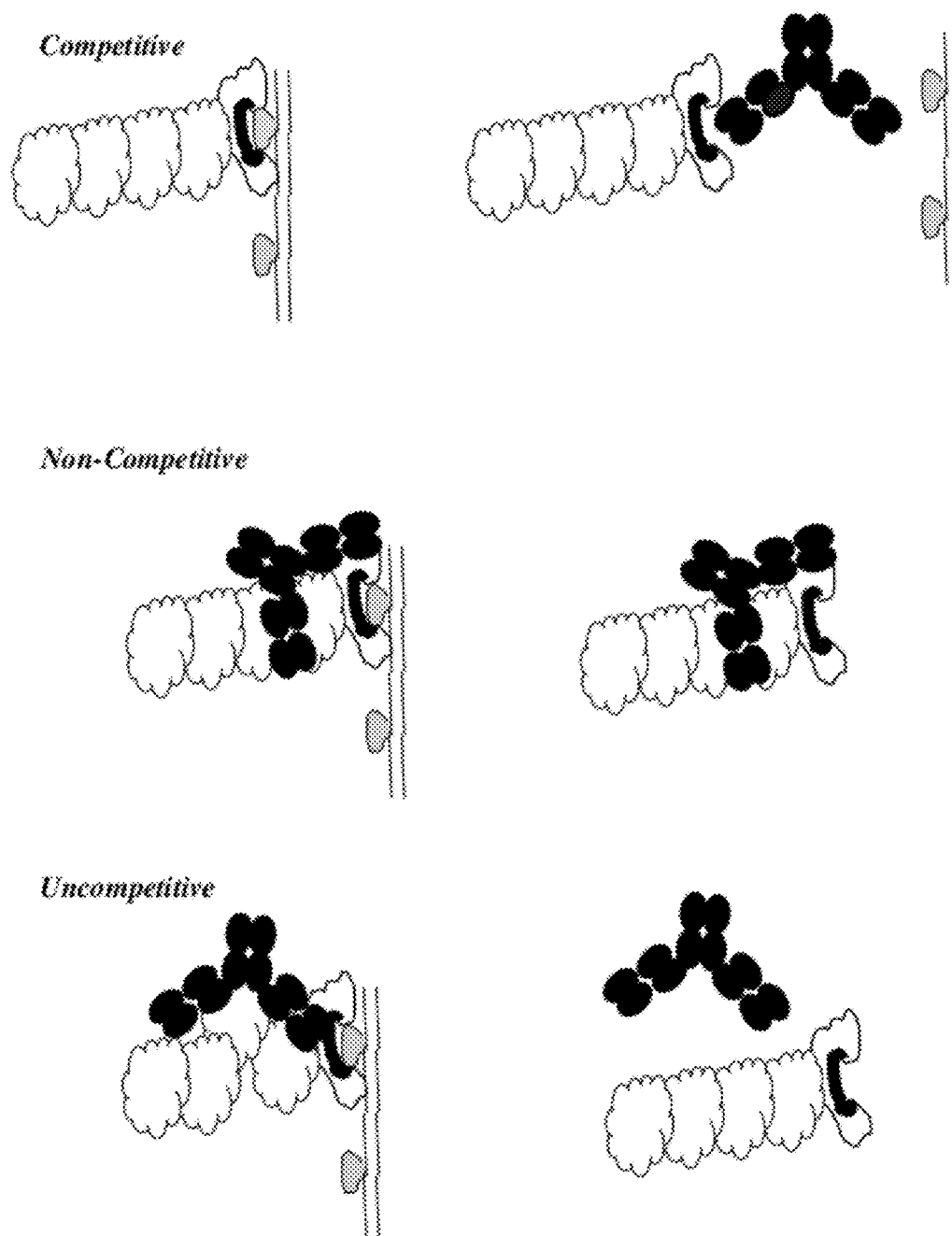


Figure 5
Extracellular LOXL2: Localization and Function

At high cell density, LOXL2 is secreted and detected bound to the matrix and, in conditioned media, a blocking antibody will, ideally, bind all states and inhibit all activities

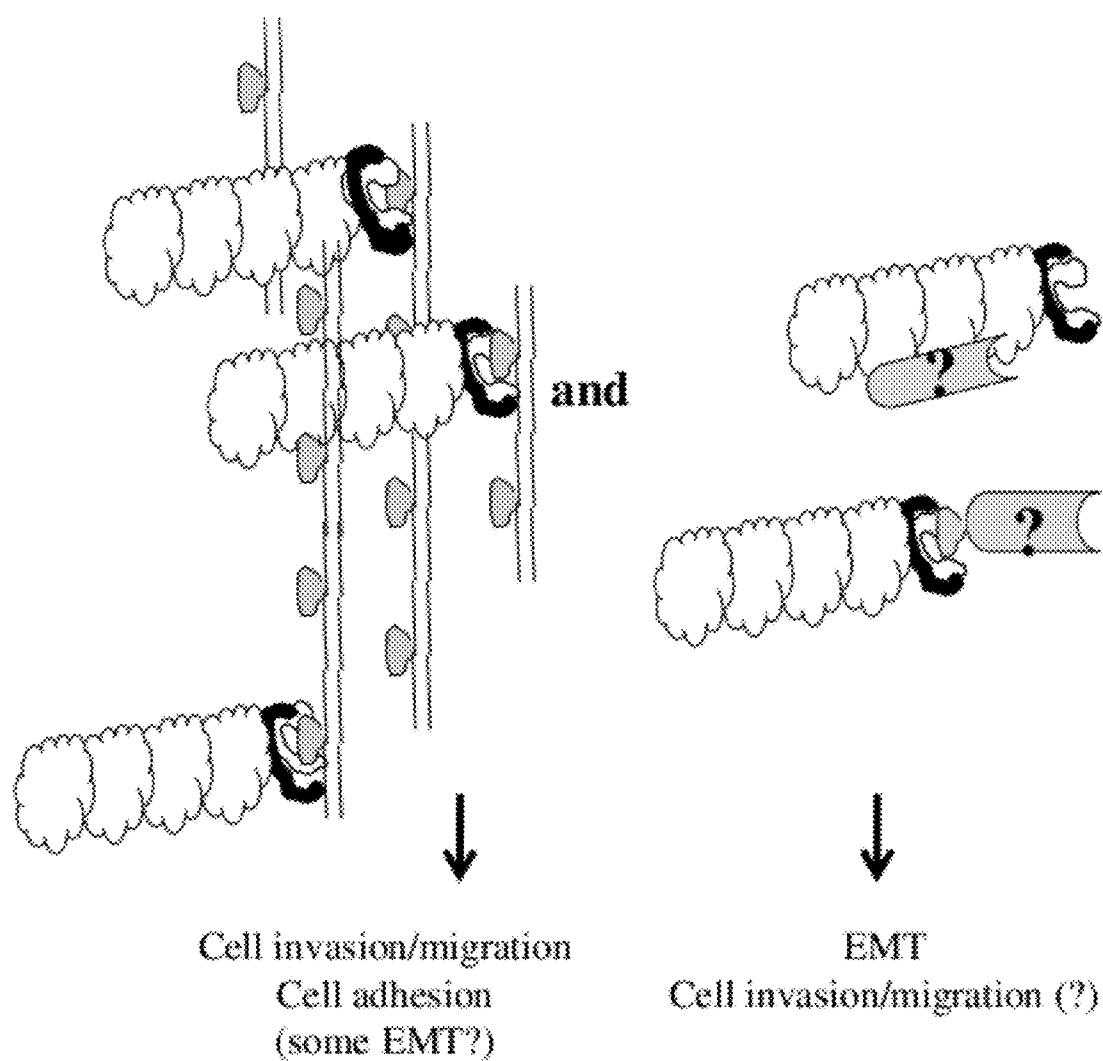


Figure 6
Murine Monoclonal Anti-LOXL2 Antibody

A. Variable Heavy Chain

MEWSRVFIFLLSVTAGVHSQVQLQQSGAELVRPGTS
VKVSCKASGYAFTYYLIEWVKQRPGQGLEWIGVI
NPGSGGTNYNEKFKGKATLTADKSSSTAYMQLSS
LTSDDSA VYFCARNWMNFDYWGQGTTTLTVSSAK
TTPPSVYPLA...(SEQ ID NO: 1)

B. Variable Light Chain

MRCLAEFLGLLVLWIPGAIGDIVMTQAAPSVSVTPG
ESVSISCRSSKSLLSNGNTYLYWFLQRPGQSPQFL
IYRMSNLASGVPDRFSGSGSGTAFTLRISRVEAED
VGYYCMQHLEYPYTFGGGTKLEIKRADAAPTV
SIFPPSTRDPRAN (SEQ ID NO: 2)

Figure 7
Anti-LOX antibody

A. Variable Heavy Chain

MGWSWVFLFLSVTAGVHSQVQLQQSGAELVKPGASVKLSC
KASGYTFRSYDINWVRQRPEQGLEWIGWIFPGDGSTKYNEK
FKGKAILTTDKSSSTAYMQLSRLTSEDSAVYFCARVYYAMD
YWGQGTSV...(SEQ ID NO: 3)

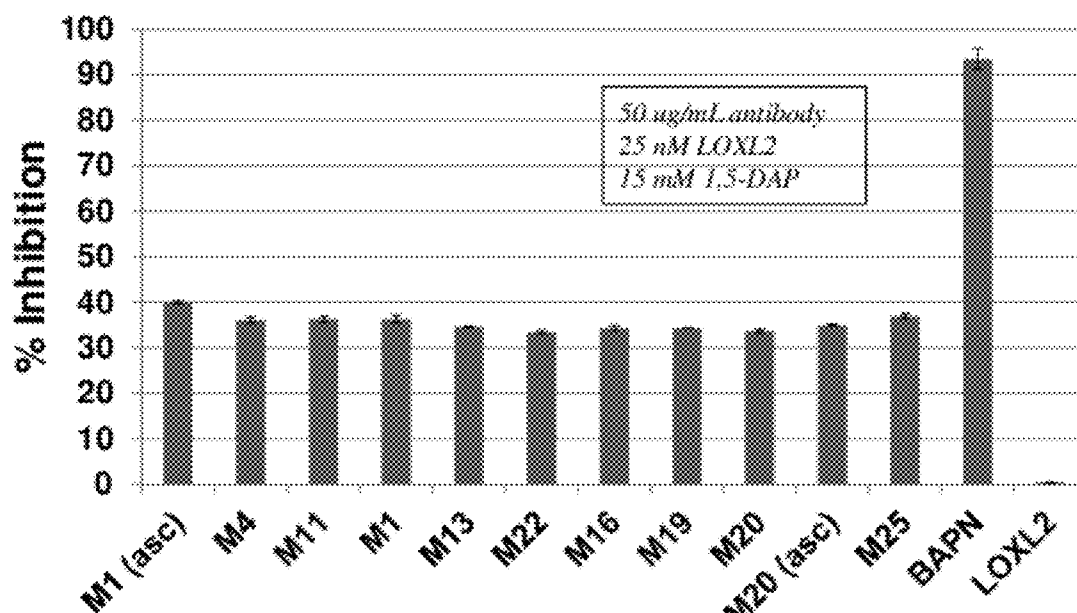
B. Variable Light Chain 1

MKLPVRLVLMFWIPASSSDVLLTQTPLSLPVSLGDQASISCRSS
QSIVHSNGNTYLEWYLOKPGQSPKLLIYKVSIRFSGVPDRF
GGSGSGTDFTLKINRVEAEDLGIYYCFQSSHIPLTFGAGTKLE
LKRAD...(SEQ ID NO: 4)

C. Variable Light Chain 2

MKLPVRLVLMFWIPASSSDVLLTQTPLSLPVSLGDQASISCRSS
QSIVHSNGNTYLEWYLOKPGQSPKLLIYKVSIRFSGVPDRFG
GSGSGTDFTLKINRVEAEDLGIYYCFQSSHIPLTFGAGTKLEL
KRAD...(SEQ ID NO: 5)

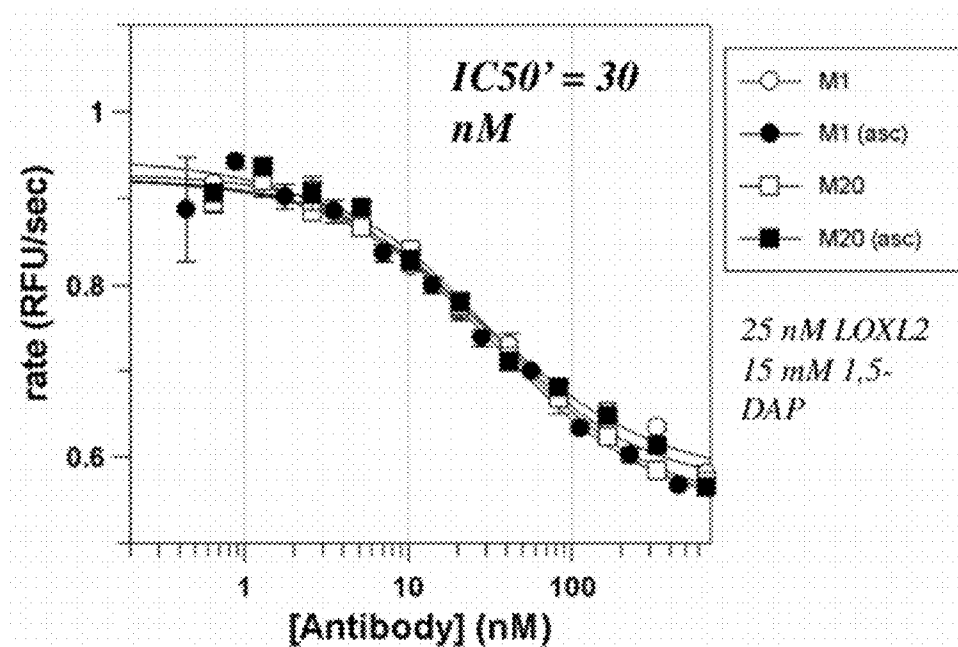
Figure 8
Anti-LOXL2 Antibodies: Protein Screen B Update
Assessment of LOXL2 Enzymatic Activity



Anti-LOXL2 Antibody designated AB0023

- α -LOXL2 antibodies repeated inhibitory activity observed in 10 ml prep material in enzymatic assay
- Inhibition also repeated in cell-based assays
- Sequence analysis confirmed that M01, M16, M19, M20 are identical

Figure 9
Anti-LOXL2 Antibody AB0023 and Enzymatic Activity



AB0023 is a partial inhibitor of LOXL2 enzymatic activity with an apparent IC_{50} of ~ 30 nM

Figure 10
Anti-LOXL2 Antibody AB0023: A Non-Competitive Inhibitor

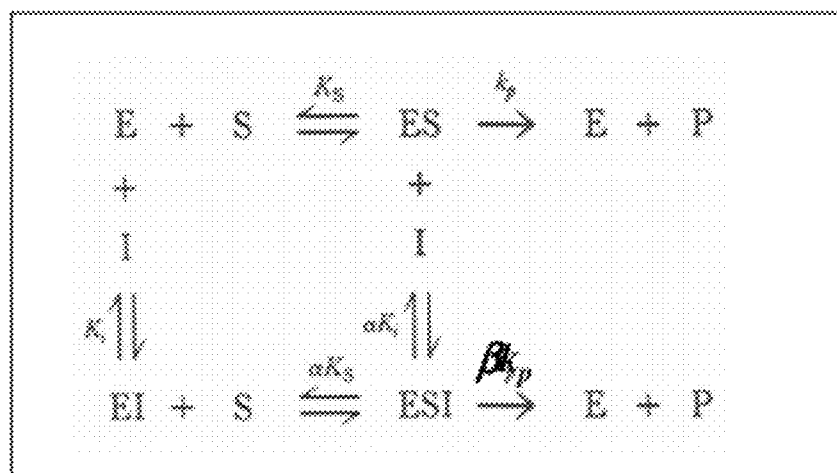
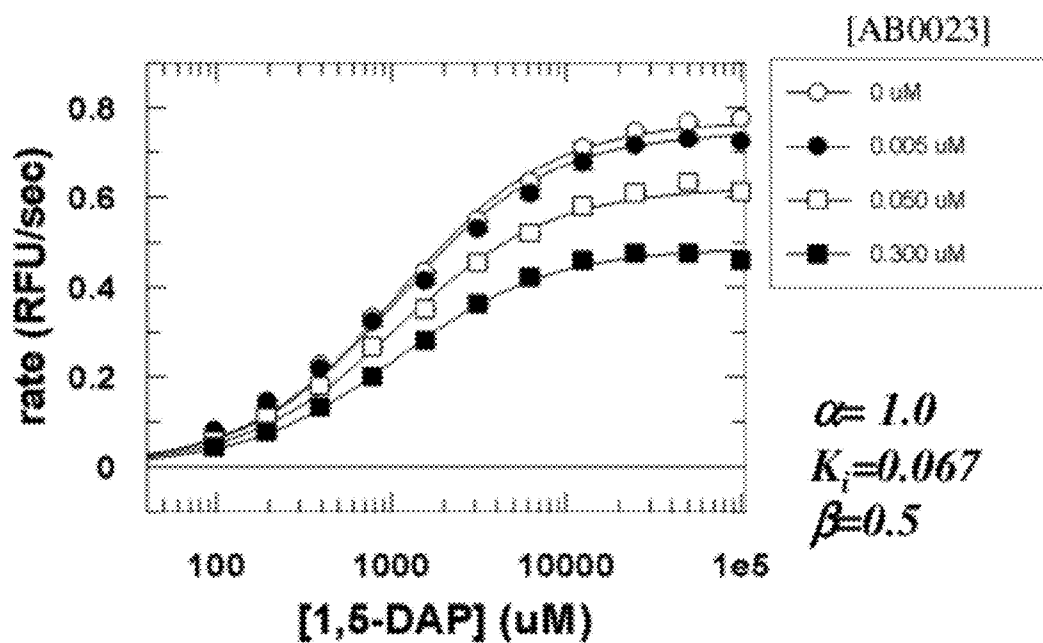
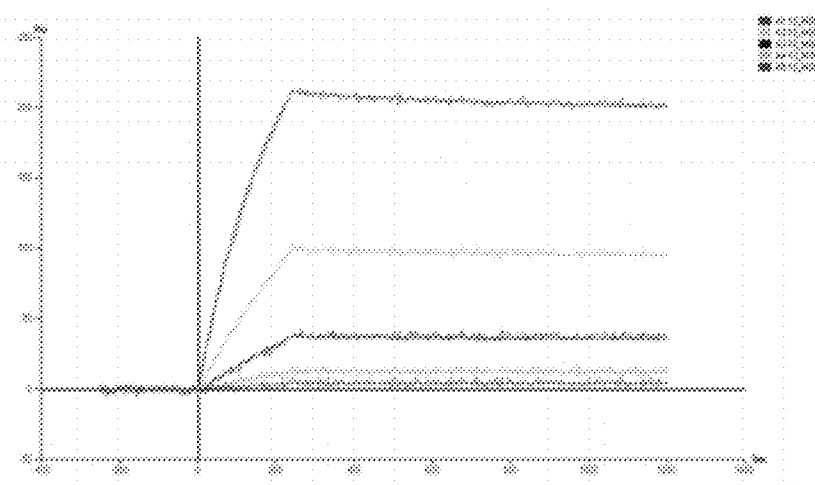


Figure 11

Anti-LOXL2 Antibody AB0023 : Binding Affinity and Off-Rate

Analysis using the ProteOn

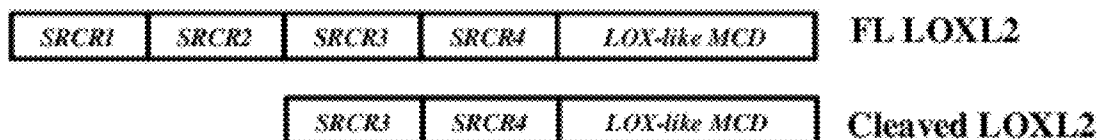
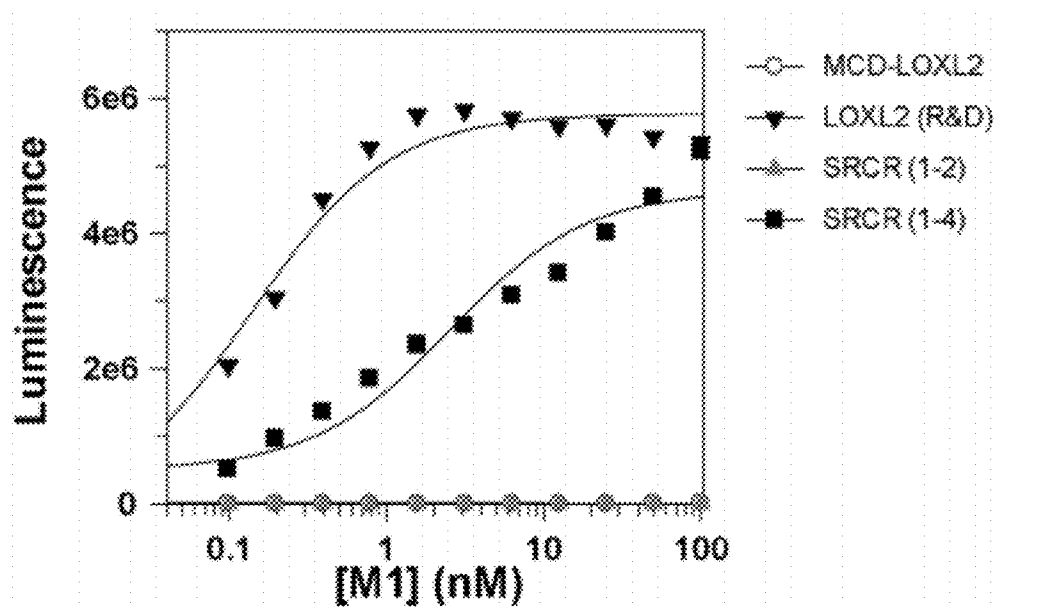
1 ug/mL AB0023 (M20) immobilized on chip

LOXL2 at varying concentrations was applied to chip

- $k_{on} = 1.68 \times 10^6 \text{ M}^{-1} \text{ s}^{-1}$
- $k_{off} = 1.17 \times 10^{-4} \text{ s}^{-1}$
- $K_D = 0.69 \text{ nM}$
- $t_{1/2} = 98.7 \text{ min}$

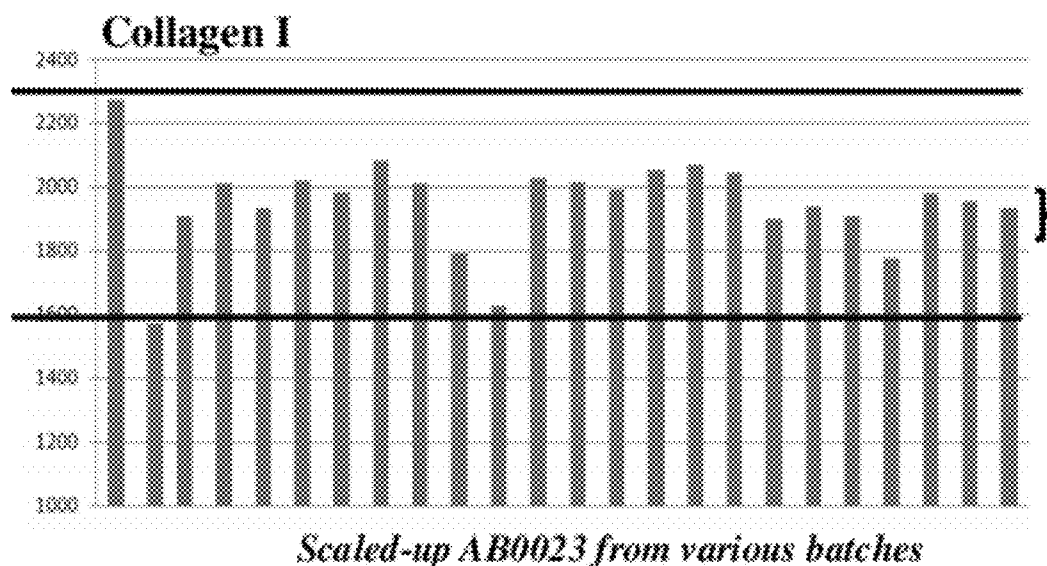
The antibody binds very tightly and releases very slowly
Kd estimate from various methods 0.1 – 1.0 nM

Figure 12
Anti-LOXL2 Antibody AB0023 Domain Mapping
AB0023 binds the SRCR 3-4 domain



AB0023 binds the SRCR 3-4 domain

Figure 13
Anti-LOXL2 antibody AB0023: Cell-Based Assays



- Consistent inhibition of migration / invasion in collagen I and collagen IV, from supernatants through 10 ml prep material and scaled-up 100 ml prep and ascites material
- Partial inhibition also observed in cell adhesion assay

FIGURE 14

A. AB0023 (hLOXL2 Protein Screen B clone M20) VH vs. Humanized Variants 1-4

CDR1 GYAFTY~~YLIE~~
 CDR2 VINPGSGGINYNEKFKG
 CDR3 NWNINFDY

Residues in Humanized AB0023 that Differ the Mouse mab (in indicated underlining):

M20 VH, pro MENSRTFLLSVTAQVRSQVQLQSGAELEKRGSTSVKVNCKASGYAFTY~~YLIE~~WVKQRFQGLERIGVI 70
 VH variant 1, proQVQLDSGAELEKRGSTSVKVNCKASGYAFTY~~YLIE~~WVKQRFQGLERIGVI 81
 VH variant 2, proQVQLDSGAELEKRGSTSVKVNCKASGYAFTY~~YLIE~~WVKQRFQGLERIGVI 81
 VH variant 3, proQVQLDSGAELEKRGSTSVKVNCKASGYAFTY~~YLIE~~WVKQRFQGLERIGVI 81
 VH variant 4, proQVQLDSGAELEKRGSTSVKVNCKASGYAFTY~~YLIE~~WVKQRFQGLERIGVI 81

M20 VH, pro NPGSGGTINYEKFKGAEFLTADKSSSTAYMQLSLSTSDDEAVTFCARNNWF~~DI~~WQGTTLVSS 125
 VH variant 1, pro NPGSGGTINYEKFKGAEFLTADKSSSTAYMQLSLSLSEDSAVTFCARNNWF~~DI~~WQGTTLVSS 116
 VH variant 2, pro NPGSGGTINYEKFKGAEFLTADKSSSTAYMQLSLSLSEDSAVTFCARNNWF~~DI~~WQGTTLVSS 116
 VH variant 3, pro NPGSGGTINYEKFKGAEFLTADKSSSTAYMQLSLSLSEDSAVTFCARNNWF~~DI~~WQGTTLVSS 116
 VH variant 4, pro NPGSGGTINYEKFKGAEFLTADKSSSTAYMQLSLSLSEDSAVTFCARNNWF~~DI~~WQGTTLVSS 116

B. AB0023 (hLOXL2 Protein Screen B clone M20) VL (Vκ) vs. Humanized Variants 1-3

CDR1 RSSKSLHSNGNTYLY
 CDR2 RMSN~~LAS~~
 CDR3 MQHLEY~~FPYT~~

Residues in Humanized AB0023 that Differ the Mouse mab (in indicated underlining):

M20 VL, pro MSCLASFLGLLVNINFGATGIVMTQDAFVSQVSTPGESVSISCSRSSKSLHSNGNTYLYWFLQNPQGSPPQ 70
 Vκ variant 1, proDIVNTQTPLSLSVTPGQFASISCSRSSKSLHSNGNTYLYWFLQNPQGSPPQ 80
 Vκ variant 2, proDIVNTQTPLSLSVTPGQFASISCSRSSKSLHSNGNTYLYWFLQNPQGSPPQ 80
 Vκ variant 3, proDIVNTQTPLSLSVTPGQFASISCSRSSKSLHSNGNTYLYWFLQNPQGSPPQ 80

M20 VL, pro FLIYRMSNLASGVFQDNPSCGSGSGTATLRISNVEAEADVGVTCMQHLEY~~FPYT~~GGGTSLKLEIK 132
 Vκ variant 1, pro FLIYRMSNLASGVFQDNPSCGSGSGTATLRISNVEAEADVGVTCMQHLEY~~FPYT~~GGGTSLKLEIK 132
 Vκ variant 2, pro FLIYRMSNLASGVFQDNPSCGSGSGTATLRISNVEAEADVGVTCMQHLEY~~FPYT~~GGGTSLKLEIK 132
 Vκ variant 3, pro FLIYRMSNLASGVFQDNPSCGSGSGTATLRISNVEAEADVGVTCMQHLEY~~FPYT~~GGGTSLKLEIK 132

Figure 15
Binding of M64 to LOX

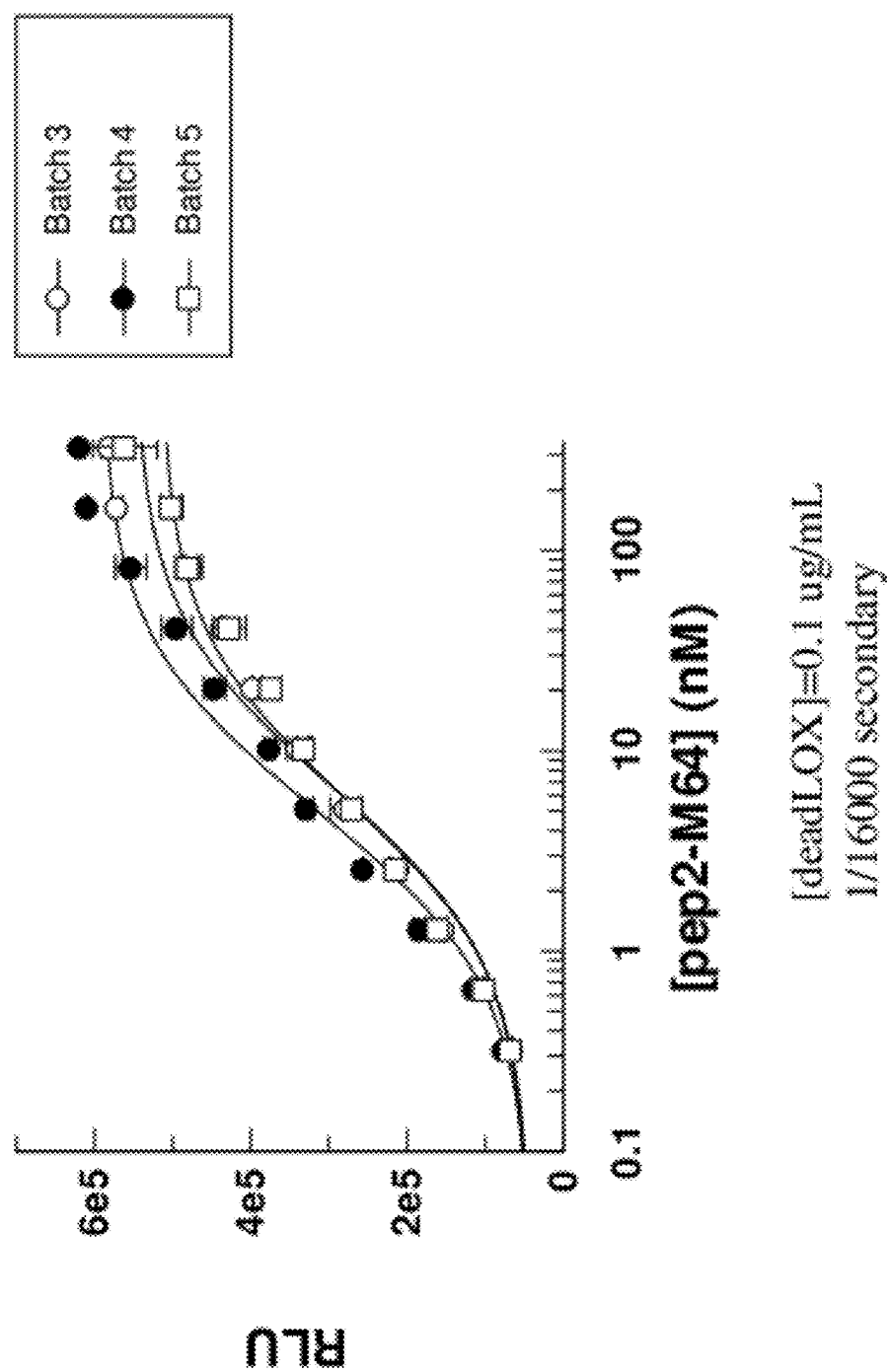
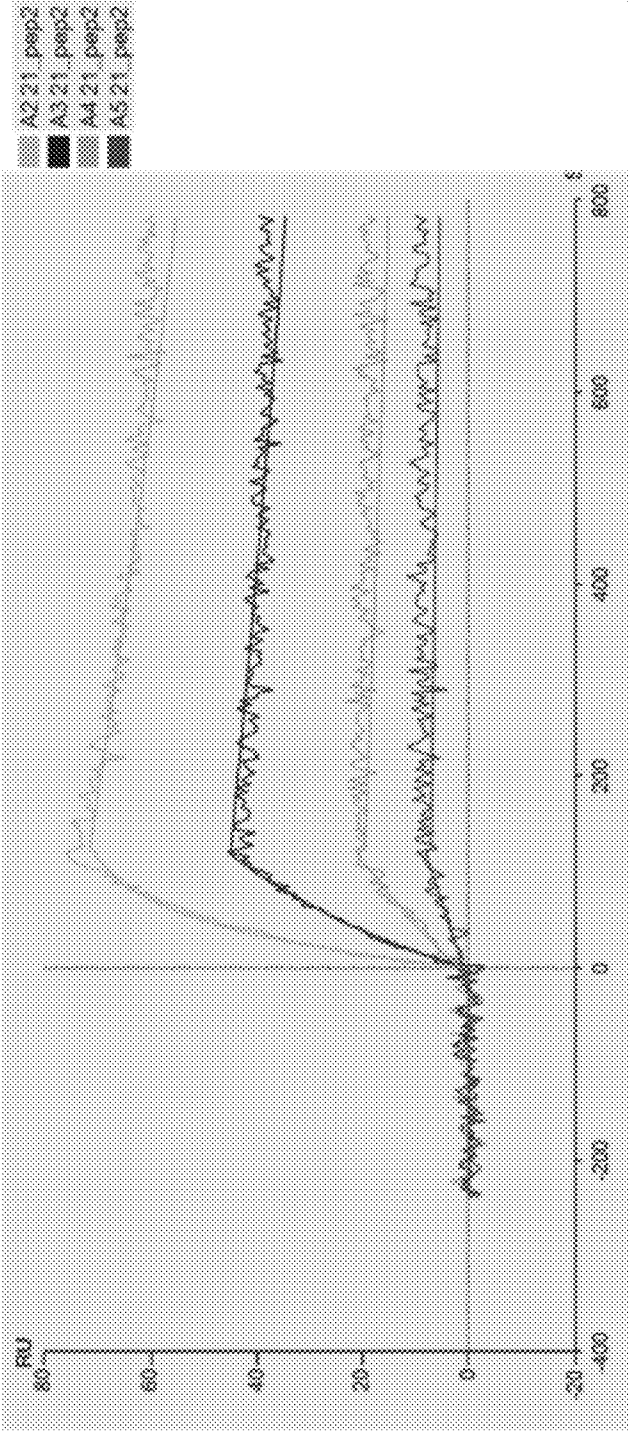


Figure 16
Binding of M64 to LOXFL via SPR



[LOXFL]=0.1 ug/mL
 $K_D=7$ nM

Figure 17

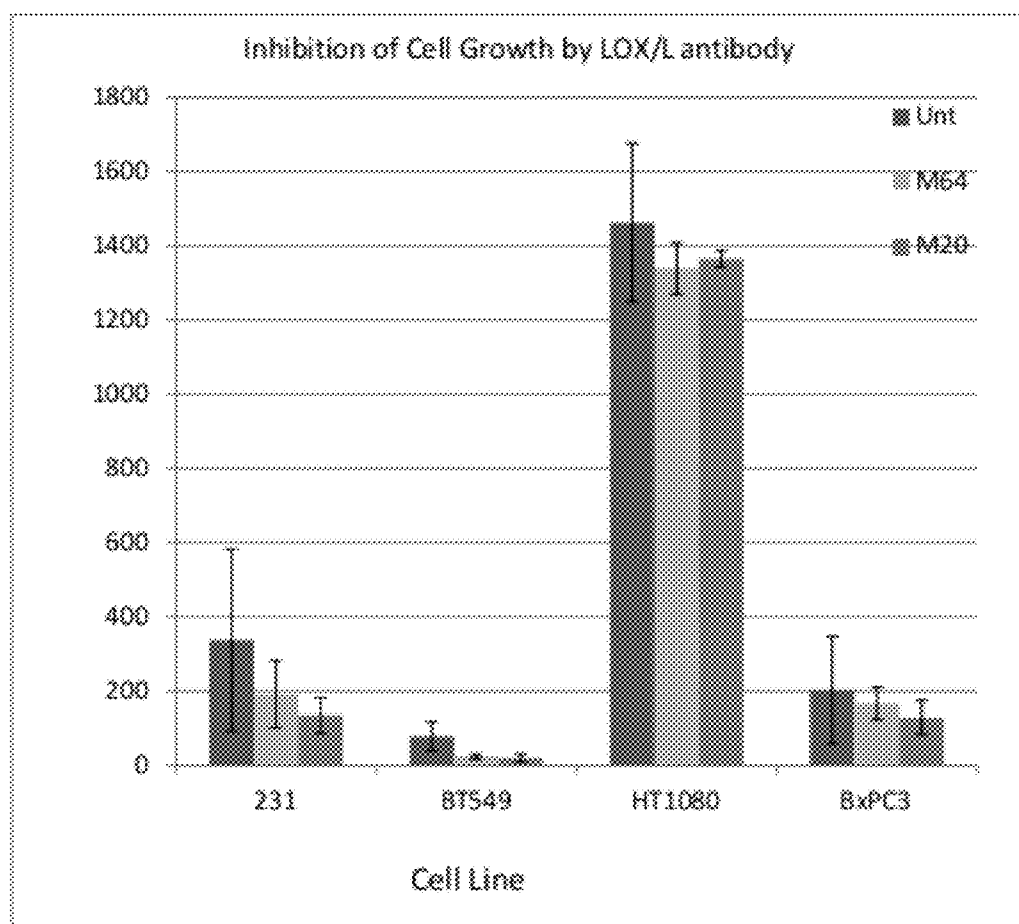
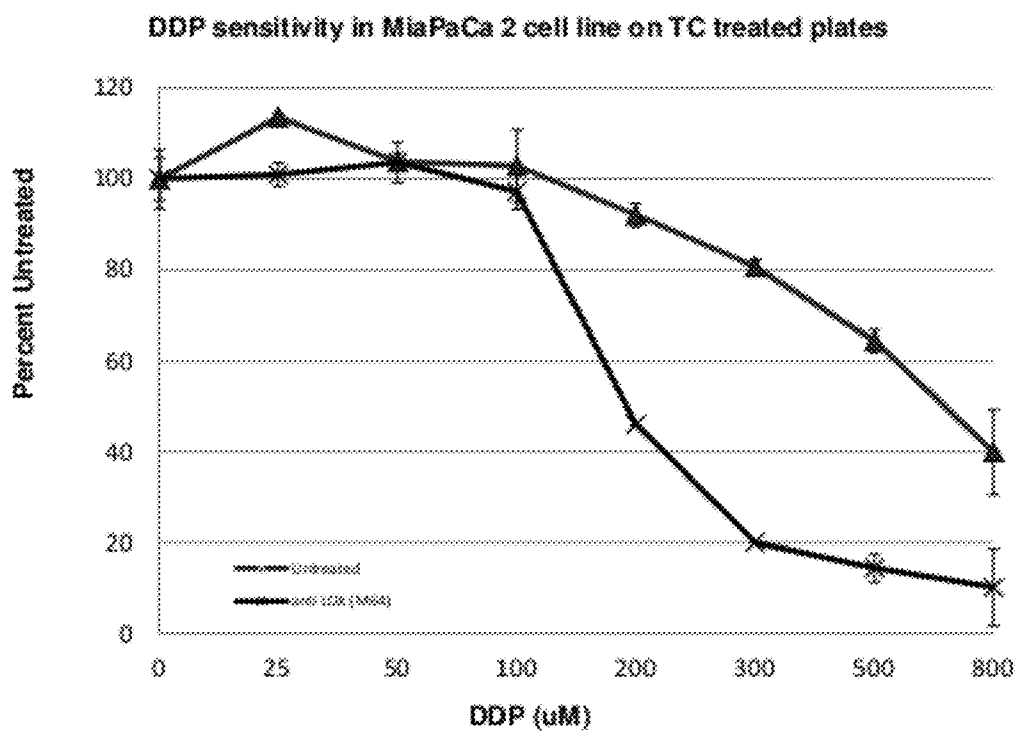


Figure 18
Cisplatin and Anti-LOX Synergy



IC50s

Cell Line	Untreated (uM)	Anti-LOX (M64) (uM)
231	261.8±72.3	242.2±14.4
HT1080	207.5±6.9	194.2±22.7
MiaPaCa 2	664.6±112.8	174.7±5.7
BT549	384±244.3	197.3±28.5

Figure 19

VK2 Kappa Protein Sequence (SEQ ID NO: 71)

MRVPAQLGLLLWLPGARCDIVMTQTPLSLSVTPGQPASISCRSSKSLHSNGNTLYWFLQKPGQSPQFLIYRMSNLAGGVPDNFSGSGSDFTLKISRVEAEDVGVY
YCMQHLEYPYTFGGGTVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLINFFPREAKVQWKVONALQSGNSQIESVTEQDSKDSITYSLSTLTLSKADYEKHKVYACEVT
HQLSSPVTKSFNRGEC

VK2 Kappa DNA Sequence (SEQ ID NO: 72)

ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGCTGCTCCAGGGCGCGATGTGATATTGTGATGACCCAGACTCCACTCTCTCTGTCCGTCACCCCTG
GACAGCCGGCTCCATCTCCCTGCAGGTCTAGTAAGAGTCTCTGCAATAGTAATGGCAACACTTACTTGTATGTCTTCAGAGGCCAGGCCAGTCTCCACAGTT
CCTGATCTATCGGATGTCCAACTTGGCTTCAGGGAGTCCAGATAGGTTGAGTGGCAGCGGGTCAAGCACTTCACTGAATAATCAGCCGGGTGGAGGCTG
AGGATGTGGGGTTTATTACTGCAATGCAACATCTAGAAATATCTTACACTTCCGGCGAGGGACCAAGGTGGAGATCAANCCGAACCTGTGGCTGCCACCATCTGTCT
TCATCTCCCGCCA TCTGATGAGCAGTTGAAATCTGGAATGCTCTCTGTGTGTGCTGTGTAATAACTTCTATCCAGAGAGGCCAAGTACAGTGGAGGTGG
ATAAGCCCTCCCAATCGGTTAACTCCAGGAGAGTGTCAAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAGCAGA
CTACGAGAACACAAAGTCTACGCTCGAAGTCACCCATCAGGGCCCTGAGCTGCCCGTCAAAAGAGCTTCAACAGGGGAGAGTGTAG

Legend:

Signal peptide; Variable Region Framework; CDR Regions; Constant region framework

Figure 20

VH3 IgG4 S241P Protein [SEQ ID NO: 76]

MGWSLLFLVAVATRVHSQVLVQSGAEVKRPGASVRYVSKASGYAFTYLLWVYRQAPSGGLEWGVNPSGGTNNYNEKPKGRATITADKSTSTAYNMFSLRSED
 TAVVFCARNWNMINEDYWGQGTITVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYHPEPTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVPVPSLSLGRITYTCN
 VDHKPSNTKVKRVESKYGPCCPAPCPAFELGGPSVFLFPPKPKDITLMISRTPEVTCVWVDVSQEDPEVFQFNWVYDGVFVHNAKTPREEQFNSTYRWSVLTVLHQID
 WLNKGKEYCKVSNRGLPSSIEKTISKARGQPREPQVYTLPPSQEEMTKNQVSLTCLVRGFPYPSDIAVEWESNGQPENNYKTTTPVLDSQGSFLYSRLTVDKSRWQEGN
 VFSCSVMHAEALHNHYTQKSLSLGLK

VH3 IgG4 S241P DNA [SEQ ID NO: 77]

ATGGSTGGAGGCTCATCTGTCTCTTGTGGCTGTGTACGGGTGTCCACTCCAGGTGCAGCTGGTGTCAGTCTGGGGCTGAGGTGAAGAGCGCTGGGGGCC
 TCAGTGAAGGTCTCTCGCAAGGCTTCTGGATACGCTTCACCTTATTACTTGTATAGAGTGGGTGAACACAGGCCCTTGGACAAGGGCTTGGATGGAGTGAATT
 AATCTGGGAAGTGGTGGTACTAATCTACATGAGAGTTCAAGGGCAGAGCCACGATCACCGCGGACAAATCCACGACACAGCCTACATGGAGCTGAGCAGCCT
 GAGATCTGAGGAGACCGGCGGTGTAATTTCTGTGCGAGAACTGGATGAACTTTGACTAGTGGGGCAAGGGAACCAACGGTACCGTCTCTCTCAGCTTCCACCAAGG
 GCCCATCGTCTTCCCGCTGGCGGCTGCTCCAGGACCTCCGAGAGCACAGCCGCTGGGCTGCTGGTCAAGGACTACTTCCCGAADCGGTGACGGTGT
 CGTGGAACTCAGGCGCCTGACCGAGCGGCGTGACACCTTCCCGGCTGTCTACAGTCTCTCAGGACTCTACTCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCA
 GCTTGGGCACGAAAGACCTACACCTGCAATGTAGATCACAAGCCCAAGCAACACCAAGGTGGACAAGAGAGTTGAGTCCAAATATGTGCCCATGSCCAATGCG
 CCAGCACTGAGTTCTGGGGGACCAACAGTCTTCTGTGTTCCCGCAAAACCCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCAAGTGGCTGGTGGT
 GACGTGAGCCAGGAAGACCCGAGGTCCAGTTCAACTGTTAGCTGGTGGATGGGTGGATATGCCAAAGACAGCAAGCCCGGGGAGGAGCAGTTCAACAGC
 ACGTACCGTGTGGTCAAGGTCTCACCGTCTTGCAACCAAGGACTGGCTGAACGGCAAGGGAGTACAAGTGAAGGTCTTCCAAACAAAGGCCCTCCCGTCTCCATCGA
 GAAACCATCTCCAAAGCCAAAGGCGAGCCCCGAGAGCCACAGGTGTACACCTGCCCCCATCCAGGAGGAGATGACCAAGAACAGGTGACGCTGACCTGACC
 TGGTCAAGGCTTCTACCCCAAGGACATCGCGCTGGAGTGGAGAGGCAATGGGCAGCTGGAGAACAACTACAGACCGCTCCCGTGGCTGGACTCCGACGG
 CTCTTCTCTCTACAGCAGGCTAACCGTGGACAAAGACAGGTGGCAGGAGGGGAATGTCTTCTCATGTCTCGTGATGCATGAGGGCTTGCACAACCACTACAC
 ACAGAAAGAGGCTCTCCCTGTCTCTGGGTAAATGA

Legend:

Signal peptide ; Variable Region Framework; CDR Regions; P = IgG4 Hinge modification (S241P); heavy chain; Constant region framework

LOX AND LOXL2 INHIBITORS AND USES THEREOF

CROSS-REFERENCE

[0001] This application is a continuation-in-part of U.S. application Ser. No. 12/185,050, filed, Aug. 1, 2008, which application claims the benefit of U.S. Provisional Application No. 60/963,282, entitled "Methods for Selecting Inhibitors of Tumor Invasion, Angiogenesis, and Metastasis," filed Aug. 2, 2007; U.S. Provisional Application No. 60/963,249, entitled "Treatment of Diseases With Inhibitors of Active Lysyl Oxidase," filed August 2, 2007; U.S. Provisional Application No. 60/963,214, entitled "Treatment of Diseases Through Inhibition of Both Lysyl Oxidase and Lysyl Oxidase-Like Proteins," filed Aug. 2, 2007; U.S. Provisional Application No. 60/963,248, entitled "Diagnosis or Monitoring of Diseases by Assessing Active Lysyl Oxidase Levels or Activity," filed Aug. 2, 2007; and U.S. Provisional Application No. 60/963,246, entitled "Combination Therapy Including Lysyl Oxidase Modulators," filed Aug. 2, 2007, each of which applications is incorporated herein in its entirety by reference.

[0002] This application is related to co-pending U.S. patent application" Ser. No. 12/185,054, filed Aug. 1, 2008, and PCT Patent Application Serial No. PCT/US2008/009354, filed Aug. 1, 2008, each of which applications is incorporated herein in its entirety by reference.

BACKGROUND OF THE INVENTION

[0003] Cancer is a serious public health problem in the United States and other developed countries. Currently, one in four deaths in the United States is due to cancer. Cancer therapy involves treating patients with chemotherapeutic drugs to kill tumor cells. However, subsets of tumor cells are frequently resistant to drug therapy and survive to re-populate at sites of origin and at distant metastatic sites, leading to detectable disease recurrence and morbidity. Many carcinoma tumor cells that have the properties of increased invasive and metastatic capacity, and altered drug resistance, are thought to have undergone a morphological transformation encompassing or similar to EMT (epithelial-mesenchymal transition). Cells undergoing EMT lose the normal adhesive properties of epithelial cells and undergo a spectrum of changes including loss of E-cadherin expression and expression of mesenchymal markers, increased motility, increased invasiveness, and increased resistance to cell death.

[0004] The leading therapies for cancer are currently surgery, radiation and chemotherapy. Chemotherapeutic approaches such as anti-tumor antibiotics, alkylating agents, nitrosourea compounds, vinca alkaloids, steroid hormones, and anti-metabolites form the bulk of therapies available to oncologists. Despite advances in the field of cancer treatment, cancer remains a major health problem.

[0005] Angiogenesis, the formation of new blood vessels out of pre-existing capillaries, is a sequence of events that is of key importance in a broad array of physiologic and pathologic processes. Normal tissue growth, such as in embryonic development, wound healing, and the menstrual cycle, is characterized by dependence on new vessel formation for the supply of oxygen and nutrients as well as removal of waste products. A large number of different and unrelated diseases are also associated with formation of new vasculature. Among certain pathologies are conditions in which angiogenesis is low, and should be enhanced to improve disease con-

ditions. More frequently, however, excessive angiogenesis is an important characteristic of various pathologies, including pathologies characterized or associated with an abnormal or uncontrolled proliferation of cells. Pathologies which involve excessive angiogenesis include, for example, cancer (both solid and hematologic tumors), cardiovascular diseases (such as atherosclerosis and restenosis), chronic inflammation (rheumatoid arthritis, Crohn's disease), diabetes (diabetic retinopathy), psoriasis, endometriosis, neovascular glaucoma and adiposity (3). These conditions may benefit from chemotherapeutic inhibition of angiogenesis.

[0006] Generally speaking, the angiogenic process entails the proliferation and migration of a normally quiescent endothelium, the controlled proteolysis of the pericellular matrix, and the synthesis of new extracellular matrix components by developing capillaries. The establishment of new intra- and intercellular contacts and the morphological differentiation of endothelial cells to capillary-like tubular networks provide support for their subsequent maturation, branching, remodeling and selective regression to form a highly organized, functional microvascular network. The autocrine, paracrine and amphicrine interactions of the vascular endothelium with its surrounding stromal components, as well as with the pro-angiogenic and angiostatic cytokines and growth factors orchestrating physiologic angiogenesis, are normally tightly regulated both spatially and temporally.

[0007] Angiogenesis is crucial to the growth of neoplastic tissues. For more than 100 years, tumors have been observed to be more vascular than normal tissues. Several experimental studies have suggested that both primary tumor growth and metastasis require neovascularization. In contrast to the well orchestrated process described above for normal tissue growth, the pathologic angiogenesis necessary for active tumor growth is generally sustained and persistent, with the initial acquisition of the angiogenic phenotype being a common mechanism for the development of a variety of solid and hematopoietic tumor types. Tumors that are unable to recruit and sustain a vascular network typically remain dormant as asymptomatic lesions in situ. Metastasis is also angiogenesis-dependent: for a tumor cell to metastasize successfully, it generally must gain access to the vasculature in the primary tumor, survive the circulation, arrest in the microvasculature of the target organ, exit from this vasculature, grow in the target organ, and induce angiogenesis at the target site. Thus, angiogenesis appears to be necessary at the beginning as well as the completion of the metastatic cascade.

[0008] The criticality of angiogenesis to the growth and metastasis of neoplasms thus provides an optimal potential target for chemotherapeutic efforts. Appropriate anti-angiogenic agents may act directly or indirectly to influence tumor-associated angiogenesis either by delaying its onset (i.e., blocking an "angiogenic switch") or by blocking the sustained and focal neovascularization that is characteristic of many tumor types. Anti-angiogenesis therapies directed against the tumor-associated endothelium and the multiple molecular and cellular processes and targets implicated in sustained pathologic angiogenesis are being actively evaluated for their safety and efficacy in multiple clinical trials. However, there has been limited success to date with the discovery and/or identification of safe and/or effective anti-angiogenic agents.

[0009] Fibrosis is the abnormal accumulation of fibrous tissue that can occur as a part of the wound-healing process in

damaged tissue. Such tissue damage may result from physical injury, inflammation, infection, exposure to toxins, and other causes.

[0010] Liver (hepatic) fibrosis, for example, occurs as a part of the wound-healing response to chronic liver injury. Fibrosis occurs as a complication of haemochromatosis, Wilson's disease, alcoholism, schistosomiasis, viral hepatitis, bile duct obstruction, exposure to toxins, and metabolic disorders. This formation of scar tissue is believed to represent an attempt by the body to encapsulate the injured tissue. Liver fibrosis is characterized by the accumulation of extracellular matrix that can be distinguished qualitatively from that in normal liver. Left unchecked, hepatic fibrosis progresses to cirrhosis (defined by the presence of encapsulated nodules), liver failure, and death.

[0011] As summarized by Li and Friedman (Gastroenterol. Hepatol. 14:618-633, 1999), actual and proposed therapeutic strategies for liver fibrosis include removal of the underlying cause (e.g., toxin or infectious agent), suppression of inflammation (using, e.g., corticosteroids, IL-1 receptor antagonists, or other agents), down-regulation of stellate cell activation using, e.g., gamma interferon or antioxidants), promotion of matrix degradation, or promotion of stellate cell apoptosis. Despite recent progress, many of these strategies are still in the experimental stage, and existing therapies are aimed at suppressing inflammation rather than addressing the underlying biochemical processes. Thus, there remains a need in the art for materials and methods for treating fibrosis, including liver and lung fibrosis.

[0012] Fibrotic tissues accumulate in the heart and blood vessels as a result of hypertension, hypertensive heart disease, atherosclerosis, and myocardial infarction. High blood pressure, or hypertension, can be caused by a variety of factors and often leads to the development of Hypertensive Heart Disease (HHD) with progression to cardiac arrest and myocardial infarction. Similarly, atherosclerosis and other ischemic heart diseases often also result in cardiac arrest. These cardiovascular diseases all exhibit an accumulation of extra-cellular matrix or fibrotic deposition which results in stiffening of the vasculature and stiffening of the cardiac tissue itself. This deposition of fibrotic material is a response to the damage induced by the hypertensive and/or sclerotic state, but the effects of this response also result in the negative effects of vascular and cardiac stiffening as well as ventricle enlargement. Additionally, it is believed that the increased cardiac fibrosis seen in cardiovascular disease disrupts or alters the signals transmitted to cardiomyocytes via the tissue scaffolding of the heart, further leading to disruption of efficient cardiac function and promoting cardiac arrest and myocardial infarction.

SUMMARY OF THE INVENTION

[0013] Epithelial-to-Mesenchymal Transition (EMT) refers to the process whereby a cell with a gene expression/phenotype characteristic of epithelial cell (i.e., expressing specific proteins, factors, and molecules) changes or alters the genes or their level of expression which results in a change in the phenotype of the cell as exhibited by the alteration or change in the genes expressed.

[0014] Compositions are needed which prevent EMT and which are effective in blocking the activity of enzymes such as LOX and LOXL2. Such inhibitors are useful in treating diseases and disorders associated with aberrant levels of LOX and LOXL2.

[0015] Antibodies that bind to enzymes can be competitive inhibitors, uncompetitive inhibitors or non-competitive inhibitors. With respect to competitive inhibition, an inhibitor usually bears structural similarity to substrate. Inhibition will be noticeable at low substrate concentrations, but can be overcome at high substrate concentrations. With respect to uncompetitive inhibition, an inhibitor binds at a site that becomes available after substrate is bound at the active site. Inhibition will be most noticeable at high substrate concentration. With respect to non-competitive inhibition, an inhibitor binds at site away from substrate binding site and relative inhibition will generally be the same at all substrate concentrations. In one embodiment, an antibody or antigen binding fragment thereof, described herein specifically binds both full-length and processed LOX or LOXL2. In one aspect, both full-length and processed LOX or LOXL2 are active forms of the enzyme.

[0016] Provided herein is an isolated antibody or antigen binding fragment thereof, that specifically binds to an epitope having an amino acid sequence set forth as SEQ ID NO: 6. The antibody or antigen binding fragment thereof, comprises a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1 and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2.

[0017] Provided herein is an isolated antibody or antigen binding fragment thereof, comprising a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1, and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2. In one embodiment, an isolated antibody or antigen binding fragment thereof, comprises a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1. In another embodiment, an isolated antibody or antigen binding fragment thereof, comprises a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2. In yet another embodiment, an isolated antibody or antigen binding fragment thereof, competes with, or specifically binds to, any of the anti-LOXL2 antibodies or antigen binding fragments thereof described herein for binding to LOXL2. Antibodies or antigen binding fragments thereof can specifically bind to LOXL2 with a binding affinity of at least 2, 5, 10, 50, 100, 500 or 1000 times greater than to at least one of LOX, LOXL1, LOXL3 or LOXL4.

[0018] Provided herein are humanized anti-LOXL2 antibodies. A humanized antibody or antigen binding fragment thereof, can specifically bind to an epitope having an amino acid sequence set forth as SEQ ID NO: 6. In one embodiment, the humanized antibody or antigen binding fragment thereof, comprises a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 25, 26, 27 or 28 and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 30, 31 or 32.

[0019] A humanized isolated antibody or antigen binding fragment thereof, can comprise a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 25, 26, 27 or 28, and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 30, 31 or 32.

[0020] A humanized antibody or antigen binding fragment thereof, can comprise a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 25, 26, 27 or 28.

[0021] A humanized antibody or antigen binding fragment thereof, can comprise a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 30, 31 or 32. Combinations of variable heavy chains and variable light chains can be made to assess binding affinity.

[0022] Provided herein is a humanized antibody or antigen binding fragment thereof, that competes with, or specifically binds to, an antibody or antigen binding fragment thereof described herein for binding to LOXL2.

[0023] Provided herein is a humanized antibody, or antigen-binding fragment thereof, which binds LOXL2, comprising a heavy chain variable region and a light chain variable region, wherein said heavy chain variable region comprises:

[0024] (i) a heavy chain FR1 having the amino acid sequence of SEQ ID NO: 33 or the amino acid sequence of SEQ ID NO: 33 but for one or more substitutions selected from the group consisting of:

[0025] (a) a substitution of glutamine (Q) by valine (V) or a conservative substitution thereof at position 24;

[0026] (b) a substitution of leucine (L) by valine (V) or a conservative substitution thereof at position 30;

[0027] (c) a substitution of valine (V) by lysine (K) or a conservative substitution thereof at position 31;

[0028] (d) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 32; and

[0029] (e) a substitution of threonine (T) by alanine (A) or a conservative substitution thereof at position 35; and a deletion of amino acid residues 1-19;

[0030] (ii) a heavy chain FR2 having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 but for one or more substitutions selected from the group consisting of:

[0031] (a) a substitution of lysine (K) by arginine (R) or a conservative substitution thereof at position 3;

[0032] (b) a substitution of arginine (R) by alanine (A) or a conservative substitution thereof at position 5, and

[0033] (iii) a heavy chain FR3 having the amino acid sequence of SEQ ID NO: 35 or the amino acid sequence of SEQ ID NO: 35 but for one or more substitutions selected from the group consisting of:

[0034] (a) a substitution of lysine (K) by arginine (R) or a conservative substitution thereof at position 1;

[0035] (b) a substitution of alanine (A) by valine (V) or a conservative substitution thereof at position 2;

[0036] (c) a substitution of leucine (L) by isoleucine (I) or a conservative substitution thereof at position 4;

[0037] (d) a substitution of serine (S) by threonine (T) or a conservative substitution thereof at position 10;

[0038] (e) a substitution of glutamine (Q) by glutamic acid (E) or a conservative substitution thereof at position 16;

[0039] (f) a substitution of threonine (T) by arginine (R) or a conservative substitution thereof at position 21;

[0040] (g) a substitution of aspartic acid (D) by glutamic acid (E) or a conservative substitution thereof at position 23;

[0041] (h) a substitution of serine (S) by threonine (T) or a conservative substitution thereof at position 25; and

[0042] (i) a substitution of phenylalanine (F) by tyrosine (Y) or a conservative substitution thereof at position 29;

[0043] and

[0044] (iv) a heavy chain FR4 having the amino acid sequence of SEQ ID NO: 36 or the amino acid sequence of SEQ ID NO: 36 but for a substitution of lysine (K) by valine (V) or a conservative substitution thereof at position 7,

[0045] and wherein said light chain variable region comprises:

[0046] (i) a light chain FR1 having the amino acid sequence of SEQ ID NO: 49 or the amino acid sequence of SEQ ID NO: 49 but for one or more substitutions selected from the group consisting of:

[0047] (a) a substitution of alanine (A) by threonine (T) or a conservative substitution thereof at position 27;

[0048] (b) a substitution of alanine (A) by proline (P) or a conservative substitution thereof at position 28;

[0049] (c) a substitution of proline (P) by leucine (L) or a conservative substitution thereof at position 29;

[0050] (d) a substitution of valine (V) by leucine (L) or a conservative substitution thereof at position 31;

[0051] (e) a substitution of glutamic acid (E) by glutamine (Q) or a conservative substitution thereof at position 37;

[0052] (d) a substitution of serine (S) by proline (P) or a conservative substitution thereof at position 38;

[0053] (f) a substitution of valine (V) by alanine (A) or a conservative substitution thereof at position 39; and a deletion of amino acid residues 1-20;

[0054] (ii) a light chain FR2 having the amino acid sequence of SEQ ID NO: 50 or the amino acid sequence of SEQ ID NO: 50 but for one or more substitutions selected from the group consisting of:

[0055] (a) a substitution of phenylalanine (F) by tyrosine (Y) or a conservative substitution thereof at position 2; and

[0056] (b) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 5;

[0057] (iii) a light chain FR3 having the amino acid sequence of SEQ ID NO: 51 or the amino acid sequence of SEQ ID NO: 51 but for one or more substitutions selected from the group consisting of:

[0058] (a) a substitution of alanine (A) by aspartic acid (D) or a conservative substitution thereof at position 14; and

[0059] (b) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 18; and

[0060] (iv) a light chain FR4 having the amino acid sequence of SEQ ID NO: 52 or the amino acid sequence of SEQ ID NO: 52 but for a substitution of leucine (L) by valine (V) or a conservative substitution thereof at position 7;

[0061] In one embodiment, the antibody, or antigen-binding fragment thereof, comprises a heavy chain variable region

FR1 having an amino acid sequence as set forth in, SEQ ID NO: 33, 37 or 44; a heavy chain variable region FR2 having an amino acid sequence as set forth in SEQ ID NO: 34, 38 or 45; a heavy chain variable region FR3 having an amino acid sequence as set forth in SEQ ID NO: 35, 39, 46, 47 or 48; a heavy chain variable region FR4 having an amino acid sequence as set forth in SEQ ID NO: 36 or 40; a light chain variable region FR1 having an amino acid sequence as set forth in SEQ ID NO: 49 or 53; a light chain variable region FR2 having an amino acid sequence as set forth in SEQ ID NO: 50, 54 or 60; a light chain variable region FR3 having an amino acid sequence as set forth in SEQ ID NO: 51, 55 or 61; and a light chain variable region FR4 having an amino acid sequence as set forth in SEQ ID NO: 52 or 56.

[0062] Provided herein are antibodies that specifically bind to LOX. In one aspect, an isolated antibody or antigen binding fragment thereof, can comprise a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 3 and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 4 or 5. In another aspect, an isolated antibody or antigen binding fragment thereof, can comprise a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 3. In yet another aspect, an isolated antibody or antigen binding fragment thereof, can comprise a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 4 or 5.

[0063] Provided herein is an isolated antibody or antigen binding fragment thereof, that competes with, or specifically binds to, an antibody or antigen binding fragment thereof of any one of the anti-LOX antibodies described herein for binding to LOX.

[0064] An anti-LOX antibody can specifically bind to LOX with a binding affinity of at least 2, 5, 10, 50, 100, 500 or 1000 times greater than to at least one of LOXL1, LOXL2, LOXL3 or LOXL4.

[0065] An isolated antibody or antigen binding fragment thereof can be labeled with a detectable label, a therapeutic label or both.

[0066] In one embodiment, an antigen binding fragment is, for example, a variable heavy chain, a variable light chain, a Fv, a scFv, a Fab, a F(ab')₂, a genetically engineered antibody, a monoclonal antibody, or a humanized antibody.

[0067] Provided herein is a kit for treating a condition associated with LOX or LOXL2, comprising a composition of an antibody or antigen binding fragment thereof of any one of the preceding embodiments and a pharmaceutically acceptable carrier or excipient. A condition associated with LOX or LOXL2 can be, for example, a tumor, a metastasis, angiogenesis, or fibrosis. A kit can further comprise a detectable label, a therapeutic label or both. Kits can further comprise written instructions describing how to conjugate the antibody or antigen binding fragment thereof with the detectable label, a therapeutic label or both. Furthermore, written instructions can describe how to administer the antibody or antigen binding fragment thereof. In one embodiment, compositions in the kit are free of pyrogens and can, in some instances, be lyophilized.

[0068] Provided herein is a method of diagnosing a condition associated with LOX or LOXL2 comprising assessing a level of LOX and/or LOXL2 in a sample of a subject by contacting said sample with an antibody or antigen binding

fragment thereof described herein, wherein a change in level of LOX and/or LOXL2 in the sample in comparison with a reference sample indicates the presence or increase of a tumor or metastasis. A condition associated with LOX or LOXL2 can be, for example, a tumor, a metastasis, angiogenesis, or a fibrotic condition. In one embodiment, an increase in LOX and/or LOXL2 levels in the sample in comparison with a reference sample indicates the presence of a tumor or metastasis or an increase in tumor or metastatic growth. A reference sample is a sample taken from the subject at an earlier time point or a sample from another individual. Levels of LOX and/or LOXL2 levels in the sample are detected by contacting the sample with any of the antibodies or antigen binding fragments thereof described herein. For detection purposes, an antibody or antigen binding fragment thereof is detectably labeled as needed depending upon the method used to assess binding.

[0069] Provided herein is a method of inhibiting LOXL2 by contacting a sample or a cellular tissue with an antibody or antigen binding fragment thereof, described herein. In one embodiment, binding of said antibody or antigen binding fragment thereof to LOXL2 inhibits enzymatic activity of LOXL2.

[0070] Provided herein is a method of inhibiting LOX by contacting a sample or cellular tissue with an antibody or antigen binding fragment thereof, described herein. In one embodiment, binding of said antibody or antigen binding fragment thereof to LOX inhibits enzymatic activity of LOX. Contacting can occur in vitro, in vivo or ex vivo. Inhibiting LOX or LOXL2 can reduce tumor growth in a subject either partially or completely. Inhibiting LOX or LOXL2 can reduce angiogenesis in a subject such that a therapeutic benefit occurs. Inhibiting LOX or LOXL2 can reduce fibrosis in a subject such that a therapeutic benefit occurs.

[0071] Provided herein is a method of reducing growth of a tumor in a subject, comprising administering an antibody or antigen binding fragment thereof, described herein. A tumor can be a primary tumor or a metastatic tumor. In one aspect, a tumor is, for example, Lung cancer (including lung adenocarcinoma, squamous cell carcinoma, large cell carcinoma, bronchioloalveolar carcinoma, non-small-cell carcinoma, small cell carcinoma, mesothelioma); breast cancer (including ductal carcinoma, lobular carcinoma, inflammatory breast cancer, clear cell carcinoma, mucinous carcinoma); colorectal cancer (colon cancer, rectal cancer); anal cancer; pancreatic cancer (including pancreatic adenocarcinoma, islet cell carcinoma, neuroendocrine tumors); prostate cancer; ovarian carcinoma (ovarian epithelial carcinoma or surface epithelial-stromal tumour including serous tumour, endometrioid tumor and mucinous cystadenocarcinoma, sex-cord-stromal tumor); liver and bile duct carcinoma (including hepatocellular carcinoma, cholangiocarcinoma, hemangioma); esophageal carcinoma (including esophageal adenocarcinoma and squamous cell carcinoma); non-Hodgkin's lymphoma; bladder carcinoma; carcinoma of the uterus (including endometrial adenocarcinoma, uterine papillary serous carcinoma, uterine clear-cell carcinoma, uterine sarcomas and leiomyosarcomas, mixed mullerian tumors); glioma, glioblastoma, medullablastoma, and other tumors of the brain; kidney cancers (including renal cell carcinoma, clear cell carcinoma, Wilm's tumor); cancer of the head and neck (including squamous cell carcinomas); cancer of the stomach (stomach adenocarcinoma, gastrointestinal stromal tumor); multiple myeloma; testicular cancer; germ cell

tumor; neuroendocrine tumor; cervical cancer; carcinoids of the gastrointestinal tract, breast, and other organs; signet ring cell carcinoma; mesenchymal tumors including sarcomas, fibrosarcomas, haemangioma, angiomas, haemangiopericytoma, pseudoangiomatous stromal hyperplasia, myofibroblastoma, fibromatosis, inflammatory myofibroblastic tumour, lipoma, angiolioma, granular cell tumour, neurofibroma, schwannoma, angiosarcoma, liposarcoma, rhabdomyosarcoma, osteosarcoma, leiomyoma or a leiomyosarcoma. In one embodiment, a tumor is, for example, a colon tumor, an ovarian tumor, a lung tumor, an esophageal tumor, a breast tumor, a prostate tumor, a carcinoma. Tumor size in the subject can be reduced by at least 10%, 25%, 50%, 70%, 90%, 95%, or more following treatment as compared to the tumor in the subject prior to treatment. In one aspect, the survival of a subject with a tumor is increased by at least 10 days, 1 month, 3 months, 6 months, 1 year, 2 years, 5 years, 10 years, or more compared to a subject that is not administered the antibody or antigen binding fragment thereof. Metastatic tumor burden of a subject can be stabilized following administration of an antibody or antigen binding fragment thereof, described herein. For instance, metastatic tumor burden can be stabilized for at least 10 days, 1 month, 3 months, 6 months, 1 year, 2 years, 5 years, 10 years or more.

[0072] An antibody or antigen-binding fragment thereof described herein can specifically bind to a secreted or mature form of hLOX but not to a preproprotein of hLOX having an amino acid sequence of SEQ ID NO: 7. In one embodiment, secreted form of hLOX has an amino acid sequence of SEQ ID NO: 8, 62 or 63. In one embodiment, the mature form of hLOX has an amino acid sequence of SEQ ID NO: 9.

[0073] Provided herein is a method of inhibiting angiogenesis in a subject by an antibody or antigen binding fragment thereof, described herein.

[0074] Provided herein is a method of inhibiting a fibrotic disease in a subject by administering an antibody or antigen binding fragment thereof, described herein. Fibrotic diseases include, but are not limited to, liver fibrosis, lung fibrosis, kidney fibrosis, cardiac fibrosis and scleroderma. In one embodiment, kidney fibrosis includes, but is not limited to, diabetic nephropathy, vesicoureteral reflux, tubulointerstitial renal fibrosis; glomerulonephritis or glomerular nephritis, including focal segmental glomerulosclerosis and membranous glomerulonephritis, and Mesangiocapillary glomerular nephritis. In one embodiment, liver fibrosis results in cirrhosis, and associated conditions such as chronic viral hepatitis, non-alcoholic fatty liver disease (NAFLD), alcoholic steatohepatitis (ASH), non-alcoholic steatohepatitis (NASH), primary biliary cirrhosis (PBC), biliary cirrhosis, and autoimmune hepatitis.

[0075] Provided herein is a method of decreasing extracellular matrix formation by contacting a sample or cellular tissue with an antibody or antigen binding fragment thereof, described herein. Administration or contacting can occur, in one example, by parenteral administration.

[0076] Provided herein is a method of monitoring a subject's response to administration of an antibody or antigen binding fragment thereof, described herein by detecting by detecting LOX and/or LOXL levels and/or activity.

[0077] In one embodiment, said antibody or antigen binding fragment thereof, is labeled with a therapeutic label.

[0078] Contemplated herein is combination therapy in which the methods further comprise co-administering a sec-

ond therapeutic agent. In one embodiment, the second therapeutic agent is an antibody or a chemotherapeutic agent.

[0079] Provided herein is a use of an antibody or antigen binding fragment thereof, described herein in the preparation of a formulation for inhibiting LOXL2 or LOX, reducing tumor growth, inhibiting angiogenesis, inhibiting a fibrotic disease or decreasing extracellular matrix formation in a subject. In one embodiment, said antibody or antigen binding fragment thereof is labeled with a therapeutic label and, optionally, a diagnostic label.

[0080] Provided herein is a use of an antibody or antigen binding fragment thereof, described herein in the preparation of a formulation for diagnosing a tumor or metastasis comprising assessing LOX and/or LOXL2 levels in a sample of a patient, wherein a change in LOX and/or LOXL2 levels in the sample in comparison with a reference sample indicates the presence of a tumor or metastasis or an increase in tumor or metastatic growth. In one embodiment, said antibody or antigen binding fragment thereof is labeled with a diagnostic label.

[0081] Provided herein are light chain polypeptides comprising the amino acid sequence:

(SEQ ID NO: 74)
DIVMTQTPLSLSVTPGQPASISCRSSKSLHNSNGNTYLYWFLQKPKQSPQ
FLIYRMSNLASGVDPDRFSGSGSGTDFTLKI SRVEAEADVGVVYCYMQHLEYF
YTFGGGTKEIKRTVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC.

Also provided are light chain polypeptides comprising the amino acid sequence of SEQ ID NO:71. Further provided are nucleic acids comprising a sequence encoding such light chain polypeptides. Also provided are nucleic acid constructs containing such nucleic acids, as well as recombinant host cells containing such constructs. Further provided are antibodies comprising such light chain polypeptides.

[0082] Provided herein are heavy chain polypeptides comprising the amino acid sequence:

(SEQ ID NO: 79)
QVQLVQSGAEVKKPGASVKVSCKASGYAFTYYLI EWVRQAPGQGLEWIGV
INPGSGGTNYNEKFKGRATITADKSTSTAYMELSSLRSEDAVYFCARNW
MNFYWGQGTITVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP
EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGKTKYTCN
VDHKPSNTKVDKRVESKYGPPCPPAPEFLGGPSVFLFPPPKDITLMIS
RTPEVTCVVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS
VLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTI SKAKGQPREPQVYTLPPS
QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK.

Also provided are heavy chain polypeptides comprising the amino acid sequence of SEQ ID NO:76. Further provided are nucleic acids comprising a sequence encoding such heavy chain polypeptides. Also provided are nucleic acid constructs containing such nucleic acids, as well as recombinant host

cells containing such constructs. Further provided are antibodies comprising such heavy chain polypeptides.

[0083] Provided herein are polypeptides comprising a light chain polypeptide and a heavy chain polypeptide, wherein the light chain polypeptide comprises the amino acid sequence of SEQ ID NO:74; or the heavy chain polypeptide comprises the amino acid sequence of SEQ ID NO:79. The heavy chain polypeptide of such polypeptides can comprise the heavy chain constant region of an IgG4 constant region polypeptide, e.g., a human or humanized IgG4 constant region polypeptide. In one example, the heavy chain polypeptide comprises a heavy chain constant region having the amino acid sequence of SEQ ID NO:84. In one example, the polypeptide comprises the amino acid sequence of SEQ ID NO:81. Also provided are nucleic acids encoding the polypeptides. Also provided are nucleic acid constructs containing such nucleic acids, as well as recombinant host cells containing such constructs.

[0084] The antibodies and polypeptides described herein above can be used in any of the methods disclosed herein, including methods of treatment and diagnosis. For example, the present disclosure provides methods of reducing growth of a tumor in a subject, by administering an antibody comprising the amino acid sequences of SEQ ID NOS: 74 and 79.

INCORPORATION BY REFERENCE

[0085] All publications, patents, and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference.

BRIEF DESCRIPTION OF THE DRAWINGS

[0086] Features of the invention are set forth with particularity in the appended claims. A better understanding of the features and advantages of the present invention will be obtained by reference to the following detailed description that sets forth illustrative embodiments, in which the principles of the invention are utilized, and the accompanying drawings.

[0087] FIG. 1 illustrates Lysyl Oxidase Enzymology. LOX/L enzymes act via a ping-pong mechanism which can be described by Michaelis-Menten kinetics.

[0088] FIG. 2 illustrates common modes of enzymatic inhibition.

[0089] FIG. 3 illustrates β APN is a competitive inhibitor of LOXL2.

[0090] FIG. 4 illustrates modes of enzymatic inhibition: LOXL2.

[0091] FIG. 5 illustrates extracellular LOXL2 localization and function of extracellular LOXL2.

[0092] FIG. 6A provides the amino acid sequences of a heavy chain variable region and FIG. 6B provides the amino acid sequences of a light chain variable region of an antibody that binds to the SRCR3-4 region of LOXL2. For each variable region, signal peptides are shown in italics, CDRs are underlined and the beginning of the constant framework is shown in bold font.

[0093] FIG. 7A provides the amino acid sequences of a heavy chain variable region and FIGS. 7B and 7C provide amino acid sequences of two light chain variable regions of antibodies that binds to LOX. For each variable region, signal peptides are shown in italics and CDRs are underlined.

[0094] FIG. 8 provides a protein screen B update using anti-LOXL2 antibodies. LOXL2 enzymatic activity was assessed.

[0095] FIG. 9 illustrates enzymatic activity of anti-LOXL2 antibody AB0023.

[0096] FIG. 10 demonstrates that anti-LOXL2 antibody AB0023 is a non-competitive inhibitor.

[0097] FIG. 11 illustrates the binding affinity and off-rate of anti-LOXL2 antibody AB0023.

[0098] FIG. 12 illustrates anti-LOXL2 antibody AB0023 domain mapping; AB0023 binds the SRCR 3-4 domain of LOXL2.

[0099] FIG. 13 shows that anti-LOXL2 antibody AB0023 demonstrates consistent inhibition of migration/invasion in collagen I and collagen IV, from supernatants through 10 ml prep material and scaled-up 100 ml prep and ascites material. Partial inhibition also observed in cell adhesion assays. In test samples, cells in the assay migrate toward serum and fluorescence is measured to determine cell count and migration. The far left bar is a control sample in which no antibody is present and the bottom layer contains serum (positive control for cell invasion). The second bar from left is a negative control in which no antibody is present and the bottom layer does not contain serum.

[0100] FIG. 14 provides amino acid sequences of the variable heavy (VH) (SEQ ID NO:24) and variable light (VL) (SEQ ID NO:29) chains of murine monoclonal antibody AB0023 (anti-hLOXL2). Complementarity determining regions (CDRs) (SEQ ID NOS: 41-42, 70 AND 57-59, respectively, in order of appearance) are shown by bold underlining. FIG. 14 also provides four humanized variants of the murine monoclonal antibody. Residues in the framework (FR) regions of the humanized variable heavy (SEQ ID NOS: 25-28, respectively, in order of appearance) and light (SEQ ID NOS: 30-32, respectively, in order of appearance) chains that differ from the murine monoclonal antibody are shown by dash marks (- - -) or by italicized underlining.

[0101] FIG. 15 demonstrates that M64 binds to LOX in a dose dependent manner. Batch 3 has a K_D of 6.6 nM, Batch 4 has a K_D of 5.0 nM and Batch 5 has a K_D of 5.7 nM.

[0102] FIG. 16 illustrates the binding affinity of anti-LOX antibody M64.

[0103] FIG. 17 demonstrates that anti-LOXL2 antibodies inhibited cell growth of four cancer derived cell lines.

[0104] FIG. 18 demonstrates a synergistic effect of an anti-LOX antibody in combination with cisplatin. IC50 values of M64 were also determined on four cell lines.

[0105] FIG. 19 provides amino acid and encoding nucleic acid sequences for the light chain of a humanized anti-LOXL2 antibody. The amino acid sequence (and encoding nucleic acid sequence) for: the signal peptide sequence is indicated by a single underline; for the variable region framework is indicated by a dashed underline; for the CDR regions is indicated by a double underline; and the constant region framework is provided as unformatted text.

[0106] FIG. 20 provides amino acid and encoding nucleic acid sequences for the heavy chain of a humanized anti-LOXL2 antibody. The amino acid sequence (and encoding nucleic acid sequence) for: the signal peptide sequence is indicated by a single underline; for the variable region framework is indicated by a dashed underline; for the CDR regions is indicated by a double underline; and the constant region framework is provided as unformatted text. Residues (pro-

line; CCA) reflecting a IgG4 hinge modification are indicated by single underlining and italics.

DETAILED DESCRIPTION OF THE INVENTION

[0107] The present invention relates to the field of medicine, including cancer diagnosis and treatment. One aspect of the invention relates to LOX and LOXL2 as indicators of disease progression and a target for therapeutic agents.

[0108] The present invention provides innovative methodology and related composition and kits for diagnosing or monitoring various diseases associated with abnormal cell proliferation, angiogenesis and fibrosis, by using agents that specifically recognize active or mature forms of lysyl oxidase (LOX) or lysyl oxidase-like (LOXL) proteins.

[0109] Methods are provided for diagnosing or monitoring cancer metastasis in a subject, comprising: assessing active LOX or LOXL2 levels or activity in the blood or in a tumor, whereby a change in active LOX or LOXL2 levels or activity in the blood or in the tumor in comparison with a reference sample, indicates the presence of metastatic tumor growth.

[0110] As described in more detail below, levels of active LOX or LOXL2 can be assessed by various methods including but are not limited to immunohistochemistry by using antibodies that specifically bind to the active or mature form of LOX or LOXL2. Enzymatic activity of active LOX or LOXL2 can be measured by using various methods including but not limited to chromogenic and fluorometric assays.

[0111] Also provided herein are antibodies or antigen-binding fragments thereof, that specifically recognize active forms of LOX or LOXL2, methods for generating antibodies against active forms of LOX or LOXL2, and method of using the antibodies to treat abnormal cell proliferation, angiogenesis and fibrosis.

I. General Definitions

[0112] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of ordinary skill in the art to which this invention belongs. All patents, applications, published applications and other publications referred to herein are incorporated by reference in their entirety. If a definition set forth in this section is contrary to or otherwise inconsistent with a definition set forth in the patents, applications, published applications and other publications that are herein incorporated by reference, the definition set forth in this section prevails over the definition that is incorporated herein by reference. The headings provided herein are for convenience only and do not limit the invention in any way.

[0113] As used herein, “a” or “an” means “at least one” or “one or more.”

[0114] The phrase “conservative amino acid substitution” refers to grouping of amino acids on the basis of certain common properties. A functional way to define common properties between individual amino acids is to analyze the normalized frequencies of amino acid changes between corresponding proteins of homologous organisms (Schulz, G. E. and R. H. Schirmer, Principles of Protein Structure, Springer-Verlag). According to such analyses, groups of amino acids may be defined where amino acids within a group exchange preferentially with each other, and therefore resemble each other most in their impact on the overall protein structure (Schulz, G. E. and R. H. Schirmer, Principles of Protein

Structure, Springer-Verlag). Examples of amino acid groups defined in this manner include:

[0115] (i) a charged group, consisting of Glu and Asp, Lys, Arg and His,

[0116] (ii) a positively-charged group, consisting of Lys, Arg and His,

[0117] (iii) a negatively-charged group, consisting of Glu and Asp,

[0118] (iv) an aromatic group, consisting of Phe, Tyr and Trp,

[0119] (v) a nitrogen ring group, consisting of His and Trp,

[0120] (vi) a large aliphatic non-polar group, consisting of Val, Leu and Ile,

[0121] (vii) a slightly-polar group, consisting of Met and Cys,

[0122] (viii) a small-residue group, consisting of Ser, Thr, Asp, Asn, Gly, Ala, Glu, Gln and Pro,

[0123] (ix) an aliphatic group consisting of Val, Leu, Ile, Met and Cys, and

[0124] (x) a small hydroxyl group consisting of Ser and Thr.

[0125] In addition to the groups presented above, each amino acid residue may form its own group, and the group formed by an individual amino acid may be referred to simply by the one and/or three letter abbreviation for that amino acid commonly used in the art as described above.

[0126] A “conserved residue” is an amino acid that is relatively invariant across a range of similar proteins. Often conserved residues will vary only by being replaced with a similar amino acid, as described above for “conservative amino acid substitution”.

[0127] The letter “x” or “xaa” as used in amino acid sequences herein is intended to indicate that any of the twenty standard amino acids may be placed at this position unless specifically noted otherwise. For the purposes of peptidomimetic design, an “x” or an “xaa” in an amino acid sequence may be replaced by a mimic of the amino acid present in the target sequence, or the amino acid may be replaced by a spacer of essentially any form that does not interfere with the activity of the peptidomimetic.

[0128] “Homology” or “identity” or “similarity” refers to sequence similarity between two peptides or between two nucleic acid molecules. Homology and identity can each be determined by comparing a position in each sequence which may be aligned for purposes of comparison. When an equivalent position in the compared sequences is occupied by the same base or amino acid, then the molecules are identical at that position; when the equivalent site occupied by the same or a similar amino acid residue (e.g., similar in steric and/or electronic nature), then the molecules can be referred to as homologous (similar) at that position. Expression as a percentage of homology/similarity or identity refers to a function of the number of identical or similar amino acids at positions shared by the compared sequences. A sequence which is “unrelated” or “non-homologous” shares less than 40% identity, though preferably less than 25% identity with a sequence of the present invention. In comparing two sequences, the absence of residues (amino acids or nucleic acids) or presence of extra residues also decreases the identity and homology/similarity.

[0129] The term “homology” describes a mathematically based comparison of sequence similarities which is used to identify genes or proteins with similar functions or motifs.

The nucleic acid (nucleotide, oligonucleotide) and amino acid (protein) sequences of the present invention may be used as a "query sequence" to perform a search against public databases to, for example, identify other family members, related sequences or homologs. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al. (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score=100, wordlength=12 to obtain nucleotide sequences homologous to nucleic acid molecules of the invention. BLAST amino acid searches can be performed with the XBLAST program, score=50, wordlength=3 to obtain amino acid sequences homologous to protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17): 3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and BLAST) can be used (see, ncbi.nlm.nih.gov).

[0130] As used herein, "identity" means the percentage of identical nucleotide or amino acid residues at corresponding positions in two or more sequences when the sequences are aligned to maximize sequence matching, i.e., taking into account gaps and insertions. Identity can be readily calculated by known methods, including but not limited to those described in *Computational Molecular Biology*, Lesk, A. M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D. W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data*, Part I, Griffin, A. M., and Griffin, H. G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, 1991; and Carillo, H., and Lipman, D., *SIAM J. Applied Math.*, 48: 1073 (1988). Methods to determine identity are designed to give the largest match between the sequences tested. Moreover, methods to determine identity are codified in publicly available computer programs. Computer program methods to determine identity between two sequences include, but are not limited to, the GCG program package (Devereux, J., et al., *Nucleic Acids Research* 12(1): 387 (1984)), BLASTP, BLASTN, and FASTA (Altschul, S. F. et al., *J. Molec. Biol.* 215: 403-410 (1990) and Altschul et al. *Nuc. Acids Res.* 25: 3389-3402 (1997)). The BLAST X program is publicly available from NCBI and other sources (BLAST Manual, Altschul, S., et al., NCBI NLM NIH Bethesda, Md. 20894; Altschul, S., et al., *J. Mol. Biol.* 215: 403-410 (1990). The well known Smith Waterman algorithm may also be used to determine identity.

[0131] The term "substantially identical" means identity between a first amino acid sequence that contains a sufficient or minimum number of amino acid residues that are i) identical to, or ii) conservative substitutions of aligned amino acid residues in a second amino acid sequence such that the first and second amino acid sequences can have a common structural domain and/or common functional activity. For example, amino acid sequences substantially identical to LOX contain a common structural domain having at least about 60%, or 65% identity, likely 75% identity, more likely 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to LOX. For example, amino acid sequences that contain a common structural domain having at least about 60%, or 65% identity, likely 75% identity, more likely 85%,

90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to LOXL2 are termed sufficiently or substantially identical. In the context of nucleotide sequence, the term "substantially identical" is used herein to refer to a first nucleic acid sequence that contains a sufficient or minimum number of nucleotides that are identical to aligned nucleotides in a second nucleic acid sequence such that the first and second nucleotide sequences encode a polypeptide having common functional activity, or encode a common structural polypeptide domain or a common functional polypeptide activity. For example, nucleotide sequences having at least about 60%, or 65% identity, likely 75% identity, more likely 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity to nucleic acid sequences provided herein are termed substantially identical.

II. Lysyl Oxidase (LOX) and Lysyl Oxidase-Like (LOXL) Proteins

[0132] Typically, solid tumors contain areas of low oxygen tension (hypoxia). Hypoxic cells present a great problem in the treatment of cancer because these cells are highly aggressive, metastatic and resistant to therapy. The underlying mechanisms contributing to these features are poorly understood. Metastasis poses a particular problem in breast cancer because there is no effective treatment for the majority of patients with detectable metastatic breast cancer (Steeg, P S. *Br. Can. Res.* 2(6): 396-9 (2000)).

[0133] The extracellular matrix (ECM) can have a major influence on tumor cells (Chang and Werb. *Trends Cell. Biol.* 11: S37-43 (2001); and Radisky et al. *Semin. Cancer Bio.* 11: 87-95 (2001)). Mice exposed to hypoxia exhibit tissue specific increases in lysyl oxidase (LOX) activity, an amine oxidase that plays an essential role in the formation and maintenance of the ECM (Brody et al. *Am. Rev. Respir. Dis.* 120: 1289-95 (2001)). A recent microarray study confirmed LOX to be a hypoxia-induced gene in a variety of cell lines (Denko, N C. *Oncogene* 22: 5907-14 (2003)). However, a biological role of LOX under hypoxic conditions was not identified. LOX initiates the covalent cross-linking of collagens and elastin in the ECM, increasing insoluble matrix deposition and tensile strength (Kagan and Li. *J. Cell. Biochem.* 88: 660-72 (2003)). LOX expression is essential for wound healing and normal connective tissue function, and knock-out mice die soon after parturition due to cardiovascular instability (Hornstra et al. *J. Biol. Chem.* 278: 14387-93 (2003)). Decreased LOX activity is associated with diseases such as Ehler-Danlos syndrome (Pinnell, S R. *J. Invest. Dermatol.* 79(Supp 1): 90S-92S (1982); Royce et al. *Biochem. J.* 192: 579-86 (1980); and Khakoo et al. *Clin. Genet.* 51: 109-14 (1997)). Increased LOX activity contributes to fibrotic and tissue remodeling diseases, such as liver cirrhosis (Kagan, H M. *Pathol. Res. Pract.* 190: 910-0 (1994); Chanki et al. *Br. J. Dermatol.* 133: 710-5 (1995); and Ooshima and Midorikawa. *Jpn. Circ. J.* 41: 1337-40 (1977)).

[0134] Elevated expression of LOX correlates with increased staging in renal cell cancer (Stassar et al. *Br. J. Cancer*, 85: 1372-82 (2001)), and increased LOX expression is observed in highly metastatic and/or invasive breast cancer cell lines (Kirschmann et al. *Breast Cancer Res. Treat.* 55: 127-36 (1999); and Kirschmann et al. *Cancer Res.* 62: 4478-83 (2002)). In contrast, LOX acts as a tumor suppressor in non-tumorigenic revertants of ras-transformed fibroblasts (Smith-Mungo and Kagan. *Matrix Biol.* 16: 387-98 (1998)). Loss of LOX is associated with tumorigenesis in several

cancer types such as gastric, colon and prostate cancers (Ren et al. *Cancer Res.* 58: 1285-90 (1998); Csiszar et al. *Int. J. Cancer* 97: 636-42 (2002); and Kaneda et al. *Cancer Res.* 64: 6410-5 (2004)). It would, thus, seem that LOX's tumor suppressive role depends on cell type and transformation status. The propeptide domain (and not the active enzyme) was recently shown to be responsible for the tumor suppressor activities. In breast cancer, increased LOX expression is associated with the early stromal reaction (Decitre et al. *Lab. Invest.* 78: 143-51 (1998)), and treatment with antisense LOX in this cancer cell type prevents in vitro invasion (Kirschmann et al. *Cancer Res.* 62: 4478-83 (2002)).

[0135] The amino acid sequence of LOXL2 shares extensive sequence homology with the conserved copper-binding and catalytic domains of both LOX and LOXL. These conserved domains are encoded by five consecutive exons within the LOX, LOXL, and LOXL2 genes that also maintain exon-intron structure conservation. Conservation of the nucleotide and deduced amino acid sequence within the carboxyl-terminal end of LOXL2, LOX, and LOXL include the copper-binding domain (WEWHSCHQHYH (SEQ ID NO: 66)) in LOX and LOXL and WIWHDCHRHYH (SEQ ID NO: 67) in LOXL2 with the four histidines that supply the nitrogen ligands for the copper coordination complex specific for lysyl oxidase proteins (Krebs and Krawetz, *Biochim. Biophys. Acta* 1202: 7-12 (1993)). The active site in LOX (DIDCQWVDITDVPPPGDY (SEQ ID NO: 68)) and in LOXL2 (DIDCQWVDITDVPPPGDY (SEQ ID NO: 69)) contains, in each, a Tyr residue (Y) at the COOH-terminal end, which participates together with a Lys residue in the formation of the quinone co-factor that is present in these proteins. Ten cysteines characteristic of LOX and LOXL are similarly conserved in LOXL2 (Kagan et al., (1994) in *Molecular Biology and Pathology of Elastic Tissue* (Mecham, R. P., and Roberts, L., eds), Ciba Foundation Symposium Series, Wiley, Chichester, UK). A growth factor and cytokine receptor domain present in the LOX and LOXL proteins has also been identified within the LOXL2-derived amino acid sequence. Four repeats of the scavenger receptor cysteine-rich domain are also present of LOXL2 (Saito et al., *J. Biol. Chem.* 272: 8157-8160 (1997), Resnick et al., *Trends Biochem. Sci.* 19: 5-8 (1994)).

[0136] Three major transcription termination sites have been noted within 3'-UTR domains of LOXL2 cDNA. The first termination site is 690 bp 3' of the termination codon, the second site is 740 bp, and the final transcription termination site is 900 bp 3' of the termination codon. These mRNAs all have 3'-UTRs differing slightly in size. Most exon-intron boundaries of the LOXL2 gene show the consensus sequence (C/T)AG-exon-GT(A/G). The sizes of the 11 exons of the LOXL2 gene range from 112 to 940 bp. Although the LOXL2 gene has 11 exons, five consecutive exons (exons 6-10), which encode the copper-binding and catalytic domains, exhibit 84% sequence similarity, and exon sizes are very similar to the corresponding exons of the LOX and LOXL genes. All the other exons in the LOXL2 gene are divergent in both sequence and size. LOXL2 has been identified in all tissues with the exception of blood leukocytes. LOXL2 mRNA has been detected in heart, liver, and pancreas; expression is significantly higher in placenta, prostate, uterus, and pancreas (ratios between 2 and 3) compared with lower expression in brain, lung, skeletal muscle, thymus, and kidney (ratios below 0.5). (Jourdan-Le Saux, et al. *J. Biol. Chem.*, 274(18): 12939-12944 (1999)).

[0137] The expression of LOX and the different LOXL proteins varies in different diseases. This may be due to a number of reasons, such as the difference in tissue distribution, processing, domains, regulation of activity, as well as other differences between the proteins. For example, LOX and LOXL are implicated in fibrotic diseases as both LOX and LOXL are highly expressed in myo-fibroblasts around fibrotic areas (Kagen, *Pathol. Res. Pract.* 190:910-919 (1994); Murawaki et al., *Hepatology* 14:1167-1173 (1991); Siegel et al., *Proc. Natl. Acad. Sci. USA* 75:2945-2949 (1978); Jourdan Le-Saux et al., *Biochem. Biophys. Res. Comm.* 199:587-592 (1994); Kim et al., *J. Cell Biochem.* 72:181-188 (1999)). LOX and the various LOXL are also implicated in a number of cancers. For example, LOXL and LOXL4 have been shown to be epigenetically silenced and can inhibit ras/extracellular signal-regulated kinase signaling pathway in human bladder cancer (Wu et al., *Cancer Res.* 67:4123-4129 (2007)). Others have shown selective upregulation and amplification of the LOXL4 gene in head and neck squamous cell carcinoma (Gorrough et al., *J. Pathol.* 212:74-82 (2007)). LOX and LOXL2 have also been implicated in a number of tumors, such as colon and esophageal cancers (Csiszar, *Prog. Nucl. Acid Res.* 70:1-32 (2001)). In breast cancer, LOX and the LOXL family members have been linked to the cancer (Kirschmann et al., *Cancer Res.* 62:448-4483 (2002)).

[0138] Lysyl oxidase catalyzes oxidative deamination of peptidyl lysine and hydroxylysine residues in collagens, and peptidyl lysine residues in elastin. The resulting peptidyl aldehydes spontaneously condense and undergo oxidation reactions to form the lysine-derived covalent cross-links required for the normal structural integrity of the extracellular matrix. In the reaction of lysyl oxidase with its substrates, hydrogen peroxide (H₂O₂) and ammonium are released in quantities stoichiometric with the peptidyl aldehyde product. See, e.g., Kagan et al., *J. Cell. Biochem.* 88:660-72 (2003).

[0139] Lysyl oxidase is secreted into the extracellular environment where it is then processed by proteolytic cleavage to a functional 30 kDa enzyme and an 18 kDa propeptide. The 30 kDa lysyl oxidase is enzymatically active whereas the 50 kDa proenzyme is not. Procollagen C-proteinases process pro-lysyl oxidase to its active form and are products of the Bmp1, Tll1 and Tll2 genes. The localization of the enzyme is mainly extracellular, although processed lysyl oxidase also localizes intracellularly and nuclearly. Sequence coding for the propeptide is moderately (60-70%) conserved among LOX and the LOXL proteins, whereas the sequence coding for the C-terminal 30 kDa region of the proenzyme in which the active site is located is highly conserved (approximately 95%). See Kagan et al., *J. Cell Biochem.* 59:329-38 (1995). LOX is induced by a number of growth factors and steroids such as TGF- β , TNF- α and interferon (Csiszar, *Prog. Nucl. Acid Res.* 70:1-32 (2001)).

[0140] Five different lysyl oxidases are known to exist in both humans and mice, LOX and four LOX related, or LOX-like proteins (LOXL, LOXL2, LOXL3, LOXL4). LOX and the LOX-like proteins are referred to collectively as "LOX/LOXL" for the purposes of the present disclosure. The five forms of lysyl oxidases reside on five different chromosomes. These family members show some overlap in structure and function, but appear to have distinct functions as well. For example, although the main activity of LOX is the oxidation of specific lysine residues in collagen and elastin outside of the cell, it may also act intracellularly, where it may regulate

gene expression. In addition, LOX induces chemotaxis of monocytes, fibroblasts and smooth muscle cells. Further, a deletion of LOX in knockout mice appears to be lethal at parturition (Hornstra et al., J. Biol. Chem. 278:14387-14393 (2003)), whereas LOXL deficiency causes no severe developmental phenotype (Bronson et al., Neurosci. Lett. 390:118-122 (2005)).

[0141] The main activity of LOX is the oxidation of specific lysine residues in collagen and elastin outside of the cell, however, it may also act intracellularly, where it may regulate gene expression (Li et al., Proc. Natl. Acad. Sci. USA 94:12817-12822 (1997), Giampuzzi et al., J. Biol. Chem. 275:36341-36349 (2000)). In addition, LOX induces chemotaxis of monocytes, fibroblasts and smooth muscle cells (Lazarus et al., Matrix Biol. 14:727-731 (1995) Nelson et al., Proc. Soc. Exp. Biol. Med. 188:346-352 (1988)). LOX itself is induced by a number of growth factors and steroids such as TGF- β , TNF- α and interferon (Csiszar, Prog. Nucl. Acid Res. 70:1-32 (2001)). Recent studies have attributed other roles to LOX in diverse biological functions such as developmental regulation, tumor suppression, cell motility, and cellular senescence. The diverse role of LOX, and its recently discovered amino oxidase family, LOX-like (LOXL), may play important roles with their intracellular and extracellular localization.

[0142] As used herein, the term "lysyl oxidase" refers to an enzyme that catalyzes the following reaction: peptidyl-L-lysyl-peptide+O₂+H₂O→peptidyl-allysyl-peptide+NH₃+H₂O₂. Other synonyms for lysyl oxidase (EC 1.4.3.13) include protein-lysine 6-oxidase and protein-L-lysine:oxygen 6-oxidoreductase (deaminating). See, e.g., Harris et al., Biochim. Biophys. Acta 341:332-44 (1974); Rayton et al., J. Biol. Chem. 254:621-26 (1979); Stassen, Biophys. Acta 438:49-60 (1976). A copper-containing quinoprotein with a lysyl adduct of tyrosyl quinone at its active center, LOX catalyzes the oxidation of peptidyl lysine to result in the formation of peptidyl α -aminoadipic- δ -semialdehyde. Once formed, this semialdehyde can spontaneously condense with neighboring aldehydes or with other lysyl groups to form intra- and interchain cross-links. See, e.g., Rucker et al., Am. J. Clin. Nutr. 67:996S-1002S (1998).

[0143] The term "LOX" refers to an enzyme having an amino acid sequence substantially identical to a polypeptide expressed or translated from one of the following sequences: EMBL/GenBank accession numbers: M94054 (SEQ ID NO: 10); AAA59525.1 (SEQ ID NO: 11)—mRNA; S45875 (SEQ ID NO: 12); AAB23549.1 (SEQ ID NO: 13)—mRNA; S78694 (SEQ ID NO: 14); AAB21243.1 (SEQ ID NO: 15)—mRNA; AF03929.1 (SEQ ID NO: 16); AAD02130.1 (SEQ ID NO: 17)—mRNA; BC074820 (SEQ ID NO: 18); AAH74820.1 (SEQ ID NO: 19)—mRNA; BC074872 (SEQ ID NO: 20); AAH74872.1 (SEQ ID NO: 21)—mRNA; M84150 (SEQ ID NO: 22); AAA59541.1 (SEQ ID NO: 23)—Genomic DNA. One embodiment of LOX is human lysyl oxidase (hLOX) preproprotein having an amino acid sequence (SEQ ID NO: 7), a secreted hLOX after cleavage of the signal peptide such as SEQ ID NO: 8 or a mature hLOX after proteolytic processing such as SEQ ID NO: 9.

[0144] LOX has highly conserved protein domains, conserved in several species including human, mouse, rat, chicken, fish and *Drosophila*. The human LOX family has a highly conserved C-terminal region containing the 205 amino acid LOX catalytic domain. The conserved region contains the copper binding (Cu), conserved cytokine receptor like

domain (CRL), and the lysyl-tyrosylquinone cofactor site (LTQ). The predicted extracellular signal sequences are represented by the hatched boxes (See FIG. 7 of U.S. Provisional Application No. 60/963,249, which is incorporated herein by reference). Twelve cysteine residues are also similarly conserved, wherein two of them reside within the prepropeptide region and ten are in the catalytically active processed form of LOX (Csiszar, Prog. Nucl. Acid Res. 70:1-32 (2001)). The conserved region also includes a fibronectin binding domain.

[0145] The prepropeptide region of LOX contains the signal peptide, and is cleaved, the cleavage site predicted to be between Cys21-Ala22, to generate a signal sequence peptide and a 48 kDa amino acid propeptide form of LOX, which is still inactive. The propeptide is N-glycosylated during passage through the Golgi that is secreted into the extracellular environment where the proenzyme, or propeptide, is cleaved between Gly168-Asp169 by a metalloendoprotease, a procollagen C-proteinase, which are products of the Bmp1, Tii1 and Tii2 genes. BMP I (bone morphogenetic protein I) is a procollagen C-proteinase that processes the propeptide to yield a functional 30 kDa enzyme and an 18 kDa propeptide. The sequence coding for the propeptide is moderately (60-70%) conserved, whereas the sequence coding for the C-terminal 30 kDa region of the proenzyme in which the active site is located is highly conserved (approximately 95%). (Kagan and Li, J. Cell. Biochem. 88:660-672 (2003); Kagan et al., J. Cell Biochem. 59:329-38 (1995)). The N-glycosyl units are also subsequently removed. LOX occurs in unprocessed and/or processed (mature) forms. The mature form of LOX is typically active although, in some embodiments, unprocessed LOX is also active.

[0146] Particular examples of a LOXL enzyme or protein are described in Molnar et al., Biochim Biophys Acta. 1647:220-24 (2003); Csiszar, Prog. Nucl. Acid Res. 70:1-32 (2001); and in WO 01/83702 published on Nov. 8, 2001, all of which are herein incorporated by reference. (It is noted that in these 3 publications, "LOXL1" was referred to as "LOXL" whereas in the present invention "LOXL" is used to refer to a lysyl oxidase-like proteins in general, not just LOXL1.) These enzymes include LOXL1, encoded by mRNA deposited at GenBank/EMBL BC015090; AAH15090.1; LOXL2, encoded by mRNA deposited at GenBank/EMBL U89942; LOXL3, encoded by mRNA deposited at GenBank/EMBL AF282619; AAK51671.1; and LOXL4, encoded by mRNA deposited at GenBank/EMBL AF338441; AAK71934.1.

[0147] Similar potential signal peptides as those described above for LOX have been predicted at the amino terminus of LOXL, LOXL2, LOXL3, and LOXL4. The predicted signal cleavage sites are between Gly25-Gln26 for LOXL, between Ala25-Gln26, for LOXL2, and between Gly25-Ser26 for LOXL3. The consensus for BMP-1 cleavage in pro-collagens and pro-LOX is between Ala/Gly-Asp, and often followed by an acidic or charged residue. A potential cleavage site to generate active LOXL is Gly303-Asp304, however, it is then followed by an atypical Pro. LOXL3 also has a potential cleavage site at Gly447-Asp448, which is followed by an Asp, processing at this site may yield an active peptide of similar size to active LOX. A potential cleavage site of BMP-I was also identified within LOXL4, at residues Ala569-Asp570 (Kim et al., J. Biol. Chem. 278:52071-52074 (2003)). LOXL2 may also be proteolytically cleaved analogously to the other members of the LOXL family and secreted (Akiri et al., Cancer Res. 63:1657-1666 (2003)).

[0148] LOX and LOXL enzymes act via a ping-pong mechanism which can be described by Michaelis-Menten kinetics (see FIG. 1).

[0149] An example of LOX or LOXL protein include the enzyme having an amino acid sequence substantially identical to a polypeptide expressed or translated from one of the following sequences: EMBL/GenBank accessions: M94054; AAA59525.1—mRNA; S45875; AAB23549.1—mRNA; S78694; AAB21243.1—mRNA; AF039291; AAD02130.1—mRNA; BC074820; AAH74820.1—mRNA; BC074872; AAH74872.1—mRNA; M84150; AAA59541.1—Genomic DNA.

[0150] The terms “LOX” and “LOXL” also encompass functional fragments or derivatives that substantially retain enzymatic activity catalyzing the deamination of lysyl residues. Typically, a functional fragment or derivative retains at least 50% of 60%, 70%, 80%, 90%, 95%, 99% or 100% of its lysyl oxidation activity. It is also intended that a LOX or a LOXL2 protein can include conservative amino acid substitutions that do not substantially alter its activity. Suitable conservative substitutions of amino acids are known to those of skill in this art and may be made generally without altering the biological activity of the resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity. See, e.g., Watson, et al., *Molecular Biology of the Gene*, 4th Edition, 1987, The Benjamin/Cummings Pub. Co., p. 224. Conservative and non-conservative amino acid substitutions have been described above.

[0151] A feature not known to be common amongst the LOX and LOXL proteins is the scavenger receptor cysteine rich (SRCR) domains. LOX and LOXL lack SRCR domains, whereas LOXL2, LOXL3, and LOXL4 each have four SRCR domains at the N-terminus. SRCR domains are found in secreted, transmembrane, or extracellular matrix proteins. SRCR domains are also known to mediate ligand binding in a number of secreted and receptor proteins (Hoheneste et al., *Nat. Struct. Biol.* 6:228-232 (1999); Sasaki et al., *EMBO J.* 17:1606-1613 (1998)). Another domain unique to LOXL is the presence of a proline rich domain (Molnar et al., *Biochimica Biophysica Acta* 1647:220-224 (2003)).

[0152] Tissue distribution may also differ amongst LOX and the various LOXL. LOX is highly expressed in the heart, placenta, testis, lung, kidney and uterus, but marginally in the brain and liver. LOXL I is expressed in the placenta, kidney, muscle, heart, lung, and pancreas, and as with LOX, has much lower expressing in the brain and liver (Kim et al., *J. Biol. Chem.* 270:7176-7182 (1995)). LOXL2 is highly expressed in the uterus, placenta, and other organs, but similar to LOX and LOXL, lowly expressed in the brain and liver (Jourdan Le-Saux et al., *J. Biol. Chem.* 274:12939:12944 (1999)). LOXL3 is highly expressed in the testis, spleen, and prostate, moderately in placenta, and not in the liver, whereas LOXL4 is highly expressed in the liver (Huang et al., *Matrix Biol.* 20:153-157 (2001); Maki and Kivirikko, *Biochem. J.* 355: 381-387 (2001); Jourdan Le-Saux et al., *Genomics* 74:211-218 (2001); Asuncion et al., *Matrix Biol.* 20:487-491 (2001)).

[0153] The expression, or implication of LOX and the different LOXL proteins, in diseases may also vary. This may be due to a number of reasons, such as the difference in tissue distribution, processing, domains, regulation of activity, as well as other differences between the proteins. For example, LOX and LOXL are implicated in fibrotic diseases as both

LOX and LOXL are highly expressed in myo-fibroblasts around fibrotic areas (Kagen, *Pathol. Res. Pract.* 190:910-919 (1994); Murawaki et al., *Hepatology* 14:1167-1173 (1991); Siegel et al., *Proc. Natl. Acad. Sci. USA* 75:2945-2949 (1978); Jourdan Le-Saux et al., *Biochem. Biophys. Res. Comm.* 199:587-592 (1994); Kim et al., *J. Cell Biochem.* 72:181-188 (1999)). LOX and the various LOXL are also implicated in a number of cancers. For example, LOXL and LOXL4 have been shown to be epigenetically silenced and can inhibit ras/extracellular signal-regulated kinase signaling pathway in human bladder cancer (Wu et al., *Cancer Res.* 67:4123-4129 (2007)). Others have shown selective upregulation and amplification of the LOXL4 gene in head and neck squamous cell carcinoma (Gorrough et al., *J. Pathol.* 212:74-82 (2007)). LOX and LOXL2 have also been implicated in a number of tumors, such as colon and esophageal cancers (Csiszar, *Prog. Nucl. Acid Res.* 70:1-32 (2001)). In breast cancer, LOX and the LOXL family members have been linked to the cancer (Kirschmann et al., *Cancer Res.* 62:448-4483 (2002)).

III. Epithelial—Mesenchymal Transition

[0154] Epithelial-to-Mesenchymal Transition (EMT) refers to the process whereby a cell with a gene expression/phenotype characteristic of epithelial cell (i.e., expressing specific proteins, factors, and molecules) changes or alters the genes or their level of expression which results in a change in the phenotype of the cell as exhibited by the alteration or change in the genes expressed.

[0155] Epithelial and mesenchymal cells represent distinct lineages, each with a unique gene expression profile that imparts attributes specific to each cell type. Conversion of an epithelial cell into a mesenchymal cell requires alterations in morphology, cellular architecture, adhesion, and/or migration capacity. Advanced tumor cells frequently exhibit a conspicuous down-regulation of epithelial markers and a loss of intercellular junctions, resulting in a loss of epithelial polarity and reduced intercellular adhesion. The loss of epithelial features is often accompanied by increased cell motility and expression of mesenchymal genes. EMT can include loss of contact inhibition, altered growth control, and/or enhanced invasiveness (Christiansen and Rajasekaran, *Cancer Res.*, 66(17): 8319-8326 (2006); and Thiery et al., *Curr. Opin. Cell. Biol.*, 15: 740-6 (2003)). Molecular and morphologic features indicative of EMT correlate with poor histologic differentiation, destruction of tissue integrity, and metastasis. EMT provides mechanisms for epithelial cells to overcome the physical constraints imposed on them by intercellular junctions and adopt a motile phenotype (Burdal et al. *Development*, 118:829-44 (1993); and Nieto et al., *Mech. Dev.*, 105:27-35 (2001)).

[0156] Commonly used molecular markers for EMT include increased expression of N-cadherin and vimentin, nuclear localization of β -catenin, and increased production of the transcription factors such as Snail1 (Snail), Snail2 (Slug), Twist, EF1/ZEB1, SIP1/ZEB2, and/or E47 that inhibit E-cadherin production. Phenotypic Markers for an EMT include, but are not limited to, an increased capacity for migration and three-dimensional invasion, as well as resistance to apoptosis. These markers have further been correlated with induction of EMT and an association with cancerous phenotypes.

[0157] The occurrence of EMT during tumor progression allows tumor cells to acquire the capacity to infiltrate surrounding tissue and ultimately to metastasize to distant sites.

Changes in gene expression within tumor cells can indicate a progression from epithelial or epithelial-like gene expression pattern to a mesenchymal or mesenchymal-like gene expression pattern. By way of example, the identification of loss of E-cadherin is correlated with metastatic carcinoma as well as resistance to cancer therapies such as EGFR inhibitors and IGF-R1 inhibitors. Analysis of many different types of cancer reveals that circulating tumor cells, or those found as micrometastases, evidence mesenchymal conversion based on changes of expression in a set of markers. These markers include, but are not limited to, EGFR, E-cadherin, ErbB3, RAB25, integrin beta 6, cadherin-2, fibroblast growth factor binding protein 1, distal-less homeo box 1, ZEB1 (transcription factor 8), SIP1, and vimentin.

[0158] By way of example, an epithelial-like gene expression profile includes expression, or increase expression of genes such as E-cadherin, ErbB3, or EGFR. An epithelial-like gene expression profile can include the expression of one or more of these genes, at least two, or at least three of these genes.

[0159] As with the previously described therapy-resistant cancers, the expression levels of E-cadherin, ErbB3, RAB25, integrin beta 6, cadherin-2, fibroblast growth factor binding protein 1, distal-less homeo box 1, ZEB1 (transcription factor 8), SIP1, TGF- β , FOXC2, GSK-313, Smad-3, Pez, Snail1, Snail2, and ILK, and vimentin represent genes that are common to EMT characteristics as well as with those epithelial-based tumor cells/cancers that develop resistance to their respective therapies. The present invention also generally relates to a method to treat a patient with cancer, and particularly a cancer that has experienced EMT. The inventors have discovered that cancers that have experienced EMT or have switched from an epithelial-like gene expression pattern to a mesenchymal-like gene expression pattern are responsive to LOX/LOXL inhibitors.

[0160] For assessment of tumor cell epithelial or mesenchymal biomarker expression, patient samples containing tumor cells, or proteins or nucleic acids produced by these tumor cells, can be used in methods described, for example, in U.S. patent application Publication Number 20070065858, which is incorporated in its entirety by reference herein. Briefly, the level of expression of the biomarker can be assessed by assessing the amount (e.g., absolute amount or concentration) of the marker in a tumor cell sample, e.g., a tumor biopsy obtained from a patient, or other patient sample containing material derived from the tumor (e.g., blood, serum, urine, or other bodily fluids or excretions as described herein above). The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (e.g., nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the sample. Likewise, tumor biopsies can also be subjected to post-collection preparative and storage techniques, e.g., fixation.

[0161] One can detect expression of biomarker proteins having at least one portion which is displayed on the surface of tumor cells which express it. It is a simple matter for the skilled artisan to determine whether a marker protein, or a portion thereof, is exposed on the cell surface. For example, immunological methods can be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods can be used to predict the presence of at least one extracellular domain (i.e., including both secreted

proteins and proteins having at least one cell-surface domain). Expression of a marker protein having at least one portion which is displayed on the surface of a cell which expresses it can be detected without necessarily lysing the tumor cell (e.g., using a labeled antibody which binds specifically with a cell-surface domain of the protein).

[0162] Expression of biomarkers can be assessed by any of a wide variety of well known methods for detecting expression of a transcribed nucleic acid or protein. Non-limiting examples of such methods include, for example, immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

[0163] Expression of a biomarker can be assessed using an antibody (e.g., a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (e.g., an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair (e.g., biotin-streptavidin), or an antibody fragment (e.g., a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a biomarker protein or fragment thereof, including a biomarker protein which has undergone either all or a portion of post-translational modifications to which it is normally subjected in the tumor cell (e.g., glycosylation, phosphorylation, methylation etc.).

[0164] Expression of a biomarker can also be assessed by preparing mRNA/cDNA (i.e., a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a biomarker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to hybridization with the reference polynucleotide. Expression of one or more biomarkers can likewise be detected using quantitative PCR to assess the level of expression of the biomarker(s). Alternatively, any of the many known methods of detecting mutations or variants (e.g., single nucleotide polymorphisms, deletions, etc.) of a biomarker can be used to detect occurrence of a biomarker in a patient.

[0165] A mixture of transcribed polynucleotides obtained from the sample can be contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (e.g., at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a biomarker nucleic acid. If polynucleotides complementary to, or homologous with, are differentially detectable on the substrate (e.g., detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of biomarkers can be assessed simultaneously using a single substrate (e.g., a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of assessing biomarker expression is used which involves hybridization of one nucleic acid with another, hybridization can be performed under stringent hybridization conditions.

[0166] When a plurality of biomarkers of the invention are used in the methods of the invention, the level of expression of each biomarker in a patient sample can be compared with the normal level of expression of each of the plurality of biomarkers in non-cancerous samples of the same type, either in a single reaction mixture (i.e., using reagents, such as different

fluorescent probes, for each biomarker) or in individual reaction mixtures corresponding to one or more of the biomarkers.

[0167] The level of expression of a biomarker in normal (i.e., non-cancerous) human tissue can be assessed in a variety of ways. This normal level of expression can be assessed by assessing the level of expression of the biomarker in a portion of cells which appears to be non-cancerous, and then comparing the normal level of expression with the level of expression in a portion of the tumor cells. As further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the biomarkers can be used. Alternatively, the normal level of expression of a biomarker can be determined by assessing expression of the biomarker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cancer in the patient, from archived patient samples, and the like.

[0168] An exemplary method for detecting the presence or absence of a biomarker protein or nucleic acid in a biological sample involves obtaining a biological sample (e.g., a tumor-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (e.g., mRNA, genomic DNA, or cDNA). The detection methods can, thus, be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample in vitro as well as in vivo. In vitro techniques for detection of mRNA include, for example, Northern hybridizations and in situ hybridizations. In vitro techniques for detection of a biomarker protein include, but are not limited to, enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitation and immunofluorescence. In vitro techniques for detection of genomic DNA include, for example, Southern hybridizations. In vivo techniques for detection of mRNA include, for example, polymerase chain reaction (PCR), Northern hybridizations and in situ hybridizations. Furthermore, in vivo techniques for detection of a biomarker protein include introducing into a subject a labeled antibody directed against the protein or fragment thereof. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

[0169] A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a biomarker, and a probe, under appropriate conditions and for a time sufficient to allow the biomarker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

[0170] For example, one method to conduct such an assay involves anchoring the biomarker or probe onto a solid phase support, also referred to as a substrate, and detecting target biomarker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of biomarker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

[0171] There are several established methods for anchoring assay components to a solid phase. These include, without

limitation, biomarker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored. Other suitable Carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the biomarker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components can be removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of biomarker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein. In one embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

[0172] It is also possible to directly detect biomarker/probe complex formation without further manipulation or labeling of either component (biomarker or probe), for example by utilizing the technique of fluorescence energy transfer (i.e., FET, see for example, Lakowicz et al., U.S. Pat. No. 5,631,169; Stavrianopoulos, et al., U.S. Pat. No. 4,868,103). A fluorophore label on the first, donor molecule is selected such that, upon excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second acceptor molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the donor protein molecule can simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the acceptor molecule label can be differentiated from that of the donor. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the acceptor molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter).

[0173] In another embodiment, determination of the ability of a probe to recognize a biomarker can be accomplished without labeling either assay component (probe or biomarker) by utilizing a technology such as real-time Biomolecular Interaction Analysis (BIA) (see, e.g., Sjolander, S. and Urbaniczky, C., 1991, Anal. Chem. 63:2338-2345 and Szabo et al., 1995, Curr. Opin. Struct. Biol. 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (e.g., BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon reso-

nance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

[0174] Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with biomarker and probe as solutes in a liquid phase. In such an assay, the complexed biomarker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, biomarker/probe complexes can be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A. P., 1993, *Trends Biochem Sci.* 18(8):284-7). Standard chromatographic techniques can also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format; for example, the relatively larger complex can be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the biomarker/probe complex as compared to the uncomplexed components can be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, e.g., Heegaard, N. H., 1998, *J. Mol. Recognit.* Winter 11(1-6):141-8; Hage, D. S., and Tweed, S. A. J. *Chromatogr B Biomed Sci Appl* Oct. 10, 1997; 699(1-2):499-525). Gel electrophoresis can also be employed to separate complexed assay components from unbound components (see, e.g., Ausubel et al., ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically used. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

[0175] In another embodiment, the level of biomarker mRNA can be determined both by in situ and by in vitro formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA. For in vitro methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from tumor cells (see, e.g., Ausubel et al., ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Pat. No. 4,843,155).

[0176] The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybrid-

ize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a biomarker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the biomarker in question is being expressed.

[0177] In one format, the mRNA is immobilized on a solid surface and contacted with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the biomarkers of the present invention.

[0178] An alternative method for determining the level of mRNA biomarker in a sample involves the process of nucleic acid amplification, e.g., by RT-PCR (the experimental embodiment set forth in Mullis, 1987, U.S. Pat. No. 4,683, 202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained sequence replication (Guatelli et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh et al., 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi et al., 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi et al., U.S. Pat. No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

[0179] For in situ methods, mRNA does not need to be isolated from the tumor cells prior to detection. In such methods, a cell or tissue sample is prepared and/or processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the biomarker.

[0180] As an alternative to making determinations based on the absolute expression level of the biomarker, determinations can be based on the normalized expression level of the biomarker. Expression levels are normalized by correcting the absolute expression level of a biomarker by comparing its expression to the expression of a gene that is not a biomarker, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level

in one sample, e.g., a patient sample, to another sample, e.g., a non-tumor sample, or between samples from different sources.

[0181] Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a biomarker (e.g., a mesenchymal biomarker), the level of expression of the biomarker is determined for 10 or more, 20 or more, 30 or more, 40 or more, or 50 or more samples of normal versus cancer cell isolates prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the biomarker. The expression level of the biomarker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that biomarker. This provides a relative expression level.

[0182] In another embodiment of the present invention, a biomarker protein is detected. One type of agent for detecting biomarker protein of the invention is an antibody capable of binding to such a protein or a fragment thereof such as, for example, a detectably labeled antibody. Antibodies can be polyclonal or monoclonal. An intact antibody, or an antigen binding fragment thereof (e.g., Fab, F(ab')₂, Fv, scFv, single binding chain polypeptide) can be used. The term "labeled," with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

[0183] Proteins from tumor cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

[0184] A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can readily adapt known protein/antibody detection methods for use in determining whether tumor cells express a biomarker of the present invention.

[0185] In one format, antibodies, or antibody fragments or derivatives, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, either the antibody or proteins can be immobilized on a solid support. Suitable solid phase supports or carriers include any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite. One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present invention. For example, protein isolated from tumor cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The

support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of bound label on the solid support can then be detected by conventional means.

[0186] For ELISA assays, specific binding pairs can be of the immune or non-immune type. Immune specific binding pairs are exemplified by antigen-antibody systems or hapten/anti-hapten systems. There can be mentioned fluorescein/anti-fluorescein, dinitrophenyl/anti-dinitrophenyl, biotin/anti-biotin, peptide/anti-peptide and the like. The antibody member of the specific binding pair can be produced by customary methods familiar to those skilled in the art. Such methods involve immunizing an animal with the antigen member of the specific binding pair. If the antigen member of the specific binding pair is not immunogenic, e.g., a hapten, it can be covalently coupled to a carrier protein to render it immunogenic. Non-immune binding pairs include systems wherein the two components share a natural affinity for each other but are not antibodies. Exemplary non-immune pairs are biotin-streptavidin, intrinsic factor-vitamin B12, folic acid-folate binding protein and the like.

[0187] A variety of methods are available to covalently label antibodies with members of specific binding pairs. Methods are selected based upon the nature of the member of the specific binding pair, the type of linkage desired, and the tolerance of the antibody to various conjugation chemistries. Biotin can be covalently coupled to antibodies by utilizing commercially available active derivatives. Some of these are biotin-N-hydroxy-succinimide which binds to amine groups on proteins; biotin hydrazide which binds to carbohydrate moieties, aldehydes and carboxyl groups via a carbodiimide coupling; and biotin maleimide and iodoacetyl biotin which bind to sulfhydryl groups. Fluorescein can be coupled to protein amine groups using fluorescein isothiocyanate. Dinitrophenyl groups can be coupled to protein amine groups using 2,4-dinitrobenzene sulfate or 2,4-dinitrofluorobenzene. Other standard methods of conjugation can be employed to couple monoclonal antibodies to a member of a specific binding pair including dialdehyde, carbodiimide coupling, homofunctional cross-linking, and heterobifunctional cross-linking. Carbodiimide coupling is an effective method of coupling carboxyl groups on one substance to amine groups on another. Carbodiimide coupling is facilitated by using the commercially available reagent 1-ethyl-3-(dimethyl-aminopropyl)-carbodiimide (EDAC).

[0188] Homobifunctional cross-linkers, including the bifunctional imidoesters and bifunctional N-hydroxysuccinimide esters, are commercially available and are employed for coupling amine groups on one substance to amine groups on another. Heterobifunctional cross-linkers are reagents which possess different functional groups. The most common commercially available heterobifunctional cross-linkers have an amine reactive N-hydroxysuccinimide ester as one functional group, and a sulfhydryl reactive group as the second functional group. The most common sulfhydryl reactive groups are maleimides, pyridyl disulfides and active halogens. One of the functional groups can be a photoactive aryl nitrene, which upon irradiation reacts with a variety of groups.

[0189] The detectably-labeled antibody or detectably-labeled member of the specific binding pair is prepared by coupling to a reporter, which can be a radioactive isotope,

enzyme, fluorogenic, chemiluminescent or electrochemical materials. Two commonly used radioactive isotopes are ¹²⁵I and ³H. Standard radioactive isotopic labeling procedures include the chloramine T, lactoperoxidase and Bolton-Hunter methods for ¹²⁵I and reductive methylation for ³H. The term “detectably-labeled” refers to a molecule labeled in such a way that it can be readily detected by the intrinsic enzymatic activity of the label or by the binding to the label of another component, which can itself be readily detected.

[0190] Enzymes suitable for use in this invention include, but are not limited to, horseradish peroxidase, alkaline phosphatase, β -galactosidase, glucose oxidase, luciferases, including firefly and renilla, β -lactamase, urease, green fluorescent protein (GFP) and lysozyme. Enzyme labeling is facilitated by using dialdehyde, carbodiimide coupling, homobifunctional cross-linkers and heterobifunctional cross-linkers as described above for coupling an antibody with a member of a specific binding pair.

[0191] The labeling method chosen depends on the functional groups available on the enzyme and the material to be labeled, and the tolerance of both to the conjugation conditions. The labeling method used in the present invention can be one of, but not limited to, any conventional methods currently employed including those described by Engvall and Pearlmann, *Immunochemistry* 8, 871 (1971), Avrameas and Temynck, *Immunochemistry* 8, 1175 (1975), Ishikawa et al., *J. Immunoassay* 4(3):209-327 (1983) and Jablonski, *Anal. Biochem.* 148:199 (1985).

[0192] Labeling can be accomplished by indirect methods such as using spacers or other members of specific binding pairs. An example of this is the detection of a biotinylated antibody with unlabeled streptavidin and biotinylated enzyme, with streptavidin and biotinylated enzyme being added either sequentially or simultaneously. Thus, according to the present invention, the antibody used to detect can be detectably-labeled directly with a reporter or indirectly with a first member of a specific binding pair. When the antibody is coupled to a first member of a specific binding pair, then detection is effected by reacting the antibody-first member of a specific binding complex with the second member of the binding pair that is labeled or unlabeled as mentioned above.

[0193] Moreover, the unlabeled detector antibody can be detected by reacting the unlabeled antibody with a labeled antibody specific for the unlabeled antibody. In this instance “detectably-labeled” as used above is taken to mean containing an epitope by which an antibody specific for the unlabeled antibody can bind. Such an anti-antibody can be labeled directly or indirectly using any of the approaches discussed above. For example, the anti-antibody can be coupled to biotin which is detected by reacting with the streptavidin-horseradish peroxidase system discussed above. Thus, in one embodiment, biotin is utilized. The biotinylated antibody is in turn reacted with streptavidin-horseradish peroxidase complex. Orthophenylenediamine, 4-chloro-naphthol, tetramethylbenzidine (TMB), ABTS, BTS or ASA can be used for chromogenic detection.

[0194] In one immunoassay format for practicing this invention, a forward sandwich assay is used in which the capture reagent has been immobilized, using conventional techniques, on the surface of a support. Suitable supports used in assays include synthetic polymer supports, such as polypropylene, polystyrene, substituted polystyrene, e.g.,

aminated or carboxylated polystyrene, polyacrylamides, polyamides, polyvinylchloride, glass beads, agarose, or nitrocellulose.

[0195] IV. Anti-LOX Antibodies and Anti-LOXL2 Antibodies

[0196] Provided herein are antibodies that can be used to diagnose angiogenesis and associated diseases, fibrosis and associated diseases, tumors or metastasis. Provided herein are antibodies that inhibit angiogenesis and associated diseases, inhibit fibrosis and associated diseases, and treat tumors or metastasis. Provided herein are antibodies that can be used to monitor efficacy of treatment regimens and protocols and the like as described throughout the present application and known in the art. Antibodies and antigen binding fragments useful in such methods are those, for example, that specifically bind LOX or LOXL2.

[0197] The disclosure also describes cell lines which produce the antibodies or functional fragments thereof, methods for producing the cell lines, and methods for producing the antibodies or functional fragments thereof.

[0198] The term “antibody” or “antibody molecule” in the various grammatical forms is used herein as a collective noun that refers to a population of immunoglobulin molecules and/or immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antibody combining site or paratope. Thus, reference to an “antibody” also includes reference to any of the antigen binding fragments of antibodies.

[0199] As used herein, “immunoreactive” refers to antibodies or fragments thereof that are specific to a sequence of amino acid residues (“binding site” or “epitope”), yet if are cross-reactive to other peptides/proteins, are not toxic at the levels at which they are formulated for administration to human use. “Epitope” refers to that portion of an antigen capable of forming a binding interaction with an antibody or antigen binding fragment thereof. Such binding interaction can be manifested as an intermolecular contact with one or more amino acid residues of a CDR. Antigen binding can involve a CDR3 or a CDR3 pair. An epitope can be a linear peptide sequence (i.e., “continuous”) or can be composed of noncontiguous amino acid sequences (i.e., “conformational” or “discontinuous”). The term “preferentially binds” means that the binding agent binds to the binding site with greater affinity than it binds unrelated amino acid sequences.

[0200] As used herein, the term “affinity” refers to the equilibrium constant for the reversible binding of two agents and is expressed as a dissociation constant (K_d). Affinity can be at least 1-fold greater, at least 2-fold greater, at least 3-fold greater, at least 4-fold greater, at least 5-fold greater, at least 6-fold greater, at least 7-fold greater, at least 8-fold greater, at least 9-fold greater, at least 10-fold greater, at least 20-fold greater, at least 30-fold greater, at least 40-fold greater, at least 50-fold greater, at least 60-fold greater, at least 70-fold greater, at least 80-fold greater, at least 90-fold greater, at least 100-fold greater, or at least 1000-fold greater, or more, than the affinity of an antibody for unrelated amino acid sequences. Affinity of an antibody to a target protein can be, for example, from about 100 nanomolar (nM) to about 0.1 nM, from about 100 nM to about 1 picomolar (pM), or from about 100 nM to about 1 femtomolar (fM) or more. As used herein, the term “avidity” refers to the resistance of a complex of two or more agents to dissociation after dilution. The terms

“immunoreactive” and “preferentially binds” are used interchangeably herein with respect to antibodies and/or antigen-binding fragments.

[0201] The term “antibody” also includes molecules which have been engineered through the use of molecular biological technique to include only portions of the native molecule as long as those molecules have the ability to bind a particular antigen or sequence of amino acids with the required specificity. Such alternative antibody molecules include classically known portions of the antibody molecules, single chain antibodies, and single chain binding molecules.

[0202] An “antibody combining site” is that structural portion of an antibody molecule comprised of heavy and light chain variable and hypervariable regions that specifically binds antigen.

[0203] As used herein, the term “CDR” or “complementarity determining region” is intended to mean the non-contiguous antigen combining sites found within the variable region of both heavy and light chain polypeptides. These particular regions have been described by Kabat et al., *J. Biol. Chem.* 252:6609-6616 (1977); Kabat et al., U.S. Dept. of Health and Human Services, “Sequences of proteins of immunological interest” (1991); by Chothia et al., *J. Mol. Biol.* 196:901-917 (1987); and MacCallum et al., *J. Mol. Biol.* 262:732-745 (1996), where the definitions include overlapping or subsets of amino acid residues when compared against each other. Nevertheless, application of either definition to refer to a CDR of an antibody or grafted antibodies or variants thereof is intended to be within the scope of the term as defined and used herein. The amino acid residues which encompass the CDRs as defined by each of the above cited references are set forth below in Table 1 as a comparison.

TABLE 1

	CDR Definitions		
	Kabat ¹	Chothia ²	MacCallum ³
V _H CDR1	31-35	26-32	30-35
V _H CDR2	50-65	53-55	47-58
V _H CDR3	95-102	96-101	93-101
V _L CDR1	24-34	26-32	30-36
V _L CDR2	50-56	50-52	46-55
V _L CDR3	89-97	91-96	89-96

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

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

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

[0204] As used herein, the term “framework” when used in reference to an antibody variable region is intended to mean all amino acid residues outside the CDR regions within the variable region of an antibody. A variable region framework is generally a discontinuous amino acid sequence between about 100-120 amino acids in length but is intended to reference only those amino acids outside of the CDRs. As used herein, the term “framework region” is intended to mean each domain of the framework that is separated by the CDRs.

[0205] “An inhibitor of LOX activity” or “an inhibitor of LOXL2 activity” can be an antibody or an antigen binding fragment thereof that directly or indirectly inhibits activity of lysyl oxidase, including but not limited to gene expression, post-translation modification, enzymatic processing or cleavage, binding to a modulator of LOX/LOXL2, enzymatic activity of LOX/LOXL2 or any other activity described herein.

[0206] As used herein, the term “antibody” refers to an isolated or recombinant binding agent that comprises the necessary variable region sequences to specifically bind an antigenic epitope. Therefore, an antibody is any form of antibody or fragment thereof that exhibits the desired biological activity, e.g., binding the specific target antigen. Thus, it is used in the broadest sense and specifically covers monoclonal antibodies (including full length monoclonal antibodies), polyclonal antibodies, human antibodies, humanized antibodies, chimeric antibodies, diabodies, multispecific antibodies (e.g., bispecific antibodies), and antibody fragments including but not limited to single chain binding polypeptides, VH, VL, Fv, scFv, Fab, and Fab2, etc., so long as they exhibit the desired biological activity. The term “human antibody” therefore refers to antibodies containing sequences of human origin, except for possible non-human CDR regions, and does not imply that the full structure of an Ig molecule be present, only that the antibody has minimal immunogenicity in a human.

[0207] The term “binding” refers to a direct association between two molecules, due to, for example, covalent, electrostatic, hydrophobic, and ionic and/or hydrogen-bond interactions, including interactions such as salt bridges and water bridges. The term “specific binding” is applicable to a situation in which an antibody or antigen binding fragment thereof does not show any significant binding to molecules other than its epitope. In one embodiment, an antibody or antigen binding fragment thereof specifically binds to a human LOX or to human LOXL2 with a dissociation constant K_d equal to or lower than about 100 nM, lower than about 10 nM, lower than about 1 nM, lower than about 0.5 nM, lower than about 0.1 nM, lower than about 0.01 nM, or lower than about 0.005 nM measured at a temperature of about 4° C., 25° C., 37° C. or 42° C.

[0208] Conventional methods can be used to prepare antibodies. For example, by using a peptide or full length lysyl oxidase protein, polyclonal antisera or monoclonal antibodies can be made using standard methods. A mammal, (e.g., a mouse, hamster, or rabbit) can be immunized with an immunogenic form of the peptide that elicits an antibody response in the mammal. Techniques for conferring enhanced immunogenicity on a peptide include conjugation to carriers or other techniques well known in the art. For example, the protein or peptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassay procedures can be used with the immunogen as antigen to assess the levels of antibodies. Following immunization, antisera can be obtained and, if desired, polyclonal antibodies isolated from the sera.

[0209] The antibodies can be generated in cell culture, in phage, or in various animals, including but not limited to cows, rabbits, goats, mice, rats, hamsters, guinea pigs, sheep, dogs, cats, monkeys, chimpanzees, apes. Therefore, an antibody useful in the present methods is typically a mammalian antibody. Phage techniques can be used to isolate an initial antibody or to generate variants with altered specificity or avidity characteristics. Such techniques are routine and well known in the art. In one embodiment, the antibody is produced by recombinant means known in the art. For example, a recombinant antibody can be produced by transfecting a host cell with a vector comprising a DNA sequence encoding the antibody. One or more vectors can be used to transfect the DNA sequence expressing at least one VL and one VH region

in the host cell. Exemplary descriptions of recombinant means of antibody generation and production include Delves, *Antibody Production: Essential Techniques* (Wiley, 1997); Shephard, et al., *Monoclonal Antibodies* (Oxford University Press, 2000); and Goding, *Monoclonal Antibodies: Principles and Practice* (Academic Press, 1993).

[0210] Antibodies also can be made according to the protocol described by Kenney, et al. ("Production of monoclonal antibodies using a secretion capture report web." *Biotechnology* 13:787-790, 1995). Briefly, mice are injected subcutaneously (s.c.), with antigen in an adjuvant formulation. For peptide antigens, peptides are conjugated to bovine serum albumin and formulated in Freund's Adjuvant (FA) prior to immunization. For protein antigens, the protein is formulated in Alhydrogel-Muramyl Dipeptide (ALD/MDP) adjuvant. Cells from the spleen and lymph nodes of the mice are isolated and fused with appropriate cells and cultured. A hybridoma library of HAT-selected cells is isolated and is cloned. Cells are sorted and sera and supernatants are screened for the presence of antibodies.

[0211] "Antibody fragments" comprise a portion of an intact antibody, and can include the antigen binding or variable region of an intact antibody. Examples of antibody fragments include Fab, Fab', F(ab')₂, Fv fragments, scFv fragments, diabodies, linear antibodies (Zapata et al., *Protein Eng.* 8(10): 1057-1062 (1995)), single-chain antibody molecules, single chain binding polypeptides, and multispecific antibodies formed from antibody fragments. Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an F(ab')₂ fragment that has two antigen combining sites and is still capable of cross-linking antigen.

[0212] A "single chain binding polypeptide" refers to a polypeptide having a heavy chain variable region, a light chain variable region and, optionally, an immunoglobulin Fc region. Such a molecule is a single chain variable fragment optionally having effector function through the presence of the immunoglobulin Fc region. Methods of preparing single chain binding polypeptides are known in the art (e.g., US Patent Application 2005/0238646).

[0213] "Fv" refers to an antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0214] A "Fab" fragment contains a "Fv" and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. F(ab')₂ antibody fragments originally were produced as pairs of Fab

fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

[0215] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

[0216] Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these can be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA1, and IgA2. The heavy-chain constant domains (Fc) that correspond to the different classes of immunoglobulins are called α , δ , ϵ , γ , and μ , respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known.

[0217] The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa or ("k") and lambda or ("λ"), based on the amino acid sequences of their constant domains.

[0218] "Single-chain Fv" or "sFv" antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. A Fv polypeptide can further include, if needed, a polypeptide linker between the VH and VL domains, which enables the sFv to form a desired structure for antigen binding. For a review of sFv, see Pluckthun in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenberg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

[0219] The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments contain a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., *Proc. Natl. Acad. Sci. USA*, 90:6444-6448 (1993).

[0220] An antibody can also be a bispecific antibody. Bispecific antibodies are monoclonal, chimeric, human or humanized antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is, for example, LOX or LOXL2, the other one is for any other antigen, such as, for example, a cell-surface protein or receptor or receptor subunit. In addition to embodiments, a bispecific antibody is specific for LOX and LOXL2.

[0221] Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities (Milstein and Cuellar, *Nature*, 305:537-539 (1983)). Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Trautner et al., *EMBO J.*, 10:3655-3659 (1991).

[0222] Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences using conventional methods known in the art. The fusion is, generally, with an immunoglobulin heavy-chain constant domain, containing at least part of the hinge, CH2, and CH3 regions. In one embodiment, the first heavy-chain constant region (CH1) containing the site necessary for light-chain binding is present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, can be inserted into separate expression vectors, and can be co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., *Methods in Enzymology*, 121:210 (1986).

[0223] According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers that are recovered from recombinant cell culture. The interface can comprise at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g., tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g., alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

[0224] Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g., F(ab')₂ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan et al., *Science* 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate F(ab')₂ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

[0225] Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby et al., *J. Exp. Med.* 175:217-225 (1992) describe the production of a fully humanized bispecific antibody F(ab')₂ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling in vitro to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells over-expressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

[0226] Various techniques for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny et al., *J. Immunol.* 148(5):1547-1553 (1992). The leucine zipper

peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) by a linker that is too short to allow pairing between the two domains on the same chain. Accordingly, the VH and VL domains of one fragment are forced to pair with the complementary VL and VH domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber et al., *J. Immunol.* 152:5368 (1994).

[0227] Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt et al., *J. Immunol.* 147:60 (1991).

[0228] Exemplary bispecific antibodies may bind to two different epitopes on a given LOX or LOXL2 polypeptide herein. Alternatively, an anti-LOX or anti-LOXL2 polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g., CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing a particular target polypeptide. Bispecific antibodies can also be used to localize cytotoxic agents to cells that express a particular target polypeptide. These antibodies possess a target binding arm and an arm that binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the target polypeptide and further binds tissue factor (TF).

[0229] The anti-LOX antibody or anti-LOXL2 antibody can also be a heteroconjugate antibody. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells (U.S. Pat. No. 4,676,980) and for treatment of HIV infection (WO 91/00360 and WO 92/200373). Antibodies can be prepared in vitro using known methods in synthetic protein chemistry, including those involving cross-linking agents. For example, immunotoxins can be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include, but are not limited to, iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Pat. No. 4,676,980.

[0230] It may be desirable to modify an anti-LOX antibody or anti-LOXL2 antibody with respect to effector function, so as to enhance, e.g., the effectiveness of the antibody in treating or preventing cancer metastasis. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated can have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron et al., *J. Exp. Med.*, 176: 1191-1195 (1992) and Shopes, *J. Immunol.*, 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity can also be prepared using heterobifunctional cross-

linkers as described in Wolff et al. *Cancer Research*, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson et al., *Anti-Cancer Drug Design*, 3: 219-230 (1989).

[0231] An “isolated antibody” is one that has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials that would interfere with diagnostic or therapeutic uses for the antibody, and can include, for example, enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In one embodiment, an antibody will be purified (1) to greater than 80%, 85%, 90%, 95%, or 99% by weight of antibody as determined by the Lowry method, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, and/or (3) to homogeneity by SDS-PAGE under reducing or non-reducing conditions using Coomassie blue or silver stain. The term “isolated antibody” includes within its scope an antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Generally, isolation of an antibody or antigen binding fragment thereof will include at least one purification step.

[0232] An antibody can be a humanized antibody or a human antibody. Humanized forms of non-human (e.g., murine) antibodies include, for example, chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, scFv, Fab, Fab', F(ab')₂, single chain binding polypeptide, VH, VL, or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Chimeric antibodies include those in which the heavy and light chain variable regions are combined with human constant regions (Fc). Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues that are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of, the FR regions are those of a human immunoglobulin consensus sequence.

[0233] A humanized antibody can also contain at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin (Jones et al., *Nature*, 321: 522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992)).

[0234] Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source that is non-human. These non-human amino acid residues are often referred to as “import” or “donor” residues, which are typically taken from an “import” or “donor” variable domain. Humanization can be essentially performed following the method of Winter and co-workers (Jones et al.,

Nature, 321:522-525 (1986); Riechmann et al., *Nature*, 332: 323-327 (1988)); Verhoeven et al. *Science*, 239:1534-1536 (1988)), by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such “humanized” antibodies include chimeric antibodies (U.S. Pat. No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

[0235] Human antibodies can also be produced using various techniques known in the art, including phage display libraries (Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)). The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)). Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Pat. Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-813 (1994); Fishwald et al., *Nature Biotechnology* 14, 845-851 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

[0236] Murine monoclonal antibodies have been developed that bind LOX or LOXL2 and block the enzymatic activity thereof. Humanized antibodies and antigen-binding fragments thereof described herein are created by humanization of the VL and VH sequences of the murine monoclonal anti-LOX and anti-LOXL2 antibodies.

[0237] Humanized immunoglobulins, including humanized antibodies, have been constructed by means of genetic engineering. Most humanized immunoglobulins that have been previously described have comprised a framework that is identical to the framework of a particular human immunoglobulin chain (i.e., an acceptor or recipient), and three CDRs from a non-human (donor) immunoglobulin chain. As described herein, humanization can also include criteria by which a limited number of amino acids in the framework of a humanized immunoglobulin chain are identified and chosen to be the same as the amino acids at those positions in the donor rather than in the acceptor, in order to increase the affinity of an antibody comprising the humanized immunoglobulin chain.

[0238] The present invention is based in part on the model that two contributing causes of the loss of affinity in prior means of producing humanized antibodies (using as examples mouse antibodies as the source of CDRs) are: (1) when the mouse CDRs are combined with a human framework, the amino acids in the frameworks close to the CDRs become human instead of mouse. Without intending to be bound by theory, these changed amino acids may slightly distort the CDRs (e.g., they may create different electrostatic

or hydrophobic forces than in the donor mouse antibody, and the distorted-CDRs may not make as effective contacts with the antigen as the CDRs did in the donor antibody); (2) also, amino acids in the original mouse antibody that are close to, but not part of, the CDRs (i.e., still part of the framework), may make contacts with the antigen that contribute to affinity. These amino acids are lost when the antibody is humanized because, generally, all framework amino acids are made human. To circumvent these issues, and to produce humanized antibodies that have a very strong affinity for a desired antigen, humanized antibodies and antigen-binding fragments thereof can be constructed using one or more of the following principles.

[0239] One principle is that as acceptor, a framework is used from a particular human immunoglobulin that is unusually homologous to the donor immunoglobulin to be humanized, or use a consensus framework from many human antibodies is used as an acceptor. For example, comparison of the sequence of a mouse heavy (or light) chain variable region against human heavy (or light) variable regions in a data bank (for example, the National Biomedical Research Foundation Protein Identification Resource or the protein sequence database of the National Center for Biotechnology Information—NCBI) shows that the extent of homology to different human regions can vary greatly, for example from about 40% to about 60%, about 70%, about 80%, or higher. By choosing as the acceptor immunoglobulin one of the human heavy chain variable regions that is most homologous to the heavy chain variable region of the donor immunoglobulin, fewer amino acids will be changed in going from the donor immunoglobulin to the humanized immunoglobulin. By choosing as the acceptor immunoglobulin one of the human light chain variable regions that is most homologous to the light chain variable region of the donor immunoglobulin, fewer amino acids will be changed in going from the donor immunoglobulin to the humanized immunoglobulin. Generally, using such techniques, there is a reduced chance of changing an amino acid near one or more of the CDRs that distorts their conformation. Moreover, the precise overall shape of a humanized antibody comprising the humanized immunoglobulin chain may more closely resemble the shape of the donor antibody, thereby also reducing the chance of distorting the CDRS.

[0240] One can also use light and heavy chains from the same human antibody as acceptor sequences, to improve the likelihood that the humanized light and heavy chains will make favorable contacts with each other. Alternatively, one can also use light and heavy chains from different human antibody germline sequences as acceptor sequences; when such combinations are used, one can readily determine whether the VH and VL bind an epitope of interest using conventional assays (e.g., an ELISA). In one example, the human antibody will be chosen in which the light and heavy chain variable regions sequences, taken together, are overall most homologous to the donor light and heavy chain variable region sequences. Sometimes greater weight will be given to the heavy chain sequence. Regardless of how the acceptor immunoglobulin is chosen, higher affinity can, in some cases, be achieved by selecting a small number of amino acids in the framework of the humanized immunoglobulin chain to be the same as the amino acids at those positions in the donor rather than in the acceptor. Methods of affinity maturation are known in the art.

[0241] Humanized antibodies generally have at least three potential advantages over mouse or chimeric antibodies for

use in human therapy. Because the effector portion of an antibody is human, it is believed to interact better with the other parts of the human immune system (e.g., destroy the target cells more efficiently by complement-dependent cytotoxicity (CDC) or antibody-dependent cellular cytotoxicity (ADCC)). Additionally, the human immune system should not recognize the framework or constant region of the humanized antibody as foreign, and therefore the antibody response against such an injected antibody should be less than against a totally foreign mouse antibody or a partially foreign chimeric antibody. Finally, mouse antibodies are known to have a half-life in the human circulation that is much shorter than the half-life of human antibodies. Humanized antibodies can, presumably, have a half-life more similar to naturally-occurring human antibodies, allowing smaller and less frequent doses to be given.

[0242] Humanization of antibodies and antigen-binding fragments thereof, can be accomplished via a variety of methods known in the art and described herein. Similarly, production of humanized antibodies can also be accomplished via methods known in the art and described herein.

[0243] Methods for modifications of framework regions are known in the art and are contemplated herein. Selection of one or more relevant framework amino acid positions to be altered depends on a variety of criteria. One criterion for selecting relevant framework amino acids to change can be the relative differences in amino acid framework residues between the donor and acceptor molecules. Selection of relevant framework positions to alter using this approach has the advantage of avoiding any subjective bias in residue determination or any bias in CDR binding affinity contribution by the residue.

[0244] Another criterion that can be used for determining the relevant amino acid positions to change can be, for example, selection of framework residues that are known to be important or to contribute to CDR conformation. For example, canonical framework residues are important for CDR conformation and/or structure. Targeting of a canonical framework residue as a relevant position to change can be used to identify a more compatible amino acid residue in context with its associated donor CDR sequence.

[0245] The frequency of an amino acid residue at a particular framework position is another criterion which can be used for selecting relevant framework amino acid positions to change. For example, comparison of the selected framework with other framework sequences within its subfamily can reveal residues that occur at minor frequencies at a particular position or positions. Positions harboring less abundant residues are similarly applicable for selection as a position to alter in the acceptor variable region framework.

[0246] The relevant amino acid positions to change also can be selected, for example, based on proximity to a CDR. In certain contexts, FR residues can participate in CDR conformation and/or antigen binding. Moreover, this criterion can similarly be used to prioritize relevant positions selected by other criteria described herein. Therefore, differentiating between residues proximal and distal to one or more CDRs represents one way to reduce the number of relevant positions to change.

[0247] Other criteria for selecting relevant amino acid framework positions to alter include, for example, residues that are known or predicted to reside in a three dimensional space near the antigen-CDR interface or predicted to modulate CDR activity. Similarly, framework residues that are

known to, or predicted to, form contacts between the heavy (V_H) and light (V_L) chain variable region interface can be selected. Such framework positions can affect the conformation and/or affinity of a CDR by modulating the CDR binding pocket, antigen (epitope) interaction or the V_H and V_L interaction. Therefore, selection of these amino acid positions for constructing a diverse population for screening of binding activity can be used to identify framework changes which replace residues having detrimental effects on CDR conformation or compensate for detrimental effects of residues occurring elsewhere in the framework.

[0248] Other framework residues that can be selected for alteration include amino acid positions that are inaccessible to solvent. Such residues are generally buried in the variable region and are, therefore, capable of influencing the conformation of the CDR or V_H and V_L interactions. Solvent accessibility can be predicted, for example, from the relative hydrophobicity of the environment created by the amino acid side chains of the polypeptide and/or by known three-dimensional structural data.

[0249] Following selection of relevant amino acid positions in the donor CDRs, as well as any relevant amino acid positions in the framework regions desired to be varied, amino acid changes at some or all of the selected positions can be incorporated into encoding nucleic acids for the acceptor variable region framework and donor CDRs. Altered framework or CDR sequences can be individually made and tested, or can be sequentially or simultaneously combined and tested.

[0250] The variability at any or all of the altered positions can range from a few to a plurality of different amino acid residues, including all twenty naturally occurring amino acids or functional equivalents and analogues thereof. In some cases, non-naturally occurring amino acids may also be considered and are known in the art.

[0251] Selection of the number and location of the amino acid positions to vary is flexible and can depend on the intended use and desired efficiency for identification of the altered variable region having a desirable activity such as substantially the same or greater binding affinity compared to the donor variable region. In this regard, the greater the number of changes that are incorporated into an altered variable region population, the more efficient it is to identify at least one species that exhibits a desirable activity, for example, substantially the same or greater binding affinity as the donor. Alternatively, where the user has empirical or actual data to the affect that certain amino acid residues or positions contribute disproportionately to binding affinity, then it can be desirable to produce a limited population of altered variable regions which focuses on changes within or around those identified residues or positions.

[0252] For example, if CDR grafted variable regions are desired, a large, diverse population of altered variable regions can include all the non-identical framework region positions between the donor and acceptor framework and all single CDR amino acid position changes. Alternatively, a population of intermediate diversity can include subsets, for example, of only the proximal non-identical framework positions to be incorporated together with all single CDR amino acid position changes to, for example, increase affinity of the humanized antibodies or antigen binding fragments. The diversity of the above populations can be further increased by, for example, additionally including all pair-wise CDR amino acid position changes. In contrast, populations focusing on

predetermined residues or positions which incorporate variant residues at as few as one framework and/or one CDR amino acid position can similarly be constructed for screening and identification of an altered antibody variable region. As with the above populations, the diversity of such focused populations can be further increased by additionally expanding the positions selected for change to include other relevant positions in either or both of the framework and CDR regions. There are numerous other combinations ranging from few changes to many changes in either or both of the framework regions and CDRs that can additionally be employed, all of which will result in a population of altered variable regions that can be screened for the identification of at least one CDR grafted altered variable region having desired activity, for example, binding activity to LOX/LOXL2. Those skilled in the art will know, or can determine, which selected residue positions in the framework or donor CDRs, or subsets thereof, can be varied to produce a population for screening and identification of an altered antibody of the invention given the teachings and guidance provided herein. Codons encoding amino acids are known in the art.

[0253] Humanized antibodies and antigen-binding fragments can be made using conventional techniques known in the art. In addition, recombinantly prepared antibodies can often be produced in large quantities, particularly when utilizing high level expression vectors.

[0254] Antibodies can be sequenced using conventional techniques known in the art and the amino acid sequences of the complementarity determining regions (CDRs) determined. In one aspect, the amino acid sequences of one or more of the CDRs is inserted into a synthetic sequence of, for example, a human antibody (or antigen-binding fragment thereof) framework to create a human antibody that could limit adverse side reactions of treating a human patient with a non-human antibody. The amino acid sequences of one or more of the CDRs can also be inserted into a synthetic sequence of, for example, into a binding protein such as an Avimer™ to create a construct for administration to a human patient. Such techniques can be modified depending on the species of animal to be treated. For example, for veterinary uses, an antibody, antigen-binding fragment or binding protein can be synthesized for administration of a primate, a cow, a horse, etc.

[0255] In another aspect, using art-recognized techniques such as those provided and incorporated herein, nucleotides encoding amino acid sequences of one or more of the CDRs can be inserted, for example, by recombinant techniques in restriction endonuclease sites of an existing polynucleotide that encodes an antibody, antigen-binding fragment or binding protein.

[0256] For high level production, the most widely used mammalian expression system is one which utilizes the gene amplification procedure offered by dihydrofolate reductase deficient ("dhfr-") Chinese hamster ovary cells. The system is well known to the skilled artisan. The system is based upon the dihydrofolate reductase "dhfr" gene, which encodes the DHFR enzyme, which catalyzes conversion of dihydrofolate to tetrahydrofolate. In order to achieve high production, dhfr-CHO cells are transfected with an expression vector containing a functional dhfr gene, together with a gene that encodes a desired protein. In this case, the desired protein is recombinant antibody heavy chain and/or light chain.

[0257] By increasing the amount of the competitive DHFR inhibitor methotrexate (MTX), the recombinant cells develop

resistance by amplifying the dhfr gene. In standard cases, the amplification unit employed is much larger than the size of the dhfr gene, and as a result the antibody heavy chain is co-amplified.

[0258] When large scale production of the protein, such as the antibody chain, is desired, both the expression level and the stability of the cells being employed are taken into account. In long term culture, recombinant CHO cell populations lose homogeneity with respect to their specific antibody productivity during amplification, even though they derive from a single, parental clone.

[0259] The present application provides an isolated polynucleotide (nucleic acid) encoding an antibody or antigen-binding fragment as described herein, vectors containing such polynucleotides, and host cells and expression systems for transcribing and translating such polynucleotides into polypeptides.

[0260] The present application also provides constructs in the form of plasmids, vectors, transcription or expression cassettes which comprise at least one polynucleotide as above.

[0261] The present application also provides a recombinant host cell which comprises one or more constructs as above. A nucleic acid encoding any antibody or antigen-binding fragments thereof described herein as provided itself forms an aspect of the present application, as does a method of production of the antibody or antigen-binding fragments thereof described herein which method comprises expression from encoding nucleic acid therefrom. Expression can conveniently be achieved by culturing under appropriate conditions recombinant host cells containing the nucleic acid. Following production by expression, an antibody or antigen-binding fragment can be isolated and/or purified using any suitable technique, then used as appropriate.

[0262] Specific antibodies, antigen-binding fragments, and encoding nucleic acid molecules and vectors described herein can be provided isolated and/or purified, e.g., from their natural environment, in substantially pure or homogeneous form, or, in the case of nucleic acid, free or substantially free of nucleic acid or genes origin other than the sequence encoding a polypeptide with the required function. Nucleic acid can comprise DNA or RNA and can be wholly or partially synthetic.

[0263] Systems for cloning and expression of a polypeptide in a variety of different host cells are well known. Suitable host cells include bacteria, mammalian cells, yeast and baculovirus systems. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary cells, HeLa cells, baby hamster kidney cells, NSO mouse melanoma cells and many others. A common bacterial host is *E. coli*.

[0264] The expression of antibodies and antibody fragments in prokaryotic cells such as *E. coli* is well established in the art. For a review, see for example Plückthun, A. *Bio/Technology* 9: 545-551 (1991). Expression in eukaryotic cells in culture is also available to those skilled in the art as an option for production of the antibodies and antigen-binding fragments described herein, see for recent reviews, for example Raff, M. E. (1993) *Curr. Opin. Biotech.* 4: 573-576; Trill J. J. et al. (1995) *Curr. Opin. Biotech.* 6: 553-560, each of which is incorporated herein by reference in its entirety.

[0265] Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter

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

[0266] Thus, a further aspect provides a host cell containing nucleic acid as disclosed herein. A still further aspect provides a method comprising introducing such nucleic acid into a host cell. The introduction can employ any available technique. For eukaryotic cells, suitable techniques can include, for example, calcium phosphate transfection, DEAE Dextran, electroporation, biolistics, liposome-mediated transfection and transduction using retrovirus or other virus, e.g., vaccinia or, for insect cells, baculovirus. For bacterial cells, suitable techniques can include, for example, calcium chloride transformation, electroporation and transfection using bacteriophage.

[0267] The introduction can be followed by causing or allowing expression from the nucleic acid, e.g. by culturing host cells under conditions for expression of the gene.

[0268] In one embodiment, the nucleic acid is integrated into the genome (e.g. chromosome) of the host cell. Integration can be promoted by inclusion of sequences which promote recombination with the genome, in accordance with standard techniques.

[0269] The present application also provides a method which comprises using a construct as stated above in an expression system in order to express the antibodies or antigen-binding fragments thereof as above.

[0270] The present application also relates to isolated nucleic acids, such as recombinant DNA molecules or cloned genes, or degenerate variants thereof, mutants, analogs, or fragments thereof, which encode an antibody or antigen-binding sequence that binds LOX or LOXL2 described herein.

[0271] In one aspect, the present application provides a nucleic acid which codes for an antibody or antigen-binding fragment thereof which binds LOX or LOXL2 as described herein.

[0272] In a further embodiment, the full DNA sequence of the recombinant DNA molecule or cloned gene of an antibody or antigen-binding fragment described herein can be operatively linked to an expression control sequence which can be introduced into an appropriate host. The application accordingly extends to unicellular hosts transformed with the cloned gene or recombinant DNA molecule comprising a DNA sequence encoding the V_H and/or V_L , or portions thereof, of the antibody.

[0273] Another feature is the expression of the DNA sequences disclosed herein. As is well known in the art, DNA sequences can be expressed by operatively linking them to an expression control sequence in an appropriate expression vector and employing that expression vector to transform an appropriate unicellular host.

[0274] Such operative linking of a DNA sequence to an expression control sequence, of course, includes, if not already part of the DNA sequence, the provision of an initiation codon, ATG, in the correct reading frame upstream of the DNA sequence.

[0275] Polynucleotides and vectors can be provided in an isolated and/or a purified form (e.g., free or substantially free of polynucleotides of origin other than the polynucleotide encoding a polypeptide with the required function). As used herein, "substantially pure" and "substantially free," refer to a solution or suspension containing less than, for example, 20% or less extraneous material, 10% or less extraneous material, 5% or less extraneous material, 4% or less extraneous material, 3% or less extraneous material, 2% or less extraneous material, or 1% or less extraneous material.

[0276] A wide variety of host/expression vector combinations can be employed in expressing the DNA sequences of this invention. Useful expression vectors, for example, can consist of segments of chromosomal, non-chromosomal and synthetic DNA sequences. Suitable vectors include derivatives of SV40 and known bacterial plasmids, e.g., *E. coli* plasmids col El, Per1, Pbr322, Pmb9 and their derivatives, plasmids such as RP4; phage DNAs, e.g., the numerous derivatives of phage λ , e.g., NM989, and other phage DNA, e.g., M13 and filamentous single stranded phage DNA; yeast plasmids such as the 2 μ plasmid or derivatives thereof; vectors useful in eukaryotic cells, such as vectors useful in insect or mammalian cells; vectors derived from combinations of plasmids and phage DNAs, such as plasmids that have been modified to employ phage DNA or other expression control sequences; and the like.

[0277] Also provided herein is a recombinant host cell which comprises one or more polynucleotide constructs. A polynucleotide encoding an antibody or antigen-binding fragment as provided herein forms an aspect of the present application, as does a method of production of the antibody or antigen-binding fragment which method comprises expression from the polynucleotide. Expression can be achieved, for example, by culturing under appropriate conditions recombinant host cells containing the polynucleotide. An antibody or antigen-binding fragment can then be isolated and/or purified using any suitable technique, and used as appropriate.

[0278] Any of a wide variety of expression control sequences—sequences that control the expression of a DNA sequence operatively linked to it—can be used in these vectors to express the DNA sequences. Such useful expression control sequences include, for example, the early or late promoters of SV40, CMV, vaccinia, polyoma or adenovirus, the lac system, the trp system, the TAC system, the TRC system, the LTR system, the major operator and promoter regions of phage λ , the control regions of fd coat protein, the promoter for 3-phosphoglycerate kinase or other glycolytic enzymes, the promoters of acid phosphatase (e.g., Pho5), the promoters of the yeast α -mating factors, and other sequences known to control the expression of genes of prokaryotic or eukaryotic cells or their viruses, and various combinations thereof.

[0279] Systems for cloning and expression of a polypeptide in a variety of different host cells are well known. Suitable host cells include bacteria, mammalian cells, yeast and baculovirus systems. Mammalian cell lines available in the art for expression of a heterologous polypeptide include Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney cells, NSO mouse melanoma cells and many others. A common, bacterial host can be, for example, *E. coli*.

[0280] The expression of antibodies or antigen-binding fragments in prokaryotic cells, such as *E. coli*, is well established in the art. For a review, see for example Plückthun, A. Bio/Technology 9: 545-551 (1991). Expression in eukaryotic cells in culture is also available to those skilled in the art (Raff, M. E. (1993) Curr. Opinion Biotech. 4: 573-576; Trill J. J. et al. (1995) Curr. Opinion Biotech 6: 553-560).

[0281] A wide variety of unicellular host cells are also useful in expressing the DNA sequences. These hosts include well-known eukaryotic and prokaryotic hosts, such as strains of *E. coli*, *Pseudomonas*, *Bacillus*, *Streptomyces*, fungi such as yeasts, and animal cells, such as CHO, YB/20, NSO, SP2/0, R1.1, B-W and L-M cells, African Green Monkey kidney cells (e.g., COS 1, COS 7, BSC1, BSC40, and BMT10), insect cells (e.g., Sf9), and human cells and plant cells in tissue culture.

[0282] It will be understood that not all vectors, expression control sequences and hosts will function equally well to express the DNA sequences. Neither will all hosts function equally well with the same expression system. However, one skilled in the art will be able to select the proper vectors, expression control sequences, and hosts without undue experimentation to accomplish the desired expression without departing from the scope of this application. For example, in selecting a vector, the host must be considered because the vector must function in it. The vector's copy number, the ability to control that copy number, and the expression of any other proteins encoded by the vector, such as antibiotic markers, will also be considered. One of ordinary skill in the art can select the proper vectors, expression control sequences, and hosts to accomplish the desired expression without departing from the scope of this application. For example, in selecting a vector, the host is considered because the vector functions in it. The vector's copy number, the ability to control that copy number, and the expression of any other proteins encoded by the vector, such as antibiotic markers, can also be considered.

[0283] The present application also provides constructs in the form of plasmids, vectors, transcription or expression cassettes as described elsewhere herein which comprise at least one polynucleotide as above. Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator sequences, polyadenylation sequences, enhancer sequences, selectable markers and other sequences as appropriate. Vectors can be plasmids, viral e.g., phage, phagemid, etc., as appropriate; For further details see, for example, Molecular Cloning: a Laboratory Manual: 2nd edition, Sambrook et al., 1989, Cold Spring Harbor Laboratory Press. Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis, sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in Short Protocols in Molecular Biology, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992. The disclosures of Sambrook et al. and Ausubel et al. are incorporated herein by reference.

[0284] In selecting an expression control sequence, a variety of factors will normally be considered. These include, for example, the relative strength of the system, its controllability, and its compatibility with the particular DNA sequence or gene to be expressed, particularly as regards potential secondary structures. Suitable unicellular hosts will be selected by consideration of, e.g., their compatibility with the chosen vector, their secretion characteristics, their ability to fold

proteins correctly, and their fermentation requirements, as well as the toxicity to the host of the product encoded by the DNA sequences to be expressed, and the ease of purification of the expression products.

[0285] A further aspect provides a host cell containing one or more polynucleotides as disclosed herein. Yet a further aspect provides a method of introducing such one or more polynucleotides into a host cell, any available technique. For eukaryotic cells, suitable techniques can include, for example, calcium phosphate transfection, DEAE Dextran, electroporation, liposome-mediated transfection and transduction using retrovirus or other virus (e.g. vaccinia) or, for insect cells, baculovirus. For bacterial cells, suitable techniques can include, for example calcium chloride transformation, electroporation and transfection using bacteriophages.

[0286] The introduction can be followed by causing or allowing expression from the one or more polynucleotides, e.g. by culturing host cells under conditions for expression of one or more polypeptides from one or more polynucleotides. Inducible systems can be used and expression induced by addition of an activator.

[0287] In one embodiment, the polynucleotides can be integrated into the genome (e.g., chromosome) of the host cell. Integration can be promoted by inclusion of sequences which promote recombination with the genome, in accordance with standard techniques. In another embodiment, the nucleic acid is maintained on an episomal vector in the host cell.

[0288] Methods are provided herein which include using a construct as stated above in an expression system in order to express a specific polypeptide.

[0289] Considering these and other factors, a person skilled in the art will be able to construct a variety of vector/expression control sequence/host combinations that will express the DNA sequences on fermentation or in large scale animal culture.

[0290] A polynucleotide encoding an antibody, antigen-binding fragment, or a binding protein can be prepared recombinantly/synthetically in addition to, or rather than, cloned. The polynucleotide can be designed with the appropriate codons for the antibody, antigen-binding fragment, or a binding protein. In general, one will select preferred codons for an intended host if the sequence will be used for expression. The complete polynucleotide can be assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge, Nature, 292:756 (1981); Nambair et al., Science, 223:1299 (1984); Jay et al., J. Biol. Chem., 259:6311 (1984).

[0291] A general method for site-specific incorporation of unnatural amino acids into proteins is described in Christopher J. Noren, Spencer J. Anthony-Cahill, Michael C. Griffith, Peter G. Schultz, Science, 244:182-188 (April 1989). This method can be used to create analogs with unnatural amino acids.

[0292] As mentioned above, a DNA sequence encoding an antibody or antigen-binding fragment thereof can be prepared synthetically rather than cloned. The DNA sequence can be designed with the appropriate codons for the antibody or antigen-binding fragment amino acid sequence. In general, one will select preferred codons for the intended host if the sequence will be used for expression. The complete sequence is assembled from overlapping oligonucleotides prepared by standard methods and assembled into a complete coding sequence. See, e.g., Edge, Nature, 292:756 (1981); Nambair et al., Science, 223:1299 (1984); Jay et al., J. Biol. Chem.,

259:6311 (1984), each of which is incorporated herein by reference in its entirety.

[0293] The term "adjuvant" refers to a compound or mixture that enhances the immune response, particularly to an antigen. An adjuvant can serve as a tissue depot that slowly releases the antigen and also as a lymphoid system activator that non-specifically enhances the immune response (Hood et al., Immunology, Second Ed., 1984, Benjamin/Cummings: Menlo Park, Calif., p. 384). Often, a primary challenge with an antigen alone, in the absence of an adjuvant, will fail to elicit a humoral or cellular immune response. Previously known and utilized adjuvants include, but are not limited to, complete Freund's adjuvant (CFA), incomplete Freund's adjuvant (IFA), saponin, mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil or hydrocarbon emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvant such as BCG (Bacille Calmette-Guerin) and *Corynebacterium parvum*. Mineral salt adjuvants include but are not limited to: aluminum hydroxide, aluminum phosphate, calcium phosphate, zinc hydroxide and calcium hydroxide. Preferably, the adjuvant composition further comprises a lipid of fat emulsion comprising about 10% (by weight) vegetable oil and about 1-2% (by weight) phospholipids. Preferably, the adjuvant composition further optionally comprises an emulsion form having oily particles dispersed in a continuous aqueous phase, having an emulsion forming polyol in an amount of from about 0.2% (by weight) to about 49% (by weight), optionally a metabolizable oil in an emulsion-forming amount of up to 15% (by weight), and optionally a glycol ether-based surfactant in an emulsion-stabilizing amount of up to about 5% (by weight).

[0294] Antibodies can also be affinity matured using known selection and/or mutagenesis methods as described above. Affinity matured antibodies can have an affinity which is two times, five times, 10 times, 20 times, 30 times or more greater than the starting antibody (generally murine, rabbit, chicken, humanized or human) from which the matured antibody is prepared. Apparent affinities can be determined by methods such as an enzyme linked immunosorbent assay (ELISA) or any other technique familiar to one of skill in the art. Avidities can be determined by methods such as a Scatchard analysis or any other technique familiar to one of skill in the art. Another technique for measuring apparent binding affinity familiar to those of skill in the art is a surface plasmon resonance technique (analyzed on a BIACORE 2000 system) (Liljeblad, et al., Glyco. J. 2000, 17:323-329). Standard measurements and traditional binding assays are described by Heeley, R. P., Endocr. Res. 2002, 28:217-229.

[0295] In one embodiment, an antibody specifically and selectively binds to the mature or active form of LOX after proteolytic processing, with a greater binding affinity (e.g., at least about 5 times, at least about 10 times, at least about 50 times, at least about 100 times, at least about 500 times, or at least about 1000 times greater), than the binding affinity to at least one of: the preproprotein of human LOX, the secreted human LOX, or other lysyl oxidase-like or lysyl oxidase-related proteins (e.g., LOXL1, LOXL2, LOXL3, and LOXL4). In one embodiment, the antibody specifically and selectively binds to LOX in unprocessed and/or processed (mature) forms. The mature form of LOX is typically active although, in some embodiments, unprocessed LOX is also active.

[0296] In another embodiment, an antibody specifically and selectively binds to the secreted form of LOX, such as a secreted human LOX after cleavage of the signal peptide, with a greater binding affinity (e.g., at least about 5 times, at least about 10 times, at least about 50 times, at least about 100 times, at least about 500 times, or at least about 1000 times greater), than the binding affinity to at least one of: the pre-protein of human LOX, the mature or active human LOX, or other lysyl oxidase-like or lysyl oxidase-related proteins (e.g., LOXL1, LOXL2, LOXL3, and LOXL4).

[0297] In yet another embodiment, an antibody specifically and selectively binds to LOXL2 with a greater binding affinity (e.g., at least about 5 times, at least about 10 times, at least about 50 times, at least about 100 times, at least about 500 times, or at least about 1000 times greater) than the binding affinity to at least one of: human LOX, the mature or active human LOX, the secreted form of LOX or other lysyl oxidase-like (LOL) or lysyl oxidase-related proteins (e.g., LOXL1, LOXL3, and LOXL4) in unprocessed, mature, active and/or secreted products. In one embodiment, the antibody specifically and selectively binds to LOXL2 in unprocessed and/or processed (mature) forms. The mature form of LOXL2 is typically active although, in some embodiments, unprocessed LOXL2 is also active.

[0298] An antibody can bind to both human LOX or human LOXL2, with a greater binding affinity (e.g., at least about 5 times, at least about 10 times, at least about 50 times, at least about 100 times, at least about 500 times, or at least about 1000 times greater), than the binding affinity to at least one of: other lysyl oxidase-like or lysyl oxidase-related proteins (e.g., LOXL1, LOXL3, and LOXL4).

[0299] Antibodies that bind to enzymes can be competitive inhibitors, uncompetitive inhibitors or non-competitive inhibitors. With respect to competitive inhibition, an inhibitor usually bears structural similarity to substrate. Inhibition will be noticeable at low substrate concentrations, but can be overcome at high substrate concentrations. With respect to uncompetitive inhibition, an inhibitor binds at site that becomes available after substrate is bound at the active site. Inhibition will be most noticeable at high substrate concentration. With respect to non-competitive inhibition, an inhibitor binds at site away from substrate binding site. Relative inhibition will generally be the same at all substrate concentrations. The mechanism of action antibodies that act as competitive inhibitors, uncompetitive inhibitors and non-competitive inhibitors is illustrated in FIG. 4. Antibodies described herein can be competitive inhibitors, uncompetitive inhibitors or non-competitive inhibitors. In one aspect, antibodies described herein can be non-competitive inhibitors.

[0300] In one aspect, antibodies described herein are non-competitive inhibitors; that is the antibodies block enzymatic activity of LOX or LOXL2 regardless of whether or not the enzymes are bound to substrate (collagen).

[0301] Binding of an antibody to LOX/LOXL2 can (1) reduce or inhibit uptake or internalization of LOX/LOXL2 (e.g., via integrin beta 1 or other cellular receptors or proteins) and/or (2) reduce or inhibit the enzymatic activity of LOX or LOXL2. It is believed that such an antibody could reduce EMT and thus is useful for the applications disclosed herein. An antibody described herein can bind to the proteolytic cleavage site of LOX or LOXL2, thereby effectively blocking (inhibiting) processing of the LOX or LOXL2 to reduce the level of active LOX or LOXL2. Such inhibition can occur

through direct binding to LOX or LOXL2 or through indirect interference including steric hindrance, enzymatic alteration of LOX or LOXL2, inhibition of transcription or translation, destabilization of mRNA transcripts, impaired export, processing, or localization of LOX or LOXL2, and the like.

[0302] Binding of LOX/LOXL2 with other proteins, such as cellular receptors (e.g., uptake receptor integrin beta1), BTK (burton agammaglobulinemia tyrosine kinase), or other integrins is also performed using the aforementioned assay, wherein instead of ECM proteins, cellular receptors (e.g., uptake receptor integrin beta1), BTK (burton agammaglobulinemia tyrosine kinase), or other integrins are used.

[0303] Those anti-LOX/LOXL2 antibodies that inhibit LOX/LOXL2 binding to ECM proteins, cellular receptors, and integrins, are selected as candidates for further development. In one embodiment, anti-LOX/LOXL2 antibodies that inhibit LOX/LOXL2 binding to ECM proteins, cellular receptors, and integrins, are non-competitive inhibitors.

[0304] In one embodiment, an antibody described herein specifically binds to the catalytic domain of LOX. This domain, in the C-terminal region, contains the elements required for catalytic activity (the copper binding site, tyrosyl and lysyl residues that contribute to the carbonyl cofactor, and 10 cysteine residues. See, Thomassin et al. "The Pro-regions of lysyl oxidase and lysyl oxidase-like 1 are required for deposition onto elastic fibers," J Biol. Chem. 2005 Dec. 30; 280(52):42848-55 for further details.

[0305] Provided herein are antibodies or antigen binding fragments thereof that bind to LOX and/or inhibit the activity of LOX. Anti-LOX antibodies and antigen binding fragments thereof that bind and/or inhibit LOX have use in the purification, diagnostic, and therapeutic methods described herein. Antibodies can bind both full-length and/or processed LOX/LOXL2.

[0306] Provided herein is an isolated antibody or antigen binding fragment thereof, comprising a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 3 and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 4 or 5.

[0307] In one aspect, provided herein is an isolated antibody or antigen binding fragment thereof, comprising a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 3. In another aspect, provided herein is an isolated antibody or antigen binding fragment thereof, comprising a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 4 or 5.

[0308] Further provided herein are antibodies or antigen binding fragments thereof, that compete with, or specifically bind to, an anti-LOX antibody or antigen binding fragment thereof described herein for binding to LOX. In one embodiment, anti-LOX antibodies described herein are non-competitive inhibitors.

[0309] Any of such antibodies or antigen binding fragments can specifically bind to LOX with a binding affinity of at least 2, 5, 10, 50, 100, 500 or 1000 times greater than to at least one of LOXL1, LOXL2, LOXL3 or LOXL4.

[0310] In one embodiment, an antibody or antigen binding fragment thereof, described herein specifically binds both full-length and processed LOX. In one aspect, both full-length and processed LOX are active forms of the enzyme.

[0311] Provided herein are antibodies or antigen binding fragments thereof that bind to LOXL2 and/or inhibit the activ-

ity of LOXL2. Anti-LOXL2 antibodies and antigen binding fragments thereof that bind and/or inhibit LOXL2 have use in the purification, diagnostic, and therapeutic methods described herein.

[0312] Provided herein is an isolated antibody or antigen binding fragment thereof, that specifically binds to an epitope having an amino acid sequence set forth as SEQ ID NO: 6. The antibody or antigen binding fragment thereof, can comprise a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1 and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2.

[0313] Also provided herein is an isolated antibody or antigen binding fragment thereof, comprising a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1, and a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2.

[0314] In one aspect, provided herein is a variable heavy chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 1. In another aspect, provided herein is a variable light chain having at least 75% amino acid sequence identity to an amino acid sequence set forth as SEQ ID NO: 2.

[0315] Further provided herein are antibodies or antigen binding fragments that compete with, or specifically bind to, any of the preceding antibodies or antigen binding fragments thereof for binding to LOXL2.

[0316] Any of such antibodies or antigen binding fragments can specifically bind to LOXL2 with a binding affinity of at least 2, 5, 10, 50, 100, 500 or 1000 times greater than to at least one of LOX, LOXL1, LOXL3 or LOXL4.

[0317] In one embodiment, an antibody or antigen binding fragment thereof, described herein specifically binds to the SRCR3-4 region of LOXL2 and, thus, binds both full-length and processed LOXL2. In one aspect, both full-length and processed LOXL2 are active forms of the enzyme. An antibody can, for example, specifically bind to an epitope having an amino acid sequence set forth as SEQ ID NO: 6. Such antibodies can serve as an uncompetitive partial inhibitor of enzymatic activity in vitro, inhibiting approximately half the enzymatic activity against a 1,5-diaminopentane substrate with an apparent IC_{50} of 20-30 nM. Such antibodies can serve as non-competitive inhibitors.

[0318] When humanizing antibodies, simultaneous incorporation of all of the FR and/or CDR encoding nucleic acids and all of the selected amino acid position changes can be accomplished by a variety of methods known to those skilled in the art, including for example, recombinant and chemical synthesis. For example, simultaneous incorporation can be accomplished by, for example, chemically synthesizing the nucleotide sequence for the acceptor variable region, fused together with the donor CDR encoding nucleic acids, and incorporating at the positions selected for harboring variable amino acid residues a plurality of corresponding amino acid codons.

[0319] Provided herein are antibodies and antigen-binding fragments thereof that bind to LOX or LOXL2. Antibodies and antigen-binding fragments thereof that bind LOX or LOXL2 can inhibit (partially or fully) or manage/treat (partially or fully) symptoms associated with and/or caused by aberrant LOX or LOXL2 expression. The application also provides cell lines which can be used to produce the antibodies,

methods for producing the cell lines, methods for expressing antibodies or antigen-binding fragments and purifying the same.

[0320] One can recognize that the antibodies and antigen-binding fragments thereof that specifically bind LOX or LOXL2 generated using the methods described herein can be tested using the assays provided herein or known in the art for the ability to bind to LOX or LOXL2 (e.g., ELISA) as well as affinity (e.g., Biacore or Surface Plasmon Resonance).

[0321] Humanized versions of anti-LOX and anti-LOXL2 antibodies have one or more of the following characteristics: retention of the inhibitory function of murine monoclonal antibodies, equivalent or increased binding affinity with a slow off rate (e.g., K_d 0.1-1 nM), binding to full length and/or processed LOX / LOXL2, non-competitive partial inhibition of enzymatic activity, equivalent or better IC_{50} (e.g., about 30 nM), inhibitory activity in cell-based migration/invasion assays, inhibition of an EMT-like change induced by secreted LOX/LOXL2 in conditioned media of tumor cells, binding to matrix-associated LOX/LOXL2 generated by live human tumor cells, cross-reactivity of binding of human LOX/LOXL2 with murine LOX/LOXL2, therapeutic effectiveness (e.g., partial or reduction in tumor size and/or symptoms), reduced toxicity and reduced immunogenicity.

[0322] Provided herein are humanized antibodies that bind to hLOX, humanized antibodies that bind to hLOX and mLOX (murine LOX), humanized antibodies that bind to hLOXL2, and humanized antibodies that bind to hLOXL2 and mLOXL2 (murine LOXL2). In one aspect, the humanized antibodies are non-competitive inhibitors.

[0323] In one embodiment, a humanized anti-LOXL2 antibody has VH chain having an amino acid sequence of SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 27 or SEQ ID NO: 28. One would understand that conservative amino acid modifications can be made using the methods described herein in one or more CDR or framework regions for affinity maturation of the antibody. Antibodies modified by such methods can be tested with respect to function using any of the assays described herein or known in the art.

[0324] In another embodiment, a humanized anti-LOXL2 antibody has VL chain having an amino acid sequence of SEQ ID NO: 30, SEQ ID NO: 31 or SEQ ID NO: 32. One would understand that conservative amino acid modifications can be made using the methods described herein in one or more CDR or framework regions for affinity maturation of the antibody. Antibodies modified by such methods can be tested with respect to function using any of the assays described herein or known in the art.

[0325] Provided herein is a humanized antibody, or antigen-binding fragment thereof, which binds LOXL2, comprising a heavy chain variable region and a light chain variable region,

[0326] wherein said heavy chain variable region comprises:

[0327] (i) a heavy chain FR1 having the amino acid sequence of SEQ ID NO: 33 or the amino acid sequence of SEQ ID NO: 33 but for one or more substitutions selected from the group consisting of:

[0328] (a) a substitution of glutamine (Q) by valine (V) or a conservative substitution thereof at position 24;

[0329] (b) a substitution of leucine (L) by valine (V) or a conservative substitution thereof at position 30;

- [0330] (c) a substitution of valine (V) by lysine (K) or a conservative substitution thereof at position 31;
- [0331] (d) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 32; and
- [0332] (e) a substitution of threonine (T) by alanine (A) or a conservative substitution thereof at position 35; and a deletion of amino acid residues 1-19;
- [0333] (ii) a heavy chain FR2 having the amino acid sequence of SEQ ID NO: 34 or the amino acid sequence of SEQ ID NO: 34 but for one or more substitutions selected from the group consisting of:
- [0334] (a) a substitution of lysine (K) by arginine (R) or a conservative substitution thereof at position 3;
- [0335] (b) a substitution of arginine (R) by alanine (A) or a conservative substitution thereof at position 5, and
- [0336] (iii) a heavy chain FR3 having the amino acid sequence of SEQ ID NO: 35 or the amino acid sequence of SEQ ID NO: 35 but for one or more substitutions selected from the group consisting of:
- [0337] (a) a substitution of lysine (K) by arginine (R) or a conservative substitution thereof at position 1;
- [0338] (b) a substitution of alanine (A) by valine (V) or a conservative substitution thereof at position 2;
- [0339] (c) a substitution of leucine (L) by isoleucine (I) or a conservative substitution thereof at position 4;
- [0340] (d) a substitution of serine (S) by threonine (T) or a conservative substitution thereof at position 10;
- [0341] (e) a substitution of glutamine (Q) by glutamic acid (E) or a conservative substitution thereof at position 16;
- [0342] (f) a substitution of threonine (T) by arginine (R) or a conservative substitution thereof at position 21;
- [0343] (g) a substitution of aspartic acid (D) by glutamic acid (E) or a conservative substitution thereof at position 23;
- [0344] (h) a substitution of serine (S) by threonine (T) or a conservative substitution thereof at position 25; and
- [0345] (i) a substitution of phenylalanine (F) by tyrosine (Y) or a conservative substitution thereof at position 29;
- [0346] and
- [0347] (iv) a heavy chain FR4 having the amino acid sequence of SEQ ID NO: 36 or the amino acid sequence of SEQ ID NO: 36 but for a substitution of lysine (K) by valine (V) or a conservative substitution thereof at position 7,
- [0348] and wherein said light chain variable region comprises:
- [0349] (i) a light chain FR1 having the amino acid sequence of SEQ ID NO: 49 or the amino acid sequence of SEQ ID NO: 49 but for one or more substitutions selected from the group consisting of:
- [0350] (a) a substitution of alanine (A) by threonine (T) or a conservative substitution thereof at position 27;
- [0351] (b) a substitution of alanine (A) by proline (P) or a conservative substitution thereof at position 28;
- [0352] (c) a substitution of proline (P) by leucine (L) or a conservative substitution thereof at position 29;
- [0353] (d) a substitution of valine (V) by leucine (L) or a conservative substitution thereof at position 31;
- [0354] (e) a substitution of glutamic acid (E) by glutamine (Q) or a conservative substitution thereof at position 37;
- [0355] (d) a substitution of serine (S) by proline (P) or a conservative substitution thereof at position 38;
- [0356] (f) a substitution of valine (V) by alanine (A) or a conservative substitution thereof at position 39; and a deletion of amino acid residues 1-20;
- [0357] (ii) a light chain FR2 having the amino acid sequence of SEQ ID NO: 50 or the amino acid sequence of SEQ ID NO: 50 but for one or more substitutions selected from the group consisting of:
- [0358] (a) a substitution of phenylalanine (F) by tyrosine (Y) or a conservative substitution thereof at position 2; and
- [0359] (b) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 5;
- [0360] (iii) a light chain FR3 having the amino acid sequence of SEQ ID NO: 51 or the amino acid sequence of SEQ ID NO: 51 but for one or more substitutions selected from the group consisting of:
- [0361] (a) a substitution of alanine (A) by aspartic acid (D) or a conservative substitution thereof at position 14; and
- [0362] (b) a substitution of arginine (R) by lysine (K) or a conservative substitution thereof at position 18;
- [0363] and
- [0364] (iv) a light chain FR4 having the amino acid sequence of SEQ ID NO: 52 or the amino acid sequence of SEQ ID NO: 52 but for a substitution of leucine (L) by valine (V) or a conservative substitution thereof at position 7;
- [0365] In one embodiment, the antibody, or antigen-binding fragment thereof, comprises a heavy chain variable region FR1 having an amino acid sequence as set forth in SEQ ID NO: 33, 37 or 44; a heavy chain variable region FR2 having an amino acid sequence as set forth in SEQ ID NO: 34, 38 or 45; a heavy chain variable region FR3 having an amino acid sequence as set forth in SEQ ID NO: 35, 39, 46, 47 or 48; a heavy chain variable region FR4 having an amino acid sequence as set forth in SEQ ID NO: 36 or 40; a light chain variable region FR1 having an amino acid sequence as set forth in SEQ ID NO: 49 or 53; a light chain variable region FR2 having an amino acid sequence as set forth in SEQ ID NO: 50, 54 or 60; a light chain variable region FR3 having an amino acid sequence as set forth in SEQ ID NO: 51, 55 or 61; and a light chain variable region FR4 having an amino acid sequence as set forth in SEQ ID NO: 52 or 56.
- [0366] Encompassed within the scope of the present application are variable heavy chains and variable light chains that are at least 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95% or up to 100% identical to the variable heavy chains and variable light chains described herein.
- [0367] Conservative substitutions are minor modification of these nucleotide sequences and/or amino acids are intended to be included as heavy and light chain encoding nucleic acids and their functional fragments. Such minor modifications include, for example, those which do not change the encoded amino acid sequence due to the degeneracy of the genetic code as well as those which result in only a conservative substitution of the encoded amino acid sequence or those that do not substantially alter the binding

capacity of the antibody. Conservative substitutions of encoded amino acids include, for example, amino acids which belong within the following groups: (1) non-polar amino acids (Gly, Ala, Val, Leu, and Ile); (2) polar neutral amino acids (Cys, Met, Ser, Thr, Asn, and Gln); (3) polar acidic amino acids (Asp and Glu); (4) polar basic amino acids (Lys, Arg and His); and (5) aromatic amino acids (Phe, Trp, Tyr, and His). Other minor modifications are included within the nucleic acids encoding heavy and light chain polypeptides of the invention so long as the nucleic acid or encoded polypeptides retain some, or all, of their function as described herein and which have use in the methods described herein. Non-conservative substitutions are those that are not identified as conservative substitutions. Using the methods described herein, one can ascertain whether it would be possible to substitute a non-conservative amino acid for a framework amino acid residue and test the function of the modified antibody using the assays described elsewhere herein.

[0368] Modified variable heavy chains and variable light chains can be screened for binding and activity using methods known in the art and described herein.

[0369] A substantial portion of a variable domain will include three CDR regions, together with their intervening framework regions. The portion can also include at least about 50% of either or both of the first and fourth framework regions, the 50% being the C-terminal 50% of the first framework region and the N-terminal 50% of the fourth framework region. Additional residues at the N-terminal or C-terminal end of the substantial part of the variable domain may be those not normally associated with naturally occurring variable domain regions. For example, construction of humanized anti-LOX or anti-LOXL2 antibodies and antigen-binding fragments described herein made by recombinant DNA techniques can result in the introduction of N- or C-terminal residues encoded by linkers introduced to facilitate cloning or other manipulation steps. Other manipulation steps include the introduction of linkers to join variable domains to further protein sequences including immunoglobulin heavy chains, other variable domains (for example in the production of diabodies) or protein labels as discussed in more detail below.

[0370] Antibodies encompassed within the present application, including, for example, those having variable heavy or light chains that have at least 50% identity to those described herein can be assessed for anti-LOX or anti-LOXL2 activity.

[0371] Provided herein is a method for identifying an antibody that inhibits metastatic tumor cell growth, comprising contacting LOX or LOXL2 or a cell expressing LOX or LOXL2 with a candidate antibody; and determining the expression or activity of the LOX or LOXL2, whereby the candidate antibody that reduces the expression or activity of LOX or LOXL2 compared to the expression or activity detected in the absence of the antibody is identified as the compound that inhibits metastatic tumor cell growth. In particular embodiments, the antibody is contacted with LOX or LOXL2 or a cell expressing LOX or LOXL2 under hypoxic conditions. In one aspect, antibodies described herein can be non-competitive inhibitors.

[0372] Also provided herein is method for identifying an antibody that increases the efficacy of chemotherapeutic agents, comprising contacting LOX or LOXL2 or a cell expressing LOX or LOXL2 with a candidate antibody; and determining the expression or activity of the LOX or LOXL2, whereby the candidate antibody that reduces the expression or activity of LOX or LOXL2 compared to the expression or

activity detected in the absence of the antibody is identified as the antibody that increases the efficacy of chemotherapeutic agents in inhibiting or reducing metastatic tumor growth.

[0373] Any suitable source of LOX or LOXL2 can be employed as an antibody target in the present method. The enzyme can be derived, isolated, or recombinantly produced from any source known in the art, including yeast, microbial, and mammalian, that will permit the generation of a suitable product that can generate a detectable reagent or will be biologically active in a suitable assay.

[0374] The enzymatic activity of LOX or LOXL2 can be assessed by any suitable method described herein or known in the art. Exemplary methods of assessing LOX or LOXL2 activity include that of Trackman et al., *Anal. Biochem.* 113: 336-342 (1981); Kagan, et al., *Methods Enzymol.* 82A:637-49 (1982); Palamakumbura et al., *Anal. Biochem.* 300:245-51 (2002); Albini et al., *Cancer Res.* 47: 3239-45 (1987); Kamath et al, *Cancer Res.* 61:5933-40 (2001); U.S. Pat. No. 4,997,854; and U.S. Patent Application No. 2004/0248871. For example, enzymatic activity can be assessed by detecting and/or quantitating "lysyl oxidase byproducts," such as H₂O₂ production; collagen pyridinium residues, ammonium production; aldehyde product production; lysyl oxidation, deoxypyridinoline (Dpd)—discussed below. One may also detect and quantitate cellular invasive capacity in vitro; cellular adhesion and growth in vitro; and metastatic growth in vivo. In vivo models include, but are not limited to suitable syngeneic models, human tumor xenograft models, orthotopic models, metastatic models, transgenic models, and gene knockout models (see, e.g., Teicher, *Tumors Models in Cancer Research* (Humana Press 2001)).

[0375] Hypoxic conditions can be induced or naturally occurring. Hypoxic areas frequently occur in the interior of solid tumor. Hypoxia can also be induced in vivo, particularly in experimental animal models, using diminution or cessation of arterial blood flow to tumor or the administration of vasoconstrictive compounds. See, e.g., U.S. Pat. No. 5,646,185. Exemplary vasoconstrictive compounds include adrenergic direct and indirect agonists such as norepinephrine, epinephrine, phenylephrine, and cocaine. The presence of a hypoxic region in a solid tumor present in a subject can be observed by a number of methods currently known in the art, including nuclear magnetic resonance (NMR) and oxygen electrode pO₂ histography. Such methods may be used in the context of the present invention (as described below), to identify hypoxic treatment target regions and to guide in administering treatment compositions to such regions. In vitro, hypoxic conditions can be induced using any suitable method. For example, cells can be maintained under anoxic (<0.1% O₂) conditions at 37° C. within an anaerobic chamber or under hypoxic (1 to 2% O₂) conditions at 37° C. within a modular incubator chamber filled with 5% CO₂ and 1 to 2% O₂ balanced with N₂. See, e.g., Erler et al., *Mol. Cell. Biol.* 24:2875-89 (2004).

[0376] The LOX or LOXL2 enzymes or LOX- or LOXL2-expressing cell can be contacted with a compound (e.g., a LOX/LOXL inhibitor such as an antibody) in any suitable manner for any suitable length of time. For tumor regions that are accessible to hypodermic delivery of agent, it may be desirable to inject the compound directly into the hypoxic region. The cells can be contacted with the compound more than once during incubation or treatment. Typically, the dose required for an antibody is in the range of about 1 micro-g/ml to 1000 micro-g/ml, more typically in the range of about 100

μg/ml to about 800 μg/ml. The exact dose can be readily determined from in vitro cultures of the cells and exposure of the cell to varying dosages of the compound. Typically, the length of time the cell is contacted with the compound is about 5 minutes, about 15 minutes, about 30 minutes, about 1 hour, about 4 hours, about 12 hours, about 36 hours, about 48 hours to about 3 days or more, even indefinitely, more typically for about 24 hours. For in vitro invasion assays, any suitable matrix may be used. In one embodiment, the matrix is reconstituted basement membrane Matrigel™ matrix (BD Sciences).

[0377] Screening methods can also include a step of measuring FAK levels. As described below, FAK (Focal Adhesion Kinase [p125FAK]) is activated as part of the cell motility process. When LOX is inhibited, FAK phosphorylation is not increased under hypoxic conditions. In a compound-screening assay, a secondary step can include the detection of phospho-FAK levels both with and without addition of the test antibody. A test inhibitory antibody will also reduce levels of phospho-FAK.

[0378] An antibody is an inhibitor of LOX or LOXL2 expression or biological activity when the antibody reduces the expression or activity of LOX or LOXL2 relative to that observed in the absence of the antibody. In one embodiment, an antibody is an inhibitor of LOX or LOXL2 when it reduces the incidence of metastasis relative to the observed in the absence of the antibody and, in further testing, inhibits metastatic tumor growth. In one aspect, antibodies described herein are non-competitive inhibitors. Tumor inhibition can be quantified using any convenient method of measurement. The incidence of metastasis can be assessed by examining relative dissemination (e.g., number of organ systems involved) and relative tumor burden in these sites. Metastatic growth can be ascertained by microscopic or macroscopic analysis, as appropriate. Tumor metastasis can be reduced by about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or greater. In some embodiments, the antibody can be assessed relative to other antibodies or compounds that do not impact LOX or LOXL2 expression or biological activity. The test antibodies can be administered at the time of tumor inoculation, after the establishment of primary tumor growth, or after the establishment of local and/or distant metastases. Single or multiple administration of the test antibody can be given using any convenient mode of administration including, but not limited to, intravenous, intraperitoneal, intratumoral, subcutaneous and intradermal.

[0379] Any suitable cell expressing LOX or LOXL2 can be employed with the present methods. As used herein, the term "cell" includes a biological cell (e.g., CHO, HeLa, etc.). The cell can be human or nonhuman. The cell can be freshly isolated (i.e., primary) or derived from a short term- or long term-established cell line. Exemplary biological cell lines include MDA-MB 231 human breast cancer cells, MDA-MB 435 human breast cancer cells, U-87 MG glioma, SCL1 squamous cell carcinoma cells, CEM, HeLa epithelial carcinoma, and Chinese hamster ovary (CHO) cells. Such cell lines are described, for example, in the Cell Line Catalog of the American Type Culture Collection (ATCC, Rockville, Md.).

[0380] A cell can express the LOX or LOXL2 or its promoter endogenously or exogenously (e.g., as a result of the stable transfer of genes). Endogenous expression by a cell as provided herein can result from constitutive or induced expression of endogenous genes.

[0381] Exogenous expression by a cell as provided herein can result from the introduction of the nucleic acid sequences encoding LOX or LOXL2 or a biologically active fragment thereof, or LOX or LOXL2 promoter nucleic acid sequence. Transformation may be achieved using viral vectors, calcium phosphate, DEAE-dextran, electroporation, biolistics, cationic lipid reagents, or any other convenient technique known in the art. The manner of transformation useful in the present invention is conventional and is exemplified in Current Protocols in Molecular Biology (Ausubel, et al., eds. 2000). Exogenous expression of the lysyl oxidase or its promoter can be transient, stable, or some combination thereof. Exogenous expression of the enzyme can be achieved using constitutive promoters, e.g., SV40, CMV, and the like, and inducible promoters known in the art. Suitable promoters are those that will function in the cell of interest.

[0382] The methods described herein are non-limiting and any other methods known in the art can also be used to test the activity of anti-LOX antibodies and anti-LOXL2 antibodies. Additional assays are described below in the Examples.

[0383] It may be necessary in some instances to introduce an unstructured polypeptide linker region between a label of the present invention and portions of the antibodies. The linker can facilitate enhanced flexibility, and/or reduce steric hindrance between any two fragments. The linker can also facilitate the appropriate folding of each fragment to occur. The linker can be of natural origin, such as a sequence determined to exist in random coil between two domains of a protein. An exemplary linker sequence is the linker found between the C-terminal and N-terminal domains of the RNA polymerase α subunit. Other examples of naturally occurring linkers include linkers found in the ICI and LexA proteins.

[0384] Within the linker, the amino acid sequence may be varied based on the preferred characteristics of the linker as determined empirically or as revealed by modeling. Considerations in choosing a linker include flexibility of the linker, charge of the linker, and presence of some amino acids of the linker in the naturally-occurring subunits. The linker can also be designed such that residues in the linker contact DNA, thereby influencing binding affinity or specificity, or to interact with other proteins. In some cases, particularly when it is necessary to span a longer distance between subunits or when the domains must be held in a particular configuration, the linker may optionally contain an additional folded domain.

[0385] In some embodiments it is preferable that the design of a linker involve an arrangement of domains which requires the linker to span a relatively short distance, preferably less than about 10 Angstroms (Å). However, in certain embodiments, linkers span a distance of up to about 50 Å.

[0386] Antibodies provided herein such that they are conjugated or linked to therapeutic and/or imaging/detectable moieties. Methods for conjugating or linking antibodies are well known in the art. Associations between antibodies and labels include any means known in the art including, but not limited to, covalent and non-covalent interactions.

[0387] In one non-limiting embodiment, antibodies can be associated with a toxin, a radionuclide, an iron-related compound, a dye, an imaging reagent, a fluorescent label or a chemotherapeutic agent that would be toxic when delivered to a cancer cell.

[0388] Alternatively, the antibodies can be associated with detectable label, such as a radionuclide, iron-related compound, a dye, an imaging agent or a fluorescent agent for immunodetection of target antigens.

[0389] Non-limiting examples of radiolabels include, for example, ^{32}P , ^{33}P , ^{43}K , ^{52}Fe , ^{57}Co , ^{64}Cu , ^{67}Ga , ^{68}Ga , ^{71}Ge , ^{75}Br , ^{76}Br , ^{77}Br , ^{77}As , ^{77}Br , ^{81}Rb , $^{81\text{M}}\text{Kr}$, $^{87\text{M}}\text{Sr}$, ^{90}Y , ^{97}Ru , ^{99}Tc , ^{100}Pd , ^{101}Rh , ^{103}Pb , ^{105}Rh , ^{109}Pd , ^{111}Ag , ^{111}In , ^{113}In , ^{119}Sb , ^{121}Sn , ^{123}I , ^{125}I , ^{127}Cs , ^{128}Ba , ^{129}Cs , ^{131}I , ^{131}Cs , ^{143}Pr , ^{153}Sm , ^{161}Tb , ^{166}Ho , ^{169}Eu , ^{177}Lu , ^{186}Re , ^{188}Re , ^{189}Re , ^{191}Os , ^{193}Pt , ^{194}Ir , ^{197}Hg , ^{199}Au , ^{203}Pb , ^{211}At , ^{212}Pb , ^{212}Bi and ^{213}Bi .

[0390] Non-limiting examples of toxins include, for example, diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolacca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crocin, *sapaonaria officinalis* inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, tricothecenes, *Clostridium perfringens* phospholipase C (PLC), bovine pancreatic ribonuclease (BPR), antiviral protein (PAP), abrin, cobra venom factor (CVF), gelonin (GEL), saporin (SAP) viscumin.

[0391] Non-limiting examples of iron-related compounds include, for example, magnetic iron-oxide particles, ferric or ferrous particles, Fe^{203} and Fe^{304} . Iron-related compounds and methods of labeling polypeptides, proteins and peptides can be found, for example, in U.S. Pat. Nos. 4,101,435 and 4,452,773, and U.S. published applications 20020064502 and 20020136693, all of which are hereby incorporated by reference in their entirety.

[0392] In certain embodiments, the subject antibodies can be covalently or non-covalently coupled to a cytotoxin or other cell proliferation inhibiting compound, in order to localize delivery of that agent to a tumor cell. For instance, the agent can be selected from the group consisting agents, enzyme inhibitors, proliferation inhibitors, lytic agents, DNA or RNA synthesis inhibitors, membrane permeability modifiers, DNA metabolites, dichloroethylsulfide derivatives, protein production inhibitors, ribosome inhibitors, inducers of apoptosis, and neurotoxins.

[0393] In certain embodiments, the subject antibodies can be coupled with an agent useful in imaging tumors. Such agents include: metals; metal chelators; lanthanides; lanthanide chelators; radiometals; radiometal chelators; positron-emitting nuclei; microbubbles (for ultrasound); liposomes; molecules microencapsulated in liposomes or nanosphere; monocrystalline iron oxide nanocompounds; magnetic resonance imaging contrast agents; light absorbing, reflecting and/or scattering agents; colloidal particles; fluorophores, such as near-infrared fluorophores. In many embodiments, such secondary functionality/moiety will be relatively large, e.g., at least 25 amu in size, and in many instances can be at least 50,100 or 250 amu in size.

[0394] In certain embodiments, the secondary functionality is a chelate moiety for chelating a metal, e.g., a chelator for a radiometal or paramagnetic ion. In additional embodiments, it is a chelator for a radionuclide useful for radiotherapy or imaging procedures.

[0395] Radionuclides useful within the present invention include gamma-emitters, positron-emitters, Auger electron-emitters, X-ray emitters and fluorescence-emitters, with beta- or alpha-emitters preferred for therapeutic use. Examples of radionuclides useful as toxins in radiation therapy include: ^{32}P , ^{33}P , ^{43}K , ^{52}Fe , ^{57}Co , ^{64}Cu , ^{67}Ga , ^{67}Cu , ^{68}Ga , ^{71}Ge , ^{75}Br , ^{76}Br , ^{77}Br , ^{77}As , ^{77}Br , ^{81}Rb , $^{81\text{M}}\text{Kr}$, $^{87\text{M}}\text{Sr}$, ^{90}Y , ^{97}Ru , ^{99}Tc , ^{100}Pd , ^{101}Rh , ^{103}Pb , ^{105}Rh , ^{109}Pd , ^{111}Ag , ^{111}In , ^{113}In , ^{119}Sb ,

^{121}Sn , ^{123}I , ^{125}I , ^{127}Cs , ^{128}Ba , ^{129}Cs , ^{131}I , ^{131}Cs , ^{143}Pr , ^{153}Sm , ^{161}Tb , ^{166}Ho , ^{169}Eu , ^{177}Lu , ^{186}Re , ^{188}Re , ^{189}Re , ^{191}Os , ^{193}Pt , ^{194}Ir , ^{197}Hg , ^{199}Au , ^{203}Pb , ^{211}At , ^{212}Pb , ^{212}Bi and ^{213}Bi . Preferred therapeutic radionuclides include ^{188}Re , ^{186}Re , ^{203}Pb , ^{212}Pb , ^{212}Bi , ^{109}Pd , ^{64}Cu , ^{67}Cu , ^{90}Y , ^{125}I , ^{131}I , ^{77}Br , ^{211}At , ^{97}Ru , ^{105}Rh , ^{198}Au and ^{199}Ag , ^{166}Ho or ^{177}Lu .

Conditions under which a chelator will coordinate a metal are described, for example, by Gasnow et al. U.S. Pat. Nos. 4,831,175, 4,454,106 and 4,472,509, each of which is incorporated herein by reference. Within the present invention, "radionuclide" and "radiolabel" are interchangeable.

[0396] ^{99}Tc is a particularly attractive radioisotope for diagnostic applications, as it is readily available to all nuclear medicine departments, is inexpensive, gives minimal patient radiation doses, and has ideal nuclear imaging properties. It has a half-life of six hours which means that rapid targeting of a technetium-labeled antibody is desirable. Accordingly, in certain preferred embodiments, the modified antibodies include a chelating agent for technetium.

[0397] In still other embodiments, the secondary functionality can be a radiosensitizing agent, e.g., a moiety that increases the sensitivity of cells to radiation. Examples of radiosensitizing agents include nitroimidazoles, metronidazole and misonidazole (see: DeVita, V. T. in Harrison's Principles of Internal Medicine, p. 68, McGraw-Hill Book Co., NY, 1983, which is incorporated herein by reference). The modified antibodies that comprise a radiosensitizing agent as the active moiety are administered and localize at the target cell. Upon exposure of the individual to radiation, the radiosensitizing agent is "excited" and causes the death of the cell.

[0398] There are a wide range of moieties which can serve as chelators and which can be derivatized to the antibodies of the present invention. For instance, the chelator can be a derivative of 1,4,7,10-tetraazacyclododecanetetraacetic acid (DOTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA) and 1-p-Isothiocyanatobenzyl-methyl-diethylenetriaminepentaacetic acid (ITC-MX). These chelators typically have groups on the side chain by which the chelator can be used for attachment to subject antagonists. Such groups include, e.g., benzyliothiocyanate, by which the DOTA, DTPA or EDTA can be coupled to, e.g., an amine group.

[0399] In one embodiment, the chelate moiety is an "NxSy" chelate moiety. As defined herein, the "NxSy chelates" include bifunctional chelators that are capable of coordinately binding a metal or radiometal and, preferably, have N2S2 or N3S cores. Exemplary NxSy chelates are described, e.g., in Fritzberg et al. (1998) PNAS 85: 4024-29; and Weber et al. (1990) Chem. 1: 431-37; and in the references cited therein.

[0400] Jacobsen et al. (PCT application WO 98/12156) provides methods and compositions, i.e., synthetic libraries of binding moieties, for identifying compounds which bind to a metal atom. The approach described in that publication can be used to identify binding moieties which can subsequently be added to the antibodies to derive the modified antibodies.

[0401] One problem frequently encountered with the use of conjugated proteins in and radiodiagnostic applications is a potentially dangerous accumulation of the radiolabeled moiety fragments in the kidney. When the conjugate is formed using an acid-or base-labile linker, cleavage of the radioactive chelate from the protein can advantageously occur. If the chelate is of relatively low molecular weight, as most of the

subject modified antibodies, antigen binding fragments and peptides are expected to be, it is not retained in the kidney and is excreted in the urine, thereby reducing the exposure of the kidney to radioactivity. However, in certain instances, it may be advantageous to utilize acid- or base-labile in the subject ligands for the same reasons they have been used in labeled proteins.

[0402] Accordingly, certain of the subject labeled/modified antibodies can be synthesized, by standard methods in the art, to provide reactive functional groups which can form acid-labile linkages with, e.g., a carbonyl group of the ligand. Examples of suitable acid-labile linkages include hydrazone and thiosemicarbazone functions. These are formed by reacting the oxidized carbohydrate with chelates bearing hydrazide, thiosemicarbazide, and functions, respectively.

[0403] Alternatively, base-cleavable which have been used for the enhanced clearance of the radiolabel from the kidneys, can be used. See, for example, Weber et al. 1990 *Bioconjug. Chem.* 1:431. The coupling of a bifunctional chelate to an antibody via a hydrazide linkage can incorporate base-sensitive ester moieties in a linker spacer arm. Such an ester-containing linker unit is exemplified by ethylene glycolbis (succinimidyl succinate), (EGS, available from Pierce Chemical Co., Rockford, Ill.), which has two terminal N-hydroxysuccinimide (NHS) ester derivatives of two 1,4-dibutyric acid units, each of which are linked to a single ethylene glycol moiety by two alkyl esters. One NHS ester may be replaced with a suitable amine-containing BFC (for example 2-aminobenzyl DTPA), while the other NHS ester is reacted with a limiting amount of hydrazine. The resulting hydrazone is used for coupling to the antagonists, forming a ligand-BFC linkage containing two alkyl ester functions. Such a conjugate is stable at physiological pH, but readily cleaved at basic pH.

[0404] Antibodies labeled by chelation of radioisotopes are subject to radiation-induced scission of the chelator and to loss of radioisotope by dissociation of the coordination complex. In some instances, metal dissociated from the complex can be re-complexed, providing more rapid clearance of non-specifically localized isotope and therefore less toxicity to non-target tissues. For example, chelator compounds such as EDTA or DTPA can be infused into patients to provide a pool of chelator to bind released radiometal and facilitate excretion of free radioisotope in the urine.

[0405] In still other embodiments, the antibodies are coupled to a Boron addend, such as a carborane. For example, carboranes can be prepared with carboxyl functions on pendant side chains, as is well known in the art. Attachment of such carboranes to amine peptides can be achieved by activation of the carboxyl groups of the carboranes and condensation with the amine group to produce the conjugate. Such modified antibodies can be used for neutron capture therapy.

[0406] The present invention also contemplates the modification of the subject antagonists with dyes, for example, useful in therapy, and used in conjunction with appropriate non-ionizing radiation. The use of light and porphyrins in methods of the present invention is also contemplated and their use in cancer therapy has been reviewed by van den Bergh, *Chemistry in Britain*, 22: 430-437 (1986), which is incorporated by reference herein in its entirety.

[0407] One embodiment of the present invention includes antagonists labeled with a fluorescent label. Common fluorescent labels include, for example, FITC, PE, Texas Red,

cytochrome c, etc. Techniques for labeling polypeptides and fragments thereof, such as those provided herein, are well-known in the art.

[0408] The term "anticancer agent" also includes the chemotherapeutic agents described below. The term anticancer agent also includes treatment with a substance that reduces hypoxia in a cell, when such agent is combined with LOX inhibition. Such a substance may include, e.g., p53. See, e.g., Matoba et al., "p53 Regulates Mitochondrial Respiration," *Science* 16 Jun. 2006 312: 1650-1653; published online 24 May 2006, and references cited there. A substance that drives cancer cells towards the respiratory pathway and away from the glycolytic pathway would be used advantageously with a LOX inhibitor insofar as LOX would not be up-regulated in this case.

[0409] Chemotherapeutics useful as active moieties which when conjugated to antagonists thereof of the present invention are specifically delivered to cells are typically, small chemical entities produced by chemical synthesis. Chemotherapeutics include cytotoxic and cytostatic drugs. Chemotherapeutics may include those which have other effects on cells such as reversal of the transformed state to a differentiated state or those which inhibit cell replication. Examples of known cytotoxic agents useful in the present invention are listed, for example, in Goodman et al., "The Pharmacological Basis of Therapeutics," Sixth Edition, A. B. Gilman et al., eds./Macmillan Publishing Co. New York, 1980. These include taxanes, such as paclitaxel and docetaxel; nitrogen such as mechlorethamine, melphalan, uracil mustard and chlorambucil; ethylenimine derivatives, such as thiopeta; alkyl sulfonates; such as busulfan; nitrosoureas, such as lomustine, semustine and streptozocin; triazines, such as dacarbazine; folic acid analogs, such as methotrexate; pyrimidine analogs, such as fluorouracil, cytarabine and azaribine; purine analogs, such as mercaptopurine and thioguanine; vinca alkaloids, such as vinblastine and vincristine; antibiotics, such as dactinomycin, daunorubicin, doxorubicin, and mitomycin; enzymes, such as platinum coordination complexes, such as cisplatin; substituted urea, such as hydroxyurea; methyl hydrazine derivatives, such as procabazine; adrenocortical suppressants, such as mitotane; hormones and antagonists, such as adrenocortisteroids (prednisone), progestins (hydroxyprogesterone caproate, acetate and megestrol acetate), estrogens (diethylstilbestrol and ethinyl estradiol), and androgens (testosterone propionate and fluoxymesterone).

[0410] Drugs that interfere with protein synthesis can also be used; such drugs are known to those skilled in the art and include puromycin, cycloheximide, and ribonuclease.

[0411] Most of the chemotherapeutic agents currently in use in treating cancer possess functional groups that are amenable to chemical cross-linking directly with an amine or carboxyl group of an agent of the present invention. For example, free amino groups are available on methotrexate, doxorubicin, daunorubicin, cytosinarabioside, bleomycin, fludarabine, and cladribine while free carboxylic acid groups are available on methotrexate, melphalan and chlorambucil.

[0412] These functional groups, that is free amino and carboxylic acids, are targets for a variety of homobifunctional and heterobifunctional chemical cross-linking agents which can crosslink these drugs directly to a free amino group of an antagonist.

[0413] Chemotherapeutic agents contemplated by the present invention also include other chemotherapeutic drugs

that are commercially available. Merely to illustrate, the chemotherapeutic can be an inhibitor of chromatin function, a inhibitor, a inhibiting drug, a DNA damaging agent, an anti-metabolite (such as folate antagonists, pyrimidine analogs, purine analogs, and sugar-modified analogs), a DNA synthesis inhibitor, a DNA interactive agent (such as an intercalating agent), a DNA repair inhibitor.

[0414] Chemotherapeutic agents may be categorized by their mechanism of action into, for example, the following groups: anti-metabolites/anti-cancer agents, such as pyrimidine analogs floxuridine, capecitabine, and cytarabine) and purine analogs, folate antagonists and related inhibitors anti-proliferative/antimitotic agents including natural products such as vinca alkaloid (vinblastine, vincristine, and microtubule such as taxane (paclitaxel, docetaxel), vinblastin, nocodazole, epothilones and navelbine, epididodophyllotoxins (etoposide, teniposide), DNA damaging agents (actinomycin, amsacrine, busulfan, carboplatin, chlorambucil, cisplatin, cyclophosphamide, cytoxan, dactinomycin, daunorubicin, doxorubicin, epirubicin, ifosphamide, melphalan, merchloroethamine, mitomycin, mitoxantrone, nitrosourea, procarbazine, taxol, taxotere, teniposide, triethylenethiophosphoramide and etoposide; antibiotics such as dactinomycin (actinomycin D), daunorubicin, doxorubicin (adriamycin), idarubicin, anthracyclines, mitoxantrone, bleomycins, plicamycin (mithramycin) and mitomycin; enzymes (L-asparaginase which systemically metabolizes L-asparagine and deprives cells which do not have the capacity to synthesize their own asparagine); antiplatelet agents; antiproliferative/antimitotic alkylating agents such as nitrogen mustards cyclophosphamide and analogs, melphalan, chlorambucil, and (hexamethylmelamine and thiotepa), alkyl nitrosoureas (BCNU) and analogs, streptozocin, trazenesdacarbazine (DTIC); antiproliferative/antimitotic antimetabolites such as folic acid analogs (methotrexate); platinum coordination complexes (cisplatin, oxiloplatinim, carboplatin), procarbazine, hydroxyurea, mitotane, aminoglutethimide; hormones, hormone analogs (estrogen, tamoxifen, goserelin, bicalutamide, nilutamide) and aromatase inhibitors (letrozole, anastrozole); anticoagulants (heparin, synthetic heparin salts and other inhibitors of thrombin); fibrinolytic agents (such as tissue plasminogen activator, streptokinase and urokinase), aspirin, dipyridamole, ticlopidine, clopidogrel; antimigratory agents; antisecretory agents (breveldin); immunosuppressives tacrolimus sirolimus azathioprine, mycophenolate; compounds (TNP-470, genistein) and growth factor inhibitors (vascular endothelial growth factor inhibitors, fibroblast growth factor inhibitors); angiotensin receptor blocker, nitric oxide donors; anti-sense oligonucleotides; antibodies (trastuzumab, rituximab); cell cycle inhibitors and differentiation inducers (tretinoin); inhibitors, topoisomerase inhibitors (doxorubicin (adriamycin), daunorubicin, dactinomycin, eniposide, epirubicin, etoposide, idarubicin, irinotecan and mitoxantrone, topotecan, irinotecan), corticosteroids (cortisone, dexamethasone, hydrocortisone, methylprednisolone, prednisone, and prednisolone); growth factor signal transduction kinase inhibitors; dysfunction inducers, toxins such as *Cholera* toxin, ricin, *Pseudomonas* exotoxin, *Bordetella pertussis* adenylate cyclase toxin, or diphtheria toxin, and caspase activators; and chromatin. Preferred dosages of the chemotherapeutic agents are consistent with currently prescribed dosages.

[0415] Additionally, other labels, such as biotin followed by streptavidin-alkaline phosphatase (AP), horseradish peroxidase are contemplated by the present invention.

[0416] As used herein, the terms “nucleic acid damaging treatment” and “nucleic acid damaging agent” refer to any treatment regimen that directly or indirectly damages nucleic acid (e.g., DNA, cDNA, genomic DNA, mRNA, tRNA or rRNA). Examples of such agents include alkylating agents, nitrosoureas, anti-metabolites, plant alkaloids, plant extracts and radioisotopes. Examples of agents also include nucleic acid damaging drugs, for example, 5-fluorouracil (5-FU), capecitabine, S-1 (Tegafur, 5-chloro-2,4-dihydroxypyridine and ozonic acid), 5-ethynyluracil, arabinosyl cytosine (ara-C), 5-azacytidine (5-AC), 2',2'-difluoro-2'-deoxycytidine (dFdC), purine antimetabolites (mercaptopurine, azathiopurine, thioguanine), gemcitabine hydrochloride (Gemzar), pentostatin, allopurinol, 2-fluoro-arabinosyl-adenine (2F-ara-A), hydroxyurea, sulfur mustard (bischloroethylsulfide), mechlorethamine, melphalan, chlorambucil, cyclophosphamide, ifosfamide, thiotepa, AZQ, mitomycin C, dianhydrogalactitol, dibromoducitol, alkyl sulfonate (busulfan), nitrosoureas (BCNU, CCNU, 4-methyl CCNU or ACNU), procarbazine, decarbazine, rebeccamycin, anthracyclins such as doxorubicin (adriamycin; ADR), daunorubicin (Cerubidine), idarubicin (Idamycin) and epirubicin (Ellence), anthracyclin analogues such as mitoxantrone, actinomycin D, non intercalating topoisomerase inhibitors such as epipodophyllotoxins (etoposide=VP16, teniposide=VM-26), podophyllotoxin, bleomycin (Bleo), pepleomycin, compounds that form adducts with nucleic acid including platinum derivatives (e.g., cisplatin (CDDP), trans analogue of cisplatin, carboplatin, iproplatin, tetraplatin and oxaliplatin), camptothecin, topotecan, irinotecan (CPT-11), and SN-38. Specific examples of nucleic acid damaging treatments include radiation (e.g., focused microwaves, ultraviolet (UV), infrared (IR), or alpha-, beta- or gamma-radiation) and environmental shock (e.g., hyperthermia).

[0417] As used herein, the terms “anti-proliferative treatment” and “anti-proliferative agent” means any treatment regimen that directly or indirectly inhibits proliferation of a cell, virus, bacteria or other unicellular or multicellular organism regardless of whether or not the treatment or agent damages nucleic acid. Particular examples of anti-proliferative agents are anti-tumor and anti-viral drugs, which inhibit cell proliferation or virus proliferation or replication. Examples include, inter alia, cyclophosphamide, azathioprine, cyclosporin A, prednisolone, melphalan, chlorambucil, mechlorethamine, busulphan, methotrexate, 6-mercaptopurine, thioguanine, cytosine arabinoside, taxol, vinblastine, vincristine, doxorubicin, actinomycin D, mithramycin, carmustine, lomustine, semustine, streptozotocin, hydroxyurea, cisplatin, mitotane, procarbazine, dacarbazine and dibromomannitol. Anti proliferative agents that cause nucleic acid replication errors or inhibit nucleic acid replication are those such as nucleoside and nucleotide analogues (e.g., AZT or 5-AZC).

[0418] In another embodiment, the anti-LOX antibody can be conjugated to a “receptor” (such streptavidin) for utilization in tumor pre-targeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a “ligand” (e.g., avidin) that is conjugated to a cytotoxic agent (e.g., a radionuclide).

[0419] Methodology for labeling polypeptides and fragments thereof including, but not limited to, those provided herein are well known in the art. When the antibodies of the present invention are labeled with a radiolabel or toxin, the antibodies can be prepared as pharmaceutical compositions which are useful for therapeutic treatment of patients where the pharmaceutical compositions are administered to the patient in an effective amount. When the antibodies of the present invention are labeled with a label that can be visualized, the antibodies can be prepared as pharmaceutical compositions which are useful for diagnostic of patients where the pharmaceutical compositions are administered to the patient in an effective amount for in vivo imaging or where the pharmaceutical compositions are tested in an in vitro assay.

V. Compositions

[0420] Each of the antibodies of the present invention can be used as a composition when combined with a pharmaceutically acceptable carrier or excipient. Such pharmaceutical compositions are useful for administration to a subject in vivo or ex vivo, and for diagnosing and/or treating a subject with the disclosed antibodies, for example.

[0421] Pharmaceutically acceptable carriers are physiologically acceptable to the administered patient and retain the therapeutic properties of the antibodies or peptides with which it is administered. Pharmaceutically-acceptable carriers and their formulations are and generally described in, for example, Remington's pharmaceutical Sciences (18th Edition, ed. A. Gennaro, Mack Publishing Co., Easton, Pa. 1990). One exemplary pharmaceutical carrier is physiological saline. The phrase "pharmaceutically acceptable carrier" as used herein means a pharmaceutically acceptable material, composition or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, involved in carrying or transporting the subject antibodies or peptides from the administration site of one organ, or portion of the body, to another organ, or portion of the body. Each carrier must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient. Nor should a pharmaceutically acceptable carrier alter the specific activity of the antagonists. Exemplary carriers and excipients have been provided elsewhere herein.

[0422] In one aspect, the present invention provides pharmaceutically acceptable or physiologically acceptable compositions including solvents (aqueous or non-aqueous), solutions, emulsions, dispersion media, coatings, isotonic and absorption promoting or delaying agents, compatible with pharmaceutical administration. Pharmaceutical compositions or pharmaceutical formulations therefore refer to a composition suitable for pharmaceutical use in a subject. The pharmaceutical compositions and formulations include an amount of an invention compound, for example, an effective amount of an antagonist of the invention, and a pharmaceutically or physiologically acceptable carrier.

[0423] Pharmaceutical compositions can be formulated to be compatible with a particular route of administration, systemic or local. Thus, pharmaceutical compositions include carriers, diluents, or excipients suitable for administration by various routes.

[0424] In a further invention, the compositions of the present invention further comprise a pharmaceutically acceptable additive in order to improve the stability of the antagonist in composition and/or to control the release rate of the composition. Pharmaceutically acceptable additives of

the present invention do not alter the specific activity of the subject antagonist. A preferable pharmaceutically acceptable additive is a sugar such as mannitol, sorbitol, glucose, xylitol, trehalose, sorbose, sucrose, galactose, dextran, dextrose, fructose, lactose and mixtures thereof. Pharmaceutically acceptable additives of the present invention can be combined with pharmaceutically acceptable carriers and/or excipients such as dextrose. Alternatively, a preferable pharmaceutically acceptable additive is a surfactant such as polysorbate 20 or polysorbate 80 to increase stability of the peptide and decrease gelling of the pharmaceutical solution. The surfactant can be added to the composition in an amount of 0.01% to 5% of the solution. Addition of such pharmaceutically acceptable additives increases the stability and half-life of the composition in storage.

[0425] The formulation and delivery methods will generally be adapted according to the site and the disease to be treated. Exemplary formulations include, but are not limited to, those suitable for parenteral administration, e.g., intravenous, intra-arterial, intramuscular, or subcutaneous administration, including formulations encapsulated in micelles, liposomes or drug-release capsules (active agents incorporated within a biocompatible coating designed for slow-release); ingestible formulations; formulations for topical use, such as creams, ointments and gels; and other formulations such as inhalants, aerosols and sprays. The dosage of the compounds of the invention will vary according to the extent and severity of the need for treatment, the activity of the administered composition, the general health of the subject, and other considerations well known to the skilled artisan.

[0426] Formulations for enteral (oral) administration can be contained in a tablet (coated or uncoated), capsule (hard or soft), microsphere, emulsion, powder, granule, crystal, suspension, syrup or elixir. Conventional nontoxic solid carriers which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, can be used to prepare solid formulations. Supplementary active compounds (e.g., preservatives, antibacterial, antiviral and antifungal agents) can also be incorporated into the formulations. A liquid formulation can also be used for enteral administration. The carrier can be selected from various oils including petroleum, animal, vegetable or synthetic, for example, peanut oil, soybean oil, mineral oil, sesame oil. Suitable pharmaceutical excipients include e.g., starch, cellulose, talc, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, magnesium stearate, sodium stearate, glycerol monostearate, sodium chloride, dried skim milk, glycerol, propylene glycol, water, ethanol.

[0427] Pharmaceutical compositions for enteral, parenteral, or transmucosal delivery include, for example, water, saline, phosphate buffered saline, Hank's solution, Ringer's solution, dextrose/saline, and glucose solutions. The formulations can contain auxiliary substances to approximate physiological conditions, such as buffering agents, tonicity adjusting agents, wetting agents, detergents and the like. Additives can also include additional active ingredients such as bactericidal agents, or stabilizers. For example, the solution can contain sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate or triethanolamine oleate. Additional parenteral formulations and methods are described in Bai (1997) J. Neuroimmunol. 80:65 75; Warren (1997) J. Neurol. Sci. 152: 31 38; and Tonegawa (1997) J. Exp. Med. 186:507 515. The

parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

[0428] Pharmaceutical compositions for intradermal or subcutaneous administration can include a sterile diluent, such as water, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid, glutathione or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose.

[0429] Pharmaceutical compositions for injection include aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. Fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Antibacterial and antifungal agents include, for example, parabens, chlorobutanol, phenol, ascorbic acid and thimerosal. Isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, and sodium chloride may be included in the composition. The resulting solutions can be packaged for use as is, or lyophilized; the lyophilized preparation can later be combined with a sterile solution prior to administration.

[0430] Pharmaceutically acceptable carriers can contain a compound that stabilizes, increases or delays absorption or clearance. Such compounds include, for example, carbohydrates, such as glucose, sucrose, or dextrans; low molecular weight proteins; compositions that reduce the clearance or hydrolysis of peptides; or excipients or other stabilizers and/or buffers. Agents that delay absorption include, for example, aluminum monostearate and gelatin. Detergents can also be used to stabilize or to increase or decrease the absorption of the pharmaceutical composition, including liposomal carriers. To protect from digestion the compound can be complexed with a composition to render it resistant to acidic and enzymatic hydrolysis, or the compound can be complexed in an appropriately resistant carrier such as a liposome. Means of protecting compounds from digestion are known in the art (see, e.g., Fix (1996) *Pharm. Res.* 13:1760 1764; Samanen (1996) *J. Pharm. Pharmacol.* 48:119 135; and U.S. Pat. No. 5,391,377, describing lipid compositions for oral delivery of therapeutic agents).

[0431] For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be through nasal sprays or suppositories (see, e.g., Sayani (1996) "Systemic delivery of peptides and proteins across absorptive mucosae" *Crit. Rev. Ther. Drug Carrier Syst.* 13:85 184). For transdermal administration, the active compound can be formulated into oint-

ments, salves, gels, or creams as generally known in the art. Transdermal delivery systems can also be achieved using patches.

[0432] For inhalation delivery, the pharmaceutical formulation can be administered in the form of an aerosol or mist. For aerosol administration, the formulation can be supplied in finely divided form along with a surfactant and propellant. In another embodiment, the device for delivering the formulation to respiratory tissue is in which the formulation vaporizes. Other delivery systems known in the art include dry powder aerosols, liquid delivery systems, inhalers, air jet nebulizers and propellant systems (see, e.g., Patton (1998) *Biotechniques* 16:141 143; Dura Pharmaceuticals, San Diego, Calif.; Aradigm, Hayward, Calif.; Aerogen, Santa Clara, Calif.; and Inhale Therapeutic Systems, San Carlos, Calif.).

[0433] Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations are known to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to cells or tissues using antibodies or viral coat proteins) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known in the art, for example, as described in U.S. Pat. Nos. 4,235,871; 4,501,728; 4,522,811; 4,837,028; 6,110,490; 6,096,716; 5,283,185; 5,279,833; Akimaru (1995) *Cytokines Mol. Ther.* 1:197 210; Alving (1995) *Immunol. Rev.* 145:5 31; and Szoka (1980) *Ann. Rev. Biophys. Bioeng.* 9:467). Biodegradable microspheres or capsules or other biodegradable polymer configurations capable of sustained delivery of small molecules including peptides are known in the art (see, e.g., Putney (1998) *Nat. Biotechnol.* 16:153 157). Compounds of the invention can be incorporated within micelles (see, e.g., Sun- tress (1994) *J. Pharm. Pharmacol.* 46:23 28; Woodle (1992) *Pharm. Res.* 9:260 265). Antagonists can be attached to the surface of the lipid monolayer or bilayer. For example, antagonists can be attached to hydrazide-PEG-(distearoylphosphatidyl-1) ethanolamine-containing liposomes (see, e.g., Zalipsky (1995) *Bioconjug. Chem.* 6: 705 708). Alternatively, any form of lipid membrane, such as a planar lipid membrane or the cell membrane of an intact cell, e.g., a red blood cell, can be used. Liposomal and lipid-containing formulations can be delivered by any means, including, for example, intravenous, transdermal (see, e.g., Vutla (1996) *J. Pharm. Sci.* 85:5 8), transmucosal, or oral administration.

[0434] Compositions of the present invention can be combined with other therapeutic moieties or imaging/diagnostic moieties as provided herein. Therapeutic moieties and/or imaging moieties can be provided as a separate composition, or as a conjugated moiety. Linkers can be included for conjugated moieties as needed and have been described elsewhere herein.

[0435] The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein et al., *Proc. Natl. Acad. Sci. USA*, 82: 3688 (1985); Hwang et al., *Proc. Natl. Acad. Sci. USA*, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Pat. No. 5,013,556.

[0436] Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin et al., *J. Biol. Chem.*, 257: 286 288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon et al., *J. National Cancer Inst.*, 81(19): 1484 (1989).

[0437] Lipofections or liposomes can also be used to deliver the anti-LOX antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein can be used. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, e.g., Marasco et al., *Proc. Natl. Acad. Sci. USA*, 90: 7889 7893 (1993). The formulation herein can also contain more than one active compound as necessary for the particular indication being treated, including, for example, those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition can comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended. The active ingredients can also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methacrylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, supra.

[0438] Formulations for in vivo administration are sterile. Sterilization can be readily accomplished via filtration through sterile filtration membranes.

[0439] Sustained-release preparations can be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ -ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT® (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37° C., resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the

mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S—S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

[0440] Various other pharmaceutical compositions and techniques for their preparation and use will be known to those of skill in the art in light of the present disclosure. For a detailed listing of suitable pharmacological compositions and associated administrative techniques one can refer to the detailed teachings herein, which can be further supplemented by texts such as Remington: The Science and Practice of Pharmacy 20th Ed. (Lippincott, Williams & Wilkins 2003).

[0441] Pharmaceutical compositions contemplated by the present invention have been described above. In one embodiment of the present invention, the pharmaceutical compositions are formulated to be free of pyrogens such that they are acceptable for administration to human patients. Testing pharmaceutical compositions for pyrogens and preparing pharmaceutical compositions free of pyrogens are well understood to one of ordinary skill in the art.

[0442] One embodiment of the present invention contemplates the use of any of the pharmaceutical compositions of the present invention to make a medicament for treating a disorder of the present invention. Medicaments can be formulated based on the physical characteristics of the patient/subject needing treatment, and can be formulated in single or multiple formulations based on the stage of the cancerous tissue. Medicaments of the present invention can be packaged in a suitable pharmaceutical package with appropriate labels for the distribution to hospitals and clinics wherein the label is for the indication of treating a disorder as described herein in a subject. Medicaments can be packaged as a single or multiple units. Instructions for the dosage and administration of the pharmaceutical compositions of the present invention can be included with the pharmaceutical packages and kits described below.

VI. Affinity Purification

[0443] Anti-LOX antibodies and anti-LOXL2 antibodies described herein are useful for affinity purification of LOX or LOXL2 from recombinant cell culture, natural sources or tissue biopsy samples (tissue and/or serum). In this process, antibodies against LOX or LOXL2 are immobilized on a suitable support, such as a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the LOX or LOXL2 to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the LOX or LOXL2, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the LOX or LOXL2 from the antibody.

VII. Packages and Kits

[0444] One embodiment of the present application includes a pharmaceutical package or kit useful for the methods provided herein. One embodiment of such pharmaceutical packages or kits includes preparations (compositions) of the antagonists as provided herein.

[0445] One aspect of the present invention relates to kits for carrying out the administration of a LOX/LOXL2 inhibitor. Another aspect of the present invention relates to kits for carrying out the combined administration of the LOX/LOXL2 inhibitor with one or more other therapeutic agent. In one embodiment, the kit comprises a LOX/LOXL2 inhibitor formulated in a pharmaceutical carrier or excipient, and at least one therapeutic agent that is not said LOX/LOXL2 inhibitor, formulated as appropriate, in one or more separate pharmaceutical preparations.

[0446] Pharmaceutical packages and kits can additionally include an excipient, a carrier, a buffering agent, a preservative or a stabilizing agent in a pharmaceutical formulation. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package. Invention kits can be designed for room temperature or cold storage.

[0447] Additionally, the preparations can contain stabilizers to increase the shelf-life of the kits and include, for example, bovine serum albumin (BSA) or other known conventional stabilizers. Where the compositions are lyophilized, the kit can contain further preparations of solutions to reconstitute the preparations. Acceptable solutions are well known in the art and include, for example, pharmaceutically acceptable phosphate buffered saline (PBS).

[0448] Additionally, the pharmaceutical packages or kits provided herein can further include any of the other moieties provided herein such as, for example, a chemotherapeutic agent as described elsewhere in more detail.

[0449] Pharmaceutical packages and kits of the present invention can further include the components for an assay provided herein, such as, for example, an ELISA assay. Alternatively, preparations of the kits are used in immunoassays, such as immunohistochemistry to test patient tissue biopsy sections. Pharmaceutical packages and kits of the present invention can further include the components for collection of a sample.

[0450] Pharmaceutical packages and kits of the present invention can further include a label specifying, for example, a product description, mode of administration and indication of treatment. Pharmaceutical packages provided herein can include any of the compositions as described herein. The pharmaceutical package can further include a label for preventing, reducing the risk of, or treating any of the disease indications described herein.

[0451] The term "packaging material" refers to a physical structure housing the components of the kit. The packaging material can maintain the components sterily, and can be made of material commonly used for such purposes (e.g., paper, corrugated fiber, glass, plastic, foil, ampules, etc.). The label or packaging insert can include appropriate written instructions. Kits of the invention therefore can additionally include labels or instructions for using the kit components in any method of the invention. A kit can include an invention compound in a pack, or dispenser together with instructions for administering the compound in a method of the invention.

[0452] Instructions can include instructions for practicing any of the methods of the invention described herein including treatment, detection, monitoring or diagnostic methods. Instructions may additionally include indications of a satisfactory clinical endpoint or any adverse symptoms that may occur, or additional information required by regulatory agencies such as the Food and Drug Administration for use on a human subject.

[0453] The instructions may be on "printed matter," e.g., on paper or cardboard within or affixed to the kit, or on a label affixed to the kit or packaging material, or attached to a vial or tube containing a component of the kit. Instructions may additionally be included on a computer readable medium, such as a disk (floppy diskette or hard disk), optical CD such as CD- or DVD-ROM/RAM, magnetic tape, electrical storage media such as RAM and ROM, IC chip and hybrids of these such as magnetic/optical storage media.

[0454] The compositions of the kit of the present invention can be formulated in single or multiple units for either a single test or multiple tests.

[0455] In preferred embodiments, the preparations of the kit are free of pyrogens. Methods for testing for the presence of, and/or specific levels of, pyrogens are routine in the art and kits are commercially available for such purpose.

[0456] Provided herein is a kit for treating a condition associated with LOX or LOXL2, containing a composition of an antibody or antigen binding fragment thereof described herein and a pharmaceutically acceptable carrier or excipient. A condition associated with LOX or LOXL2 can be, for example, a tumor, a metastasis, angiogenesis, or fibrosis. In one embodiment, antibodies in such kits can comprise a detectable label, a therapeutic label or both. In another embodiment, antibodies in such kits can be lyophilized.

[0457] Another aspect of the present invention relates to kits for carrying out the combined administration of the LOX or LOXL2 inhibitor with other therapeutic compounds. In one embodiment, the kit comprises a LOX or LOXL2 inhibitor formulated in a pharmaceutical carrier, and at least one cytotoxic agent, formulated as appropriate, in one or more separate pharmaceutical preparations.

VIII. Diagnostic Methods

[0458] The present invention also provides methods for diagnosing, monitoring, staging or detecting the diseases described above by using agents that recognize different forms of LOX or LOXL2. For example, as described above, antibodies against different forms of LOX or LOXL2, the preproprotein, secreted, mature or active form, can be used for these purposes. Methods of diagnosing, monitoring, staging or detecting the diseases described above by using agents that recognize different forms of LOX or LOXL2 are intended to encompass all of the diseases and indications described herein.

[0459] As described above, active LOX or LOXL2 is cleaved and can be detected by virtue of its change in molecular weight (immunoblot) or by use of antibodies that detect the uncleaved vs. cleaved form of LOX/LOXL, along with cellular localization by using various detection methods such as immunohistochemistry (IHC).

[0460] It is believed that the extracellular matrix and conditioned medium should contain proteolytically processed, active LOX or LOXL whereas uncleaved, inactive LOX/LOXL should be localized intracellularly. Some active, cleaved LOX/LOXL can also be detected inside the cell as a consequence of uptake from the extracellular space.

[0461] Samples from individuals can be collected and analyzed by determining inactive or active LOX levels. This analysis can be performed prior to the initiation of treatment using lysyl oxidase-specific therapy to identify tumors having elevated active LOX/LOXL expression or activity. Such diagnosis analysis can be performed using any sample, including but not limited to cells, protein or membrane extracts of cells,

biological fluids such as sputum, blood, serum, plasma, or urine, or biological samples such as tissue samples, formalin-fixed or frozen tissue sections.

[0462] Any suitable method for detection and analysis of inactive and/or active LOX/LOXL can be employed. As used herein, the term “sample” refers to a sample from a human, animal, or to a research sample, e.g., a cell, tissue, organ, fluid, gas, aerosol, slurry, colloid, or coagulated material. Samples also include, but are not limited to, protein or membrane extracts of cells, biological fluids such as sputum, blood, serum, plasma, or urine, or biological samples such as formalin-fixed or frozen tissue sections employing antibodies described herein. The term “sample” can also refer to a cell, tissue, organ, or fluid that is freshly taken from a human or animal, or to a cell, tissue, organ, or fluid that is processed or stored. The sample can be tested *in vivo*, e.g., without removal from the human or animal, or it can be tested *in vitro*. The sample can be tested after processing, e.g., by histological methods.

[0463] Various diagnostic assay techniques known in the art can be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases (Zola, *Monoclonal Antibodies: A Manual of Techniques*, CRC Press, Inc. (1987) pp. 147-158). The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety directly or indirectly produces a detectable signal. For example, the detectable moiety can be any of those described herein such as, for example, a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate (FITC), Texas red, cyanin, photocyran, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, β -galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety can be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

[0464] Provided herein is a method of diagnosing a condition associated with LOX or LOXL2 comprising assessing a level of LOX and/or LOXL2 in a sample of a subject, wherein a change in level of LOX and/or LOXL2 in the sample in comparison with a reference sample indicates the presence or increase of a tumor or metastasis. In one aspect, the condition associated with LOX or LOXL2 is a tumor, a metastasis, angiogenesis, or fibrosis. An increase in LOX and/or LOXL2 levels in the sample in comparison with a reference sample can indicate the presence of a tumor or metastasis or an increase in tumor or metastatic growth. The reference sample can be a sample taken from the subject at an earlier time point or a sample from another individual. The level of LOX and/or LOXL2 levels in the sample can be detected by contacting the sample with an antibody or antigen binding fragment thereof described herein. In one embodiment, the antibody or antigen binding fragment thereof is detectably labeled.

[0465] In one embodiment, a method is provided for diagnosing cancer metastasis in a subject, comprising: assessing active LOX or LOXL2 levels or activity in the blood, whereby a change in active LOX or LOXL2 levels or activity (e.g., in gene expression, enzymatic activity, etc.) in the blood in comparison with a reference sample, indicates the presence of metastatic tumor growth. In some instances, the active LOX

or LOXL2 levels or activities in the blood can be lower than those when measured earlier, which can indicate that the subject is at a greater risk of cancer metastasis; that the cancer has metastasized; or that cancer metastasis has increased. The reference sample may derive from the same subject, taken from the same tumor at a different time point or from other site of the body, or from another individual.

[0466] In another embodiment, a method is provided for diagnosing cancer metastasis in a subject having a tumor, comprising: assessing active LOX or LOXL2 levels or activity in the tumor, whereby a change in active LOX or LOXL2 levels or activity in the tumor in comparison with a reference sample indicates the presence of metastatic tumor growth. In some instances, the active LOX or LOXL2 levels or activities in the tumor can be higher than those when measured earlier, which can indicate that the subject is at a greater risk of cancer metastasis; that the cancer has metastasized; or that cancer metastasis has increased. The reference sample can derive from the same subject, taken from the same tumor at a different time point or from other site of the body, or from another individual.

[0467] Also provided herein is a method for staging tumor growth or metastasis in a subject, comprising assessing LOX and/or LOXL2 (e.g., hLOX or hLOXL2) levels in a tumor of the subject, whereby a change in LOX and/or LOXL2 level (e.g., in gene expression or enzymatic activity) in the tumor in comparison with a reference sample, indicates the presence of metastatic tumor growth. In some instances, the LOX and/or LOXL2 levels or activities in the tumor may be higher than those when measured earlier for the same subject, or higher than those in a reference sample taken from a normal tissue, which may indicate that the patient is at a greater risk of tumor metastasis; that the tumor has metastasized; or that tumor metastasis has increased.

[0468] Staging of solid tumor cancers is well known. The TNM system is one of the most commonly used staging systems. This system has been accepted by the International Union Against Cancer (UICC) and the American Joint Committee on Cancer (AJCC). Most medical facilities use the TNM system as their main method for cancer reporting. PDQ®, the NCI's comprehensive cancer database, also uses the TNM system. The TNM system, referred to herein as “staging,” is based on the extent of the tumor, the extent of spread to the lymph nodes, and the presence of metastasis.

[0469] Also provided here is a method for monitoring a subject's response to a therapy including a modulator of LOX/LOXL2 such as the treatment of cancer, tumors, and fibrotic diseases. The method comprises: detecting a change in the level of C-reactive protein in the subject after administration of a modulator of LOX or LOXL2 to the subject, wherein the change indicates that the LOX or LOXL2 modulator has a therapeutic effect on the subject. A C-reactive protein is an important pharmacodynamic marker for systemic inflammation. It is believed that a reduced level of C-reactive protein (e.g., in the blood sample of the subject) as compared to that prior to the administration of the LOX or LOXL2 inhibitor is indicative of the subject's response to the therapy using an inhibitor of LOX or LOXL2.

[0470] Measurement of active LOX or LOXL2 levels can take the form of an immunological assay, which detects the presence of an active LOX or LOXL2 protein with an antibody to the protein, preferably an antibody specifically binding to active LOX or LOXL2. Antigen-binding fragments of anti-LOX/LOXL antibodies can also be used.

[0471] Immunoassays also can be used in conjunction with laser induced fluorescence (see, for example, Schmalzing and Nashabeh, *Electrophoresis* 18:2184-93 (1997); and Bao, J. *Chromatogr. B. Biomed. Sci.* 699:463-80 (1997), each of which is incorporated herein by reference). Liposome immunoassays, such as flow-injection liposome immunoassays and liposome immunosensors also can be used to determine active LOX or LOXL levels according to a method of the invention (Rongen et al., *J. Immunol. Methods* 204:105-133 (1997). Immunoassays, such as enzyme-linked immunosorbent assays (ELISAs), can be particularly useful in a method of the invention. A radioimmunoassay also can be useful for determining whether a sample is positive for active LOX or LOXL2 or for determining the level of active LOX or LOXL2. A radioimmunoassay using, for example, an iodine-125 labeled secondary antibody, can be used.

[0472] In addition, one can measure the activity of active LOX or LOXL2, thus ignoring the amount of inactive enzyme. Enzymatic activity of active LOX or LOXL2 can be measured in a number of ways, using a soluble elastin or soluble collagen with labeled lysine as a substrate. Details of an activity assay are given in Royce et al., "Copper metabolism in mottled mouse mutants. The effect of copper therapy on lysyl oxidase activity in brindled (Mobr) mice," *Biochem J.* 1982 Feb. 15; 202(2): 369-371. An exemplary assay is a chromogenic assay, such as that described by Palamakumbura, et al. "A fluorometric assay for detection of lysyl oxidase enzyme activity in biological samples," *Anal Biochem.* 2002 Jan. 15; 300(2):245-51.

[0473] In addition to measuring the level of LOX or LOXL2 in the blood (or urine), one can measure secondary products of LOX or LOXL2 activity. For example, deoxypyridinoline (Dpd) is formed by the enzymatic action of lysyl oxidase on lysine residues. Dpd is released into the circulation as a result of osteoclastic degradation of bone. It cannot be re-used, is cleared by the kidney and is excreted unchanged in urine. Thus, a test based on the Immunodiagnostic Systems (IDS) Gamma BCT Dpd assay, using a coated tube RIA using an anti-Dpd monoclonal antibody can be used to measure enzymatic activity.

[0474] Anti-LOX antibodies and anti-LOXL2 antibodies described herein can also be used in the diagnosis of diseases or conditions associated with aberrant collagen metabolism such as various fibrotic conditions, for example, lung fibrosis, as well as in proliferative vitreous retinopathy, surgical scarring, systemic sclerosis, scleroderma, wound contraction, hypertrophic scars, fibromatosis (especially Dupuytren's disease), and keloids.

IX. Therapeutic Methods

[0475] The pharmaceutical formulations according to the present invention can be used to treat a wide variety of diseases and disorders such as, for example, cancer, metastasis, fibrosis and aberrant angiogenesis.

[0476] Provided herein is a method of inhibiting LOXL2 by contacting a sample, or a cellular tissue with any of the anti-LOXL2 antibodies or antigen binding fragments thereof described herein. Binding of said antibody or antigen binding fragment thereof to LOXL2 inhibits enzymatic activity of LOXL2.

[0477] Also provided herein is a method of inhibiting LOX by contacting a sample or cellular tissue with any of the anti-LOX antibodies or antigen binding fragments thereof

described herein. Binding of said antibody or antigen binding fragment thereof to LOX inhibits enzymatic activity of LOX.

[0478] In either of such methods, contacting can occur in vitro, in vivo or ex vivo.

[0479] Inhibition of LOX or LOXL2 can have one or more effects in a subject such as, for example, reduction in tumor growth, reduction in angiogenesis, reduction in a fibrotic disease, and/or decreasing extracellular matrix formation. Fibrotic diseases include, but are not limited to liver fibrosis, lung fibrosis, kidney fibrosis, cardiac fibrosis, and scleroderma.

[0480] Provided herein are methods of treating diseases and disorders associated with aberrant expression of LOX or LOXL2. Diseases and disorder include, but are not limited to tumors (e.g., primary or metastatic), angiogenesis related conditions and fibrotic conditions.

[0481] As used herein, "prevention" refers to prophylaxis, prevention of onset of symptoms, prevention of progression of a disease or disorder associated with fibrosis or correlated with LOX/LOXL2 activity. As used herein, "treat" or "treatment" means stasis or a postponement of development of the symptoms associated a disease or disorder described herein. The terms further include ameliorating existing uncontrolled or unwanted symptoms, preventing additional symptoms, and ameliorating or preventing the underlying metabolic causes of symptoms. Thus, the terms denote that a beneficial result has been conferred on a mammalian subject with a disease or symptom, or with the potential to develop such disease or symptom. A response is achieved when the patient experiences partial or total alleviation, or reduction of signs or symptoms of illness, and specifically includes, without limitation, prolongation of survival. The expected progression-free survival times can be measured in months to years, depending on prognostic factors including the number of relapses, stage of disease, and other factors. Prolonging survival includes without limitation times of at least 1 month (mo), about at least 2 months (mos.), about at least 3 mos., about at least 4 mos., about at least 6 mos., about at least 1 year, about at least 2 years, about at least 3 years, or more. Overall survival can also be measured in months to years. The patient's symptoms can remain static or can decrease.

[0482] Pharmaceutical compositions of the present invention are administered in therapeutically effective amounts which are effective for producing some desired therapeutic effect at a reasonable benefit/risk ratio applicable to any medical treatment. For the administration of the present pharmaceutical compositions to human patients, the pharmaceutical compositions of the present invention can be formulated by methodology known by one of ordinary skill in the art to be substantially free of pyrogens such that they do not induce an inflammatory response.

[0483] As used herein, the term "therapeutically effective amount" or "effective amount" refers to an amount of a therapeutic agent that when administered alone or in combination with another therapeutic agent to a cell, tissue, or subject is effective to prevent or ameliorate the disease condition or the progression of the disease. A therapeutically effective dose further refers to that amount of the compound sufficient to result in amelioration of symptoms, e.g., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient administered alone, a therapeutically effective dose refers to that ingredient alone. When applied to

a combination, a therapeutically effective dose refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously. For example, when in vivo administration of an anti-LOX/anti-LOXL2 antibody is employed, normal dosage amounts can vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 µg/kg/day to 50 mg/kg/day, optionally about 100 µg/kg/day to 20 mg/kg/day, 500 µg/kg/day to 10 mg/kg/day, or 1 mg/kg/day to 10 mg/kg/day, depending upon the route of administration.

[0484] An effective response of the present invention is achieved when the patient experiences partial or total alleviation or reduction of signs or symptoms of illness, and specifically includes, without limitation, prolongation of survival. The expected progression-free survival times may be measured in months to years, depending on prognostic factors including the number of relapses, stage of disease, and other factors. Prolonging survival includes without limitation times of at least 1 month (mo), about at least 2 mos., about at least 3 mos., about at least 4 mos., about at least 6 mos., about at least 1 year, about at least 2 years, about at least 3 years, or more. Overall survival is also measured in months to years. The patient's symptoms may remain static, and the tumor burden may not increase.

[0485] A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the effective amount (ED50) of the pharmaceutical composition required. For example, the physician or veterinarian can start doses of the compounds of the invention employed in the pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

[0486] As used herein, the term "subject" means mammalian subjects. Exemplary subjects include, but are not limited to humans, monkeys, dogs, cats, mice, rats, cows, horses, goats and sheep. In some embodiments, the subject has cancer and can be treated with the agent of the present invention as described below.

[0487] Regardless of the route of administration selected, the compounds of the present invention, which are used in a suitably hydrated form, and/or the pharmaceutical compositions of the present invention are formulated into pharmaceutically acceptable dosage forms such as described below or by other conventional methods known to those of skill in the art.

[0488] Actual dosage levels of the active ingredients in the pharmaceutical compositions of this invention may be varied so as to obtain an amount of the active ingredient that is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient.

[0489] The selected dosage level will depend upon a variety of factors including the activity of the particular compound of the present invention employed, the route of administration, the time of administration, the rate of excretion of the particular compound being employed, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular composition employed, the age, sex, weight, condition, general health and prior medical history of the patient being treated, and like factors well known in the medical arts.

[0490] In one aspect provided herein, administration of the antibodies results in an improvement the subject's condition.

In another aspect, administration of the antibodies prevents the subject's condition from worsening and/or prolongs survival of the patient.

[0491] The patient can be a mammal such as a human or a non-human. Such a patient can be symptomatic or asymptomatic.

[0492] Compositions can be administered locally, regionally or systemically by any suitable route provided herein.

[0493] In one aspect, symptoms of the patient are ameliorated. Amelioration can be manifested as, for example, reduction in pain, reduced tumor size, elimination of tumors, prevention of increases in tumor size or progression or of disease, prevention of formation of metastasis, or inhibition of metastatic growth, inhibition of fibrosis, inhibition of angiogenesis, or a combination thereof.

[0494] If needed, for cancer treatments, methods can further include surgical removal of the cancer and/or administration of an anti-cancer agent or treatment. Administration of such an anti-cancer agent or treatment can be concurrent with administration of the compositions disclosed herein. Anti-cancer agents have been provided elsewhere herein.

[0495] In one aspect, administration of any of the antibodies provided herein reduces or eliminates the need for the patient to undergo surgery or treatment with one or more anti-cancer agents or treatments.

[0496] Indications that can be treated using the pharmaceutical formulations of the present invention include those involving undesirable or uncontrolled cell proliferation. Such indications include benign tumors, various types of cancers such as primary tumors and tumor metastasis, restenosis (e.g., coronary, carotid, and cerebral lesions), hematological disorders, abnormal stimulation of endothelial cells (atherosclerosis), insults to body tissue due to surgery, abnormal wound healing, abnormal angiogenesis, diseases that produce fibrosis of tissue, macular degeneration, glaucoma; age-related macular degeneration (wet AMD and dry AMD), atherosclerosis, rheumatoid arthritis, multiple sclerosis, liver fibrosis, kidney fibrosis, lung fibrosis, scleroderma, atherosclerosis, and Alzheimer's disease, repetitive motion disorders, disorders of tissues that are not highly vascularized, and proliferative responses associated with organ transplants.

[0497] Liver fibrosis includes, but is not limited to, cirrhosis, and associated conditions such as chronic viral hepatitis, non-alcoholic fatty liver disease (NAFLD), alcoholic steatohepatitis (ASH), non-alcoholic steatohepatitis (NASH), primary biliary cirrhosis (PBC), biliary cirrhosis, and autoimmune hepatitis.

[0498] Lung fibrosis includes, but is not limited to, idiopathic pulmonary fibrosis (IPF) or cryptogenic fibrosing alveolitis, chronic fibrosing interstitial pneumonia, interstitial lung disease (ILD), diffuse parenchymal lung disease (DPLD), emphysema and chronic obstructive pulmonary disease (COPD), and chronic asthma.

[0499] Cardiac fibrosis includes, but is not limited to, congestive heart failure, cardiomyopathy, and post-myocardial infarction defects in heart function.

[0500] Kidney fibrosis includes, but is not limited to, diabetic nephropathy, vesicoureteral reflux, tubulointerstitial renal fibrosis; glomerulonephritis or glomerular nephritis, including focal segmental glomerulosclerosis and membranous glomerulonephritis, and Mesangiocapillary glomerular nephritis.

[0501] Generally, cells in a benign tumor retain their differentiated features and do not divide in a completely uncon-

trolled manner. A benign tumor is usually localized and non-metastatic. Specific types benign tumors that can be treated using the present invention include hemangiomas, hepatocellular adenoma, cavernous haemangioma, focal nodular hyperplasia, acoustic neuromas, neurofibroma, bile duct adenoma, bile duct cystadenoma, fibroma, lipomas, leiomyomas, mesotheliomas, teratomas, myxomas, nodular regenerative hyperplasia, trichomas, pyogenic granulomas, moles, uterine fibroids, thyroid adenomas, adrenocortical adenomas, and pituitary adenomas.

[0502] In a malignant tumor cells become undifferentiated, do not respond to the body's growth control signals, and multiply in an uncontrolled manner. The malignant tumor is invasive and capable of spreading to distant sites (metastasizing). Malignant tumors are generally divided into two categories: primary and secondary. Primary tumors arise directly from the tissue in which they are found. A secondary tumor, or metastasis, is a tumor which is originated elsewhere in the body but has now spread to a distant organ. The common routes for metastasis are direct growth into adjacent structures, spread through the vascular or lymphatic systems, and tracking along tissue planes and body spaces (peritoneal fluid, cerebrospinal fluid, etc.)

[0503] Specific types of cancers or malignant tumors, either primary or secondary, that can be treated using this invention include, but are not limited to, lung cancer (including lung adenocarcinoma, squamous cell carcinoma, large cell carcinoma, bronchioloalveolar carcinoma, non-small-cell carcinoma, small cell carcinoma, mesothelioma); breast cancer (including ductal carcinoma, lobular carcinoma, inflammatory breast cancer, clear cell carcinoma, mucinous carcinoma); colorectal cancer (colon cancer, rectal cancer); anal cancer; pancreatic cancer (including pancreatic adenocarcinoma, islet cell carcinoma, neuroendocrine tumors); prostate cancer; ovarian carcinoma (ovarian epithelial carcinoma or surface epithelial-stromal tumour including serous tumour, endometrioid tumor and mucinous cystadenocarcinoma, sex-cord-stromal tumor); liver and bile duct carcinoma (including hepatocellular carcinoma, cholangiocarcinoma, hemangioma); esophageal carcinoma (including esophageal adenocarcinoma and squamous cell carcinoma); non-Hodgkin's lymphoma; bladder carcinoma; carcinoma of the uterus (including endometrial adenocarcinoma, uterine papillary serous carcinoma, uterine clear-cell carcinoma, uterine sarcomas and leiomyosarcomas, mixed mullerian tumors); glioma, glioblastoma, medulloblastoma, and other tumors of the brain; kidney cancers (including renal cell carcinoma, clear cell carcinoma, Wilm's tumor); cancer of the head and neck (including squamous cell carcinomas); cancer of the stomach (stomach adenocarcinoma, gastrointestinal stromal tumor); multiple myeloma; testicular cancer; germ cell tumor; neuroendocrine tumor; cervical cancer; carcinoids of the gastrointestinal tract, breast, and other organs; signet ring cell carcinoma; mesenchymal tumors including sarcomas, fibrosarcomas, haemangioma, angiomatosis, haemangiopericytoma, pseudoangiomatous stromal hyperplasia, myofibroblastoma, fibromatosis, inflammatory myofibroblastic tumour, lipoma, angiolipoma, granular cell tumour, neurofibroma, schwannoma, angiosarcoma, liposarcoma, rhabdomyosarcoma, osteosarcoma, leiomyoma or a leiomyosarcoma.

[0504] The term "metastasis" means the ability of tumor cells to invade host tissues and metastasize to distant, often specific organ sites. As is known, this is the salient feature of

lethal tumor growths. Metastasis formation occurs via a complex series of unique interactions between tumor cells and normal host tissues and cells. In the context of the present invention, lysyl oxidase activity is critical in the metastatic growth of tumors, i.e., the growth of metastases, particularly under hypoxic conditions. As hypoxic tumors are also the most aggressive and resistant to traditional chemotherapy, agents modulating lysyl oxidase expression and/or function provide a novel therapy against metastatic tumors, particularly chemo-resistant tumors. "Metastasis" is distinguished from invasion. As described in "Understanding Cancer Series: Cancer," in the world wide web site: cancer.gov/cancer-topics/understandingcancer/cancer; invasion refers to the direct migration and penetration by cancer cells into neighboring tissues.

[0505] Hematologic disorders include abnormal growth of blood cells which can lead to dysplastic changes in blood cells and hematologic malignancies such as various leukemias. Examples of hematologic disorders include but are not limited to acute myeloid leukemia, acute promyelocytic leukemia, acute lymphoblastic leukemia, chronic myelogenous leukemia, the myelodysplastic syndromes, and sickle cell anemia.

[0506] Acute myeloid leukemia (AML) is the most common type of acute leukemia that occurs in adults. Several inherited genetic disorders and immunodeficiency states are associated with an increased risk of AML. These include disorders with defects in DNA stability, leading to random chromosomal breakage, such as Bloom's syndrome, Fanconi's anemia, Li-Fraumeni kindreds, ataxia-telangiectasia, and X-linked agammaglobulinemia.

[0507] Acute promyelocytic leukemia (APML) represents a distinct subgroup of AML. This subtype is characterized by promyelocytic blasts containing the 15; 17 chromosomal translocation. This translocation leads to the generation of the fusion transcript comprised of the retinoic acid receptor and a sequence PML.

[0508] Acute lymphoblastic leukemia (ALL) is a heterogeneous disease with distinct clinical features displayed by various subtypes. Reoccurring cytogenetic abnormalities have been demonstrated in ALL. The most common cytogenetic abnormality is the 9; 22 translocation. The resultant Philadelphia chromosome represents poor prognosis of the patient.

[0509] Chronic myelogenous leukemia (CML) is a clonal myeloproliferative disorder of a pluripotent stem cell. CML is characterized by a specific chromosomal abnormality involving the translocation of chromosomes 9 and 22, creating the Philadelphia chromosome. Ionizing radiation is associated with the development of CML.

[0510] The myelodysplastic syndromes (MDS) are heterogeneous clonal hematopoietic stem cell disorders grouped together because of the presence of dysplastic changes in one or more of the hematopoietic lineages including dysplastic changes in the myeloid, erythroid, and megakaryocytic series. These changes result in cytopenias in one or more of the three lineages. Patients afflicted with MDS typically develop complications related to anemia, neutropenia (infections), or thrombocytopenia (bleeding). Generally, from about 10% to about 70% of patients with MDS develop acute leukemia.

[0511] Administration of LOX or LOX2 inhibitors has been found to reduce the size of existing tumors, to prevent metastases, and to reduce the size of (or even eliminate)

existing metastases (see, e.g., Molnar et al. (2003) *Biochim Biophys. Acta.* 1647:220-224).

[0512] Provided herein is a method of reducing tumor growth in a subject, by administering any of the anti-LOX or anti-LOXL2 antibodies or antigen binding fragments thereof described herein. In one embodiment, a tumor is a primary tumor. In another embodiment, a tumor is a metastatic tumor. Metastatic tumor burden of a subject can be stabilized by administering antibodies as described herein. Tumor in the subject can be reduced by at least 10%, 25%, 50%, 70%, 90%, 95%, or more as compared to the tumor in the subject prior to treatment.

[0513] When an antibody or antigen binding fragment thereof specifically binds to LOXL2, examples of tumors include, but are not limited to, a colon tumor, an esophageal tumor, a breast tumor, a prostate tumor, a squamous carcinoma or a spindle cell carcinoma.

[0514] When an antibody or antigen binding fragment thereof specifically binds to LOX, examples of tumors include, but are not limited to, a breast tumor, a lung tumor, a kidney tumor, a uterine tumor, a liver tumor, or a head and neck tumor.

[0515] Provided herein is a method for preventing or reducing tumor growth, metastatic tumor growth, in a subject in vivo, comprising administering to a subject in need thereof an effective amount of an inhibitor of LOX or LOXL2 activity; and optionally, a pharmaceutically acceptable carrier or excipient, thereby preventing or reducing tumor growth, for example by at least 25%, 50%, 75%, 90%, or 95%, in the subject treated. A detailed description of suitable compositions for use in the present treatment methods is given above. Such methods are useful, for example, when the tumor is hypoxic. Hypoxic tumors can be readily identified using routine methods in the art. See, e.g., U.S. Pat. No. 5,674,693.

[0516] Also, provided herein is a method of treating metastasis in a subject with cancer in vivo, comprising administering to a subject in need thereof an effective amount of a LOX or LOXL2 inhibitor, thereby inhibiting metastasis, for example, by at least 25%, 50%, 75%, 90%, or 95%, in the subject treated. In one embodiment, inhibitors specifically inhibit human LOX or human LOXL2. Antibodies to be used in these methods have been described above. The antibody may be desirable to minimize cross-reactions with other members of the LOX or LOXL2 families and, thus, reduce the potential adverse side effects due to complications and normal tissue toxicity.

[0517] Also provided herein is a method of increasing or enhancing the chances of survival of a subject with metastatic tumor, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody, thereby increasing or enhancing the chances of survival of the subject treated by a certain period of time, for example, by at least 10 days, 1 month, 3 months, 6 months, 1 year, 1.5 years, 2 years, 3 years, 4 years, 5 years, 8 years, 10 years, or more. The increase in survival of a subject can be defined, for example, as the increase in survival of a preclinical animal model of cancer metastases (e.g., a mouse with metastatic cancer), by a certain period of time, for example, by at least 10 days, 1 month, 3 months, 6 months, or 1 year, or at least 2 times, 3 times, 4 times, 5 times, 8 times, or 10 times, more than a control animal model (that has the same type of metastatic cancer) without the treatment with the inventive method. Alternatively, the increase in survival of a mammal can also be defined, for example, as the increase in

survival of a patient with cancer metastases by a certain period of time, for example, by at least 10 days, 1 month, 3 months, 6 months, 1 year, 1.5 years, 2 years, 3 years, 4 years, 5 years, 8 years, 10 years or more than a patient with the same type of metastatic cancer but without the treatment with the inventive method. The control patient may be on a placebo or treated with supportive standard care such as chemical therapy, biologics and/or radiation that do not include the inventive method as a part of the therapy.

[0518] Also provided herein is a method of stabilizing metastatic tumor burden of a subject, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody, thereby stabilizing metastatic tumor burden of a subject for a certain period of time, for example, for at least 10 days, 1 month, 3 months, 6 months, 1 year, 1.5 years, 2 years, 3 years, 4 years, 5 years, 8 years, 10 years or more. Stabilization of the metastatic tumor burden of a subject can be defined as stabilization of metastatic tumor burden of a preclinical animal model with metastatic tumor burden (e.g., a mouse with metastatic tumor) for a certain period of time, for example, for at least 10 days, 1 month, 3 months, 6 months, or 1 year more than a control animal model (that has the same type of metastatic tumor) without the treatment with the inventive method.

[0519] The present treatment methods also include a method to increase the efficacy of chemotherapeutic agents, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient, thereby increasing the efficacy of chemotherapeutic agents (which are described in more detail above). Also contemplated are methods involving the delivery of LOX inhibitory formulations in combination with radiation therapy. Radiation therapy may be used to treat almost every type of solid tumor, including cancers of the brain, breast, cervix, larynx, lung, pancreas, prostate, skin, spine, stomach, uterus, or soft tissue sarcomas. Radiation can also be used to treat leukemia and lymphoma (cancers of the blood-forming cells and lymphatic system, respectively). Radiation dose to each site depends on a number of factors, including the type of cancer and whether there are tissues and organs nearby that may be damaged by radiation. Radiation will typically be delivered as X-rays, where the dosage is dependent on the tissue being treated. Radiopharmaceuticals, also known as radionucleotides, may also be used to treat cancer, including thyroid cancer, cancer that recurs in the chest wall, and pain caused by the spread of cancer to the bone (bone metastases). Radionuclides have been described in more detail above.

[0520] The subject to be treated or diagnosed by the present methods includes a subject having or being at risk of having metastatic tumor growth. Such tumors can be a In one aspect, a tumor is, for example, Lung cancer (including lung adenocarcinoma, squamous cell carcinoma, large cell carcinoma, bronchioloalveolar carcinoma, non-small-cell carcinoma, small cell carcinoma, mesothelioma); breast cancer (including ductal carcinoma, lobular carcinoma, inflammatory breast cancer, clear cell carcinoma, mucinous carcinoma.); colorectal cancer (colon cancer, rectal cancer); anal cancer; pancreatic cancer (including pancreatic adenocarcinoma, islet cell carcinoma, neuroendocrine tumors); prostate cancer; ovarian carcinoma (ovarian epithelial carcinoma or surface epithelial-stromal tumour including serous tumour, endometrioid tumor and mucinous cystadenocarcinoma, sex-

cord-stromal tumor); liver and bile duct carcinoma (including hepatocellular carcinoma, cholangiocarcinoma, hemangioma); esophageal carcinoma (including esophageal adenocarcinoma and squamous cell carcinoma); non-Hodgkin's lymphoma; bladder carcinoma; carcinoma of the uterus (including endometrial adenocarcinoma, uterine papillary serous carcinoma, uterine clear-cell carcinoma, uterine sarcomas and leiomyosarcomas, mixed müllerian tumors); glioma, glioblastoma, medulloblastoma, and other tumors of the brain; kidney cancers (including renal cell carcinoma, clear cell carcinoma, Wilm's tumor); cancer of the head and neck (including squamous cell carcinomas); cancer of the stomach (stomach adenocarcinoma, gastrointestinal stromal tumor); multiple myeloma; testicular cancer; germ cell tumor; neuroendocrine tumor; cervical cancer; carcinoids of the gastrointestinal tract, breast, and other organs; signet ring cell carcinoma; mesenchymal tumors including sarcomas, fibrosarcomas, haemangioma, angiomatosis, haemangiopericytoma, pseudoangiomatous stromal hyperplasia, myofibroblastoma, fibromatosis, inflammatory myofibroblastic tumour, lipoma, angiolipoma, granular cell tumour, neurofibroma, schwannoma, angiosarcoma, liposarcoma, rhabdomyosarcoma, osteosarcoma, leiomyoma or a leiomyosarcoma. In one non-limiting embodiment, the tumor is a breast tumor, a pancreas tumor, a lung tumor, a cervical tumor, a colon tumor or a head and neck tumor.

[0521] The present invention also provides a method for preventing or reducing the risk of tumor metastasis in a subject, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient, thereby preventing or reducing preventing or reducing the risk of tumor metastasis. The inhibitor can be an antibody or an antigen binding fragment thereof. The subject in need of such a prophylactic can be an individual who is genetically predisposed to cancer or at a high risk of developing cancer due to various reasons such as family history of cancer and carcinogenic environment.

[0522] Examples of the human gene that is involved in the onset or development of cancer include, but are not limited to, VHL (the Von Hippel Landau gene involved in Renal Cell Carcinoma); P16/INK4A (involved in lymphoma); E-cadherin (involved in metastasis of breast, thyroid, gastric cancer); hMLH1 (involved in DNA repair in colon, gastric, and endometrial cancer); BRCA1 (involved in DNA repair in breast and ovarian cancer); LKB1 (involved in colon and breast cancer); P15/INK4B (involved in leukemia such as AML and ALL); ER (estrogen receptor, involved in breast, colon cancer and leukemia); O6-MGMT (involved in DNA repair in brain, colon, lung cancer and lymphoma); GST-pi (involved in breast, prostate, and renal cancer); TIMP-3 (tissue metalloprotease, involved in colon, renal, and brain cancer metastasis); DAPK1 (DAP kinase, involved in apoptosis of B-cell lymphoma cells); P73 (involved in apoptosis of lymphomas cells); AR (androgen receptor, involved in prostate cancer); RAR-beta (retinoic acid receptor-beta, involved in prostate cancer); Endothelin-B receptor (involved in prostate cancer); Rb (involved in cell cycle regulation of retinoblastoma); p53 (an important tumor suppressor gene); P14ARF (involved in cell cycle regulation); RASSF1 (involved in signal transduction); APC (involved in signal transduction); Caspase-8 (involved in apoptosis); TERT (involved in senescence); TERC (involved in senescence); TMS-1 (involved in apoptosis); SOCS-1 (involved in growth factor

response of hepatocarcinoma); PITX2 (hepatocarcinoma breast cancer); MINT1; MINT2; GPR37; SDC4; MYO1D1; MDR1; THBS1; PTC1; and pMDR1, as described in Santini et al. (2001) *Ann. of Intern. Med.* 134:573-586, which is herein incorporated by reference in its entirety. Nucleotide sequences of these genes can be retrieved from the website of the National Center for Biotechnology Information (NCBI).

[0523] It should be noted that, although leukemia is a cancer of the blood, it might affect other organs, or, in effect, metastasize. In acute leukemias, the abnormal cells may collect in the central nervous system, the testicles, the skin and any other organ in the body. Because leukemia already involves all of the bone marrow in the body, and in many cases, has spread to other organs such as the liver, spleen, and lymph nodes, the staging of leukemia depends on other information that reflects the patient's outlook for survival. Leukemias include, for example, Acute lymphoblastic leukemia (ALL), Chronic lymphocytic leukemia (CLL), Acute myelogenous leukemia (AML), Chronic myelogenous leukemia (CML) and Hairy cell leukemia (HCL). Different staging systems are used for different types of chronic leukemia. Some types do not have any staging system. Methods of staging are described in more detail below.

[0524] Treatment of abnormal cell proliferation due to insults to body tissue during surgery can be possible for a variety of surgical procedures, including joint surgery, bowel surgery, and keloid scarring. Diseases that produce fibrotic tissue include emphysema. Repetitive motion disorders that can be treated using the present invention include carpal tunnel syndrome. An example of cell proliferative disorders that can be treated using the invention is a bone tumor. Provided herein is a method for preventing or reducing the risk of abnormal cell proliferation due to insults to body tissue during surgery or a disease that produces fibrotic tissue in a subject, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient, thereby preventing or reducing abnormal cell proliferation due to insults to body tissue during surgery. The inhibitor can be an antibody or an antigen binding fragment thereof. The subject in need of such a prophylactic can be an individual who is genetically predisposed to cancer or at a high risk of developing cancer due to various reasons such as family history of cancer and carcinogenic environment. In one embodiment, the disease can be, for example, joint surgery, bowel surgery, keloid scarring, a disease that produces fibrotic tissue, repetitive motion disorders of a bone tumor.

[0525] The proliferative responses associated with organ transplantation that can be treated using this invention include those proliferative responses contributing to potential organ rejections or associated complications. Specifically, these proliferative responses can occur during transplantation of the heart, lung, liver, kidney, and other body organs or organ systems. Provided herein is a method of treating an abnormal proliferative response associated with organ transplantation, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient, thereby preventing or reducing abnormal cell proliferation due to organ transplantation. Transplantation can include, for example, transplant of heart, lung, liver, kidney, and other body organs or organ systems.

[0526] The indication for the inventive composition also includes fibrosis. Fibrosis results from abnormal accumulation of fibrous tissue that can occur as a part of the wound-healing process in damaged tissue. Such tissue damage may result from physical injury, inflammation, infection, exposure to toxins, and other causes. Examples of fibrosis include liver fibrosis, lung fibrosis, kidney fibrosis, cardiac fibrosis and scleroderma. The compounds and agents of the described invention are also contemplated for the treatment, prevention, and/or amelioration of fibrotic conditions.

[0527] Fibrotic tissues accumulate in the heart and blood vessels as a result of hypertension, hypertensive heart disease, atherosclerosis, and myocardial infarction. High blood pressure, or hypertension, can be caused by a variety of factors and often leads to the development of Hypertensive Heart Disease (HHD) with progression to cardiac arrest and myocardial infarction. Similarly, atherosclerosis and other ischemic heart diseases often also result in cardiac arrest. These cardiovascular diseases all exhibit an accumulation of extra-cellular matrix or fibrotic deposition which results in stiffening of the vasculature and stiffening of the cardiac tissue itself. This deposition of fibrotic material is a response to the damage induced by the hypertensive and/or sclerotic state, but the effects of this response also result in the negative effects of vascular and cardiac stiffening as well as ventricle enlargement. Additionally, it is believed that the increased cardiac fibrosis seen in cardiovascular disease disrupts or alters the signals transmitted to cardiomyocytes via the tissue scaffolding of the heart, further leading to disruption of efficient cardiac function and promoting cardiac arrest and myocardial infarction. Given the identified role of increased extracellular matrix deposition in cardiac fibrosis, the compounds of the present invention are useful for the prevention, treatment, and/or amelioration of cardiac fibrosis by the inhibition of LOX/LOXL2.

[0528] The present invention also provides compositions, methods, systems, medical devices or kits for the treatment or prevention of cardiac fibrosis associated with cardiovascular diseases such as hypertensive heart disease (HHD), myocardial infarction (MI), atherosclerosis, restenosis (e.g. coronary, carotid, and cerebral lesions), and heart disease associated with cardiac ischemic events.

[0529] The post MI-healing response can induce expression of LOX/LOXL2 but if this process continues unchecked, excessive cross-linking leads to extracellular matrix remodeling or fibrosis that results in cardiac dysfunction. The enzymes that break down matrices and cross-linked collagen or elastin appear to function more slowly or less efficiently and are outpaced by the cross-linking events. As LOX/LOXL2 also plays a role in epithelial-mesenchymal transition (EMT), this contributes further to cardiomyocyte remodeling and cardiomyocyte hypertrophy, in addition to matrix remodeling.

[0530] Initial reparative fibrosis induced by the MI may be helpful (e.g., prevents aneurysm and related damage) and can be allowed to proceed unhindered. However, while not wishing to be bound to a particular theory or mechanism of action, the inventors believe that anti-LOX/LOXL2 treatment initiated following this reparative fibrosis phase could attenuate reactive (mal-adaptive) fibrosis that leads to cardiac dysfunction. For example, anti-LOX/LOXL2 treatment can be initiated 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 36, or 48 hours after MI, inclusive of all integers in-between. Additionally, anti-LOX/LOXL2 treatment can be initiated 2, 3, 4, 5, 6, 7, 8,

9, 10, 11, 12, 13, or 14 days after MI. Similarly, increases in blood pressure (hypertension) result in increased collagen deposition and reduced protein degradation in cardiac tissue. (Berk et al., *J. Clin. Invest.*, 117(3): 568-575 (2007)). Anti-LOX/LOXL2 treatment initiated following diagnosis and/or establishment of Hypertensive Heart Disease or hypertension can prevent, reduce, or ameliorate fibrosis associated with hypertension. Such anti-LOX/LOXL2 treatment is initiated 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13 or 14 days after increases in hypertension or systemic blood pressure are diagnosed or detected.

[0531] As another example, biomarkers may be used to determine when an inappropriate level of cross-linking might be occurring: for example, LOX levels have been shown to correlate with C reactive protein (CRP), a commonly used biomarker, and treatment could begin when CRP levels are elevated above appropriate normal levels. More directly, methods and test kits exist to measure the release of cross-linked collagen telopeptides in urine or blood. Elevated levels of these collagen fragments could indicate a transition from reparative fibrosis to reactive (mal-adaptive) fibrosis. In addition, measures of cardiac function and output, including those associated with efficient contraction of the ventricle, can be made.

[0532] An inhibitor of LOX/LOXL2 can be delivered to a subject prior to, concurrently, or post a pathological cardiac condition or disease, such as hypertension, hypertensive heart disease (HHD), myocardial infarction (MI), atherosclerosis, and restenosis, to prevent the onset of, to reduce the risk of, or to retreat pathological fibrosis associated with such a pathological cardiac condition or disease. For example, an inhibitor of LOX/LOXL2 can be administered at least 1 hr, 2 hrs, 3 hrs, 5 hrs, or 10 hrs, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, or 14 days after the onset of such a pathological cardiac condition or disease.

[0533] Additionally, a limited duration of treatment is envisioned. Treatment should be sustained only long enough to prevent or attenuate reactive fibrosis to prevent or reduce cardiac dysfunction. For example, short-lived FAB antibody fragments are used when shorter durations of treatment are desired. Alternatively, full-length antibodies that have a longer half-life in serum can be used, with limited dosing over 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 weeks, inclusive of all days in-between. Standard tests of cardiac function can be used to monitor progress and adjust dosing as necessary, along with assessment of relevant biomarkers discussed above. Limited duration of treatment adds to the safety of this approach.

[0534] Fibrosis of the liver is implicated in the pathology of numerous hepatic diseases. As previously noted, fibrosis occurs as a complication of haemochromatosis, Wilson's disease, alcoholism, schistosomiasis, viral hepatitis, bile duct obstruction, exposure to toxins, and metabolic disorders. Left unchecked, hepatic fibrosis progresses to cirrhosis (defined by the presence of encapsulated nodules), liver failure, and death. The chronic insults to the liver from such sources as parasites and viral infection (e.g. HBV, HCV, HIV, schistosomiasis) or the long term stress from alcohol consumption inevitably result in remodeling of the liver, presumably to encapsulate the damaged area and protect the remaining liver tissue from damage. (Li and Friedman, *Gastroenterol. Hepatol.* 14:618-633, 1999). Liver fibrosis results in extracellular matrix changes, including 3-10 fold increases in total collagen content and replacement of the low density basement membrane with high-density matrix, which impair the meta-

bolic and synthesis function of hepatocytes, hepatic stellate cells and endothelial cells. (Girogescu, M., Non-invasive Biochemical Markers of Liver Fibrosis, *J. Gastrointest. Liver Dis.*, 15(2): 149-159 (2006)). The compounds of the instant invention are thus useful for the prevention, treatment, and/or amelioration of fibrotic liver diseases, and such use is contemplated herein by inhibition of LOX/LOXL2.

[0535] Like liver fibrosis, kidney fibrosis can result from various diseases and insults to the kidneys. Examples of such diseases and insults include chronic kidney disease, metabolic syndrome, diabetes and resultant glomerular nephritis. It has become recognized that metabolic syndrome is a cluster of abnormalities including diabetic hallmarks such as insulin resistance as well as central or visceral obesity and hypertension. In nearly all cases, dysregulation of glucose results in the stimulation of cytokine release and upregulation of extracellular matrix deposition. Additional factors contributing to chronic kidney disease, diabetes, metabolic syndrome, and glomerular nephritis include hyperlipidemia, hypertension, and proteinuria, all of which result in further damage to the kidneys and further stimulate the extracellular matrix deposition. Thus, regardless of the primary cause, insults to the kidneys result in kidney fibrosis and the concomitant loss of kidney function. (Skena, F. and Gesualdo, L., Pathogenic Mechanisms of Diabetic Nephropathy, *J. Am. Soc. Nephrol.*, 16: S30-33 (2005); Whaley-Connell, A., and Sower, J. R., Chronic Kidney Disease and the Cardiometabolic Syndrome, *J. Clin. Hypert.*, 8(8): 546-48 (2006)). The compounds of the instant invention are thus useful for the prevention, treatment, and/or amelioration of fibrotic kidney diseases (chronic kidney disease, diabetic nephropathy, glomerular nephritis, metabolic syndrome), and such use is contemplated herein.

[0536] Fibrosis of the lung includes many syndromes and diseases. Exemplary diseases include Idiopathic pulmonary fibrosis (IPF), Idiopathic Interstitial Pneumonia, and Acute Respiratory Distress Syndrome (ARDS). The pathogenesis of most lung fibroses, including the aforementioned diseases are not well understood, however all are characterized by an influx of inflammatory cells and a subsequent increase in the synthesis and deposition of collagen-rich extracellular matrix. (Chua et al., *Am J. Respir. Cell. Mol. Biol.*, 33:9-13 (2005); Tzortzaki et al., *J. Histochem. & Cytochem.*, 54(6): 693-700 (2006); Armstrong et al., *Am. J. Respir. Crit. Care Med.*, 160: 1910-1915 (1999)). Given the identified role of increased collagen and extracellular matrix deposition in lung fibroses, the compounds of the present invention are useful for the prevention, treatment, and/or amelioration of lung fibroses by the inhibition of LOX/LOXL2.

[0537] Scleroderma is an autoimmune disorder, in which there is an overproduction of abnormal collagen. This excess collagen accumulates throughout the body, causing hardening (sclerosis), scarring (fibrosis), and other damage. The damage may affect the appearance of the skin, or it may involve only the internal organs. The symptoms and severity of scleroderma vary from person to person. Given the identified role of increased collagen in scleroderma, the compounds of the present invention are useful for the prevention, treatment, and/or amelioration of scleroderma by the inhibition of LOX/LOXL2.

[0538] Abnormal angiogenesis that can be treated or prevented by using this invention include those abnormal angiogenesis accompanying rheumatoid arthritis, ischemic-reperfusion related brain edema and injury, cortical ischemia, ovarian hyperplasia and hypervascularity, (polycystic ovary

syndrome), endometriosis, psoriasis, diabetic retinopathy, and other ocular angiogenic diseases such as retinopathy of prematurity (retrolental fibroplastic), muscular degeneration, corneal graft rejection, neurovascular glaucoma and Oster-Weber syndrome.

[0539] Diseases associated with abnormal angiogenesis require or induce vascular growth. For example, corneal angiogenesis involves three phases: a pre-vascular latent period, active neovascularization, and vascular maturation and regression. The identity and mechanism of various angiogenic factors, including elements of the inflammatory response, such as leukocytes, platelets, cytokines, and eicosanoids, or unidentified plasma constituents have yet to be revealed.

[0540] Anti-LOX antibodies and anti-LOXL2 antibodies described herein can be used for treating diseases associated with undesired or abnormal angiogenesis. The method comprises administering to a patient suffering from undesired or abnormal angiogenesis a LOX/LOXL inhibitor in combination with anti-neoplastic agent or anti-angiogenic agent that is not said LOX/LOXL inhibitor. The particular dosage of these agents required to inhibit (partially or completely) angiogenesis and/or angiogenic diseases can depend on the severity of the condition, the route of administration, and related factors that can be decided by the attending physician. Generally, accepted and effective daily doses are the amount sufficient to effectively inhibit angiogenesis and/or angiogenic diseases.

[0541] According to this embodiment, the pharmaceutical formulations of the present invention can be used to treat a variety of diseases associated with undesirable angiogenesis such as retinal/choroidal neovascularization and corneal neovascularization. Examples of retinal/choroidal neovascularization include, but are not limited to, Best's disease, myopia, optic pits, Stargardt's disease, Paget's disease, vein occlusion, artery occlusion, sickle cell anemia, sarcoid, syphilis, pseudoxanthoma elasticum carotid atherosclerotic diseases, chronic uveitis/vitritis, mycobacterial infections, Lyme's disease, systemic lupus erythematosus, retinopathy of prematurity, Eales disease, diabetic retinopathy, macular degeneration, Bechet's disease, infections causing a retinitis or chorioiditis, presumed ocular histoplasmosis, pars planitis, chronic retinal detachment, hyperviscosity syndromes, toxoplasmosis, trauma and post-laser complications, diseases associated with rubella (neovascularization of the angle) and diseases caused by the abnormal proliferation of fibrovascular or fibrous tissue including all forms of proliferative vitreoretinopathy. Examples of corneal neovascularization include, but are not limited to, epidemic keratoconjunctivitis, Vitamin A deficiency, contact lens overwear, atopic keratitis, superior limbic keratitis, pterygium keratitis sicca, Sjögren's, acne rosacea, phlyctenulosis, diabetic retinopathy, retinopathy of prematurity, corneal graft rejection, Mooren ulcer, Terrien's marginal degeneration, marginal keratolysis, polyparthritis, Wegener's sarcoidosis, Scleritis, periphthoid radial keratotomy, neovascular glaucoma and retrolental fibroplasia, syphilis, Mycobacteria infections, lipid degeneration, chemical burns, bacterial ulcers, fungal ulcers, Herpes simplex infections, Herpes zoster infections, protozoan infections and Kaposi's sarcoma.

[0542] In yet another embodiment, the pharmaceutical formulations of the present invention can be used for treating chronic inflammatory diseases associated with abnormal angiogenesis. The method comprises administering to a patient suffering from a chronic inflammatory disease asso-

ciated with abnormal angiogenesis a LOX/LOXL2 inhibitor in combination with anti-neoplastic agent or anti-angiogenic agent that is not said LOX/LOXL2 inhibitor. The chronic inflammation depends on continuous formation of capillary sprouts to maintain an influx of inflammatory cells. The influx and presence of the inflammatory cells produce granulomas and thus, maintains the chronic inflammatory state. Inhibition of angiogenesis using the compounds described herein can prevent the formation of the granulomas, thereby alleviating the disease. Examples of chronic inflammatory disease include, but are not limited to, inflammatory bowel diseases such as Crohn's disease and ulcerative colitis, psoriasis, sarcoidosis, and rheumatoid arthritis.

[0543] Inflammatory bowel diseases such as Crohn's disease and ulcerative colitis are characterized by chronic inflammation and angiogenesis at various sites in the gastrointestinal tract. For example, Crohn's disease occurs as a chronic transmural inflammatory disease that most commonly affects the distal ileum and colon but may also occur in any part of the gastrointestinal tract from the mouth to the anus and perianal area. Patients with Crohn's disease generally have chronic diarrhea associated with abdominal pain, fever, anorexia, weight loss and abdominal swelling. Ulcerative colitis is also a chronic, nonspecific, inflammatory and ulcerative disease arising in the colonic mucosa and is characterized by the presence of bloody diarrhea. These inflammatory bowel diseases are generally caused by chronic granulomatous inflammation throughout the gastrointestinal tract, involving new capillary sprouts surrounded by a cylinder of inflammatory cells. Inhibition of angiogenesis by the pharmaceutical formulations of the present invention should inhibit the formation of the sprouts and prevent the formation of granulomas. The inflammatory bowel diseases also exhibit extra intestinal manifestations, such as skin lesions. Such lesions are characterized by inflammation and angiogenesis and can occur at many sites other the gastrointestinal tract. Inhibition of angiogenesis by the pharmaceutical formulations of the present invention should reduce the influx of inflammatory cells and prevent the lesion formation. Therefore, provided herein is a method of treating an inflammatory bowel disease, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient.

[0544] Sarcoidosis, another chronic inflammatory disease, is characterized as a multisystem granulomatous disorder. The granulomas of this disease can form anywhere in the body and, thus, the symptoms depend on the site of the granulomas and whether the disease is active. The granulomas are created by the angiogenic capillary sprouts providing a constant supply of inflammatory cells. By using the pharmaceutical formulations of the present invention to inhibit angiogenesis, such granulomas formation can be inhibited. Psoriasis, also a chronic and recurrent inflammatory disease, is characterized by papules and plaques of various sizes. Treatment using the pharmaceutical formulations of the present invention should prevent the formation of new blood vessels necessary to maintain the characteristic lesions and provide the patient relief from the symptoms. Therefore, provided herein is a method of prevent the formation of new blood vessels necessary to maintain the characteristic lesions and provide the patient relief from the symptoms, comprising administering to a subject in need thereof an effective amount

of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, a pharmaceutically acceptable carrier or excipient.

[0545] Rheumatoid arthritis (RA) is also a chronic inflammatory disease characterized by non-specific inflammation of the peripheral joints. It is believed that the blood vessels in the synovial lining of the joints undergo angiogenesis. In addition to forming new vascular networks, the endothelial cells release factors and reactive oxygen species that lead to pannus growth and cartilage destruction. The factors involved in angiogenesis can actively contribute to, and help maintain, the chronically inflamed state of rheumatoid arthritis. Treatment using the pharmaceutical formulations of the present invention alone or in conjunction with other anti-RA agents may prevent the formation of new blood vessels necessary to maintain the chronic inflammation and provide the RA patient relief from the symptoms. Other anti-RA agents are conventional and known in the art. Therefore, provided herein is a method of preventing or treating RA, comprising administering to a subject in need thereof an effective amount of an anti-LOX antibody or an anti-LOXL2 antibody; and optionally, one or more other anti-RA agents.

[0546] In addition to the use of the anti-LOX antibodies or anti-LOXL2 antibodies alone in the treatment of the indications described above, combination therapy is also contemplated herein. The methods provided herein can further include administering an anti-cancer agent or treatment to the patient.

[0547] Provided herein is a method of treating any of the indications described above by administering an anti-LOX antibody and an anti-LOXL2 antibody.

[0548] In one aspect, this invention features methods for inhibiting the invasiveness and metastasis of tumor cells, by contacting the cells with at least one cytotoxic agent and at least one anti-LOX antibody or anti-LOXL2 antibody. In general, the method includes a step of contacting metastatic tumor cells with an amount of at least one cytotoxic agent and at least one anti-LOX antibody or anti-LOXL2 antibody, which, in combination, is effective to reduce or inhibit the invasiveness or metastatic potential of the cell. Alternatively, according to the present invention, an anti-LOX antibody or an anti-LOXL2 antibody can be combined with a chemotherapeutic agent to sensitize tumor cells (e.g., transition from the EMT state to the MET state) to be killed by the chemotherapeutic agent, thus not only preventing or inhibiting tumor invasion and metastasis but also inhibiting primary tumor growth.

[0549] Any suitable anticancer agent may also be employed in the present methods.

[0550] As used herein the term "chemotherapeutic agent" or "chemotherapeutic" (or "chemotherapy," in the case of treatment with a chemotherapeutic agent) is meant to encompass any non-proteinaceous (i.e., non-peptidic) chemical compound useful in the treatment of cancer. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide (CYTOXANTM); alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, triethylenephosphoramide, triethylenethiophosphoramide and trimethylolomelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including synthetic analogue topotecan); bryostatin; callystatin; CC-1065 (including its

adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (articularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CBI-TMI); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosoureas such as carmustine, chlorozotocin, foremustine, lomustine, nimustine, ranimustine; antibiotics such as the enediyne antibiotics (e.g., calicheamicin, especially calicheamicin gamma 11 and calicheamicin phi 11, see, e.g., Agnew, Chem. Intl. Ed. Engl., 33: 183-186 (1994); dynemicin, including dynemicin A; bisphosphonates, such as clodronate; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromomorphores), aclacinomysins, actinomycin, anthramycin, azaserine, bleomycins, cactinomycin, carabacin, carminomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (Adramycin™) (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins such as mitomycin C, mycophenolic acid, nogalamycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptonigrin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as demopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogues such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine; androgens such as calusterone, dromostanolone propionate, epitostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replinisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; eniluracil; amsacrine; bestabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; maytansinoids such as maytansine and ansamitocins; mitoguanzone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; losoxantrone; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK™; razoxane; rhizoxin; sizofiran; spirogermanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verracurin A, roridin A and anguidine); urethane; vindesine; dacarbazine; mannomustine; mitobronitol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiopeta; taxoids, e.g., paclitaxel (TAXOL™, Bristol Meyers Squibb Oncology, Princeton, N.J.) and docetaxel (TAXOTERE™, Rhone-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine (Gemzar™); 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; vinblastine; platinum; etoposide (VP-16); ifosfamide; mitoxantrone; vancristine; vinorelbine (Navelbine™); novantrone; teniposide; edatrexate; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoids such as retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above. Also included in the definition of "chemo-

therapeutic agent" are anti-hormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens and selective estrogen receptor modulators (SERMs), including, for example, tamoxifen (including Nolvadex™), raloxifene, droloxifene, 4-hydroxytamoxifen, trioxifene, keoxifene, LY117018, onapristone, and toremifene (Fareston™); inhibitors of the enzyme aromatase, which regulates estrogen production in the adrenal glands, such as, for example, 4(5)-imidazoles, aminoglutethimide, megestrol acetate (Megace™), exemestane, formestane, fadrozole, vorozole (Rivisor™), letrozole (Femara™), and anastrozole (Arimidex™); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

[0551] In one non-limiting example, this invention includes methods for synergistically inhibiting the invasiveness and metastasis of tumor cells, by contacting the cells with at least cisplatin and at least one anti-LOX antibody (see FIG. 18). One practicing methods described herein would understand that an anti-LOX2 antibody could be used in such methods.

[0552] In one embodiment, the anti-neoplastic agent in combination with the LOX/LOXL modulator is a tyrosine kinase inhibitor. For example, ZD1839 (Iressa™ of Astra-Zeneca K.K.) shows a competitive effect for ATP in ATP binding site of EGFR (epidermal growth factor receptor) tyrosine kinase, and inhibits tyrosine kinase activity by inhibiting autophosphorylation of tyrosine kinase. As a result, the anticancer effect is expressed by blocking an EGFR-equiping signal transduction (ligands such as epidermal growth factor (EGF) are bound to the extracellular domain of EGFR, followed by activation of EGFR tyrosine kinase in the intracellular domain, causing not only autophosphorylation of EGFR but also phosphorylation of various intracellular target proteins, then transducing a proliferation signal from the cell surface to nucleus, then transducing the proliferation signals from the cancer cell surface to nucleus, and resulting in proliferation, infiltration, metastasis, angiogenesis of cancer cells), in association with proliferation, infiltration, differentiation and metastasis. IMC-C225 or cetuximab (Erbitux™) which is an EGFR-targeting monoclonal antibody) recognizes the receptor part of EGFR on a cell membrane surface and inhibits the autophosphorylation of EGFR thereby inhibiting the tyrosine kinase activity. Herceptin is a monoclonal antibody against Her2/Neu which is homologous to EGFR, and imatinib mesylate (GLEEVEC™, formerly STI-571) can inhibit both tyrosine kinase activities of BCR-Abl and c-kit (non-patent document No. 2). Sorafenib (Nexavar™) is a small molecular inhibitor of Raf kinase, PDGF (platelet-derived growth factor), VEGF receptor 2 & 3 kinases and c-Kit.

[0553] As used herein, monoclonal antibodies against tumor antigens are antibodies elicited against antigens expressed by tumors and leukemic cells, preferably tumor-specific antigens. The monoclonal antibody also includes fully human and humanized antibody.

[0554] Other examples of therapeutic antibodies for cancer therapy include Trastuzumab (HERCEPTIN™; Overexpression of HER2 protein is associated with more aggressive disease and poorer prognosis in the clinic); Rituximab (RIT-UXAN™) that is raised against CD20 on lymphoma cells and selectively deplete normal and malignant CD20+ pre-B and mature B cells; Alemtuzumab (CAMPATH™), a monoclonal antibody that specifically targets CD52 antigen that is found

on B and T lymphocytes and used for the treatment of chronic lymphocytic leukemia (CLL) and lymphoma; and Gemtuzumab zogamicin (MYLOTARG™), an antibody conjugate that combines a specific antibody against CD33 with a chemotherapeutic drug (zogamicin) and is indicated for the treatment of relapsed adult acute myelocytic leukemia.

[0555] In another embodiment, anti-angiogenic agent is combined with a LOX/LOXL inhibitor to treat cancer and other diseases associated with abnormal or undesirable angiogenesis. Examples of anti-angiogenic agents include, but are not limited to, retinoid acid and derivatives thereof, 2-methoxyestradiol, ANGIOSTATIN™, ENDOSTATIN™, suramin, squalamine, tissue inhibitor of metalloproteinase-1, tissue inhibitor of metalloproteinase-2, plasminogen activator inhibitor-1, plasminogen activator inhibitor-2, cartilage-derived inhibitor, paclitaxel, platelet factor 4, protamine sulphate (clupeine), sulphated chitin derivatives (prepared from queen crab shells), sulphated polysaccharide peptidoglycan complex (sp-pg), staurosporine, modulators of matrix metabolism, including for example, proline analogs ((1-azetidino-2-carboxylic acid (LACA), cishydroxyproline, d,l-3, 4-dehydropyrolidine, thiaproline, α -dipyridyl, β -aminopropionitrile fumarate, 4-propyl-5-(4-pyridinyl)-2(3h)-oxazolone; methotrexate, mitoxantrone, heparin, interferons, 2 macroglobulin-serum, chimp-3, chymostatin, β -cyclodextrin tetradecasulfate, eponemycin; fumagillin, gold sodium thiomalate, d-penicillamine (CDPT), beta-1-anticollagenase-serum, alpha-2-antiplasmin, bisantrene, lobenzarit disodium, n-2-carboxyphenyl-4-chloroanthranilic acid disodium or "CCA", thalidomide; angiostatic steroid, carboglynamidazole; metalloproteinase inhibitors such as BB94. Other anti-angiogenesis agents include antibodies, preferably monoclonal antibodies against these angiogenic growth factors: bFGF, aFGF, FGF-5, VEGF isoforms, VEGF-C, HGF/SF and Ang-1/Ang-2. Ferrara N. and Alitalo, K. "Clinical application of angiogenic growth factors and their inhibitors" (1999) *Nature Medicine* 5:1359-1364.

[0556] Exemplary anti-fibrotic agents include, but are not limited to the compounds such as β -aminopropionitrile (BAPN), as well as the compounds disclosed in U.S. Pat. No. 4,965,288 to Palfreyman, et al., issued Oct. 23, 1990, entitled "Inhibitors of lysyl oxidase, relating to inhibitors of lysyl oxidase and their use in the treatment of diseases and conditions associated with the abnormal deposition of collagen; U.S. Pat. No. 4,997,854 to Kagan, et al., issued Mar. 5, 1991, entitled "Anti-fibrotic agents and methods for inhibiting the activity of lysyl oxidase in situ using adjacently positioned diamine analogue substrate," relating to compounds which inhibit LOX for the treatment of various pathological fibrotic states, which are herein incorporated by reference. Further exemplary inhibitors are described in U.S. Pat. No. 4,943,593 to Palfreyman, et al., issued Jul. 24, 1990, entitled "Inhibitors of lysyl oxidase," relating to compounds such as 2-isobutyl-3-fluoro-, chloro-, or bromo-allylamine; as well as, e.g., U.S. Pat. No. 5,021,456; U.S. Pat. No. 5,505,714; U.S. Pat. No. 5,120,764; U.S. Pat. No. 5,182,297; U.S. Pat. No. 5,252,608 (relating to 2-(1-naphthylloxymethyl)-3-fluoroallylamine); and U.S. Patent Application No. 2004/0248871, which are herein incorporated by reference. Exemplary anti-fibrotic agents also include the primary amines reacting with the carbonyl group of the active site of the lysyl oxidases, and more particularly those which produce, after binding with the carbonyl, a product stabilized by resonance, such as the following primary amines: ethylenediamine, hydrazine, phenyl-

hydrazine, and their derivatives, semicarbazide, and urea derivatives, aminonitriles, such as beta-aminopropionitrile (BAPN), or 2-nitroethylamine, unsaturated or saturated haloamines, such as 2-bromo-ethylamine, 2-chloroethylamine, 2-trifluoroethylamine, 3-bromopropylamine, p-halobenzylamines, selenohomocysteine lactone. In another embodiment, the anti-fibrotic agents are copper chelating agents, penetrating or not penetrating the cells. Additional exemplary compounds include indirect inhibitors such compounds blocking the aldehyde derivatives originating from the oxidative deamination of the lysyl and hydroxylysyl residues by the lysyl oxidases, such as the thiolamines, in particular D-penicillamine, or its analogues such as 2-amino-5-mercapto-5-methylhexanoic acid, D-2-amino-3-methyl-3-((2-acetamidoethyl)dithio)butanoic acid, p-2-amino-3-methyl-3-((2-aminoethyl)dithio)butanoic acid, sodium-4-((p-1-dimethyl-2-amino-2-carboxyethyl)dithio)butane sulphinate, 2-acetamidoethyl-2-acetamidoethanethiol sulphinate, sodium-4-mercaptobutanesulphinate trihydrate.

[0557] The present methods can be performed on cells in culture, e.g., in vitro or ex vivo, or can be performed on cells present in a subject, e.g., as part of an in vivo therapeutic protocol. The therapeutic regimen can be carried out on a human or on other animal subjects. The anti-LOX antibody or anti-LOX2 antibody provided herein can be administered in any order relative to the chemotherapeutic agent. Sometimes, the anti-LOX antibody or anti-LOX2 antibody and the agent are administered simultaneously or sequentially. They can be administered at different sites and on different dosage regimens. The enhanced therapeutic effectiveness of the combination therapy of the present invention represents a promising alternative to conventional highly toxic regimens of anticancer agents. Chemotherapeutic agents to be employed in such methods have been described in more detail above.

EXAMPLES

[0558] The application may be better understood by reference to the following non-limiting examples, which are provided as exemplary embodiments of the application. The following examples are presented in order to more fully illustrate embodiments of the invention and should in no way be construed, however, as limiting the broad scope of the application. While certain embodiments of the present application have been shown and described herein, it will be obvious that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments described herein may be employed in practicing the methods described herein.

Example 1

Methods of Generating Murine Monoclonal Anti-LOX and Anti-LOXL2 Antibodies

[0559] Mice (BALB/c (00467)) were injected subcutaneously (s.c.), 5 times at 2-3 week intervals with 0.05 mg antigen (Ag) in an adjuvant formulation. For peptide Ags, peptides were conjugated to bovine serum albumin and formulated in Freund's Adjuvant (FA) prior to immunization. For protein Ags, the protein was formulated in Alhydrogel-Muramyl Dipeptide (ALD/MDP) adjuvant.

[0560] Mice were injected with Ag formulated in PBS, each day for 3 days via a combination of s.c., intraperitoneally (i.p.) and intravenous (i.v.) routes, 0.05 to 0.1 mg/route.

[0561] Cells from the spleen and lymph nodes of the mice were isolated and fused with P3X63-Ag8.653 myeloma cells using 50% polyethylene glycol.

[0562] Cells were cultured and a hybridoma library of HAT-selected cells was isolated essentially as described in Kenney, et al. ("Production of monoclonal antibodies using a secretion capture report web." Biotechnology 13:787-790, 1995).

[0563] The hybridoma library was cloned using a fluorescent activated cell sorter with automatic cell deposition unit.

[0564] Single viable cells were sorted into 96-well plates based upon the analysis criteria of forward-scatter, side-scatter and propidium iodide fluorescence as described by Kenney et al.

[0565] Sera and supernatants were screened by enzyme linked immunosorbant assay (ELISA) using Ag-coated microtiter plate wells, which were then incubated with mouse plasma or hybridoma supernatant, followed by goat mouse IgG (Fc-specific) antibody-HRP conjugate, followed by TMB substrate solution and stop reagent.

[0566] The plate wells were washed to remove unbound antibody or antigen between all incubations and results determined.

[0567] VH and VL amino acid sequences of an anti-LOXL2 murine monoclonal antibody identified using the described methods are provided in FIG. 6A and FIG. 6B, respectively. For each variable region, signal peptides are shown in *italics*, CDRs are underlined and the beginning of the constant framework is shown in bold font.

[0568] A VH amino acid sequence of an anti-LOX murine monoclonal antibody identified using the described methods is provided in FIG. 7A. Two VL amino acid sequences of anti-LOX murine monoclonal antibodies identified using the described methods are provided in FIGS. 7B and 7C. For each variable region, signal peptides are shown in *italics*, CDRs are underlined.

Example 2

[0569] Anti-LOXL2 antibodies were screened using a protein screen B update to assess enzymatic activity of LOXL2.

[0570] Antibody candidates were initially chosen based on ELISA point tests. ELISA on multiple antigens was performed by Antibody Solutions and antibodies showing strong ELISA signal in the antigen of interest were selected for further characterization in enzymatic assays. LOXL2 produces hydrogen peroxide when the substrate 1,5-diaminopentane is deaminated and the enzyme regenerated.

[0571] Antibodies were assessed for their ability to inhibit enzymatic activity using a biochemical assay that couples the production of peroxide (liberated by LOXL2) to HRP and measuring the conversion of amplex red to a fluorescent product. Antibody hybridoma supernatant (10 μ L) was added to 40 μ L enzyme mixture (62.5 mM sodium borate pH 8.0, 5 units/mL HRP, 125 nM LOXL2, 10 ppm antifoam) and incubated at room temperature for 1 hour in a 96 well full area black plate. Enzymatic reaction was started with the addition of 50 μ L of substrate solution (50 mM sodium borate, 100 μ M amplex red reagent, 20 mM 1,5-diaminopentane (DAP), 10 ppm antifoam) and read in a Molecular Devices M5 plate reader at 37° C. The plate reader was configured to read fluorescence (ex=544 nm, em=590 nm) in kinetics mode for 1 hour. Data

was recorded as the slope of the fluorescence response to time. These slopes were compared to a control in which hydridoma media was added to the enzyme mixture. Slopes less than that of control were considered inhibitors.

[0572] Antibodies M1 (asc), M4, M11, M1, M13, M22, M16, M19, M20, M20 (asc) and M25 test antibodies were tested against BAPN (a competitive inhibitor of LOXL2) as a positive control and LOXL2 as a negative control (see FIG. 8).

[0573] One anti-LOXL2 antibody was designated AB0023. Anti-LOXL2 antibodies repeated inhibitory activity observed in 10 ml preparation materials in the enzymatic assay. Inhibition was also repeated in cell-based assays (see below). Sequence analysis confirmed that the amino acid sequences of M01, M16, M19 and M20 are identical.

Example 3

Anti-LOXL2 Antibody AB0023 and Enzymatic Activity

[0574] Enzymatic Activity of anti-LOXL2 antibodies can be assessed and IC50s determined.

[0575] M1, M1 (asc), M20 and M20 (asc) were assessed in the presence of 25 nM LOXL2 and 15 mM 1.5 DAP over increasing concentrations of antibody.

IC50 Determinations

[0576] Dose responses on selected antibodies were carried out against LOXL2 using the coupled enzymatic assay described above. A dilution series of antibody was created in PBST (0.01% tween-20) and 10 μ L of this was added to 40 μ L of enzyme mixture (62.5 mM sodium borate pH 8.0, 5 units/mL HRP, 125 nM LOXL2, 10 ppm antifoam) and incubated at room temperature for 1 hour in a 96 well full area black plate. Enzymatic reaction was started with the addition of 50 μ L of substrate solution (50 mM sodium borate, 100 μ M amplex red reagent, 20 mM 1,5-diaminopentane, 10 ppm antifoam) and read in an M5 plate reader using conditions described above. The slopes of the fluorescence response as a function of time were plotted against antibody concentration and the data was fit to a four parameter fit using GraFit. The midpoint of this plot is the apparent IC50 and is the concentration at which fifty percent of the total response is inhibited.

[0577] Ab0023 was found to be a partial inhibitor of LOXL2 enzymatic activity with an apparent IC50 of approximately 30 nM (see FIG. 9).

[0578] Based upon the use of a partial inhibitor in clinic for therapeutic treatment (i.e., Nevirapine—an approved HIV-1 drug described by Spence et al. (1995) Science 267), a partial inhibitor of LOXL2 can also be used in therapeutic applications.

Example 4

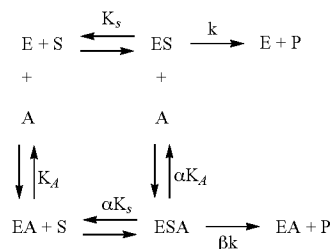
Anti-LOXL2 Antibody AB0023 is a Non-Competitive Inhibitor

[0579] The activity of anti-LOXL2 antibody AB0023 was assessed over increasing concentrations of 1.5 DAP and over increasing concentrations of antibody (1 μ M, 0.005 μ M, 0.050 μ M, and 0.300 μ M).

Mode of Inhibition

[0580] Mode of inhibition of antibodies against LOXL2 was conducted using the model described below. In these

experiments, the dependence of the steady state rate on the concentration of 1,5-diaminopentane was monitored under increasing concentrations of antibody. The purpose was to assess whether the K_m for substrate, k_{cat} or both change in the presence of antibody. Collected data was analyzed globally with GraFit using the model shown in figure below. E represents enzyme, S represents substrate, A represents antibody, and P represents product. Parameter α describes the effect of the compound on substrate affinity. An α value equal to one describes a situation in which the compound binds equally well the free enzyme and the enzyme-substrate complex (non-competitive inhibition like). Values less than one describe an interaction in which the compound binds the enzyme-substrate complex (uncompetitive inhibition like). Values greater than one correspond to the compound binding the free enzyme better than the enzyme-substrate complex (competitive inhibition like). The β value describes the effect of the modulator on the rate of the enzyme. Inhibitors have values less than one (for a complete inhibitor ($\beta=0$)) and activators have values greater than one. K_A is the dissociation constant of the compound, K_s is the Michaelis constant for the substrate and k is the catalytic rate of the enzyme. The steady state rates were determined from the slope of the fluorescence response as a function of time as described above (IC50 determination). Data was plotted as the dependence of steady state rate on the concentration of substrate (1,5-diaminopentane) at several fixed concentrations of antibody and analyzed with GraFit.



[0581] Anti-LOXL2 antibody AB0023 was determined to be a non-competitive inhibitor based on the following results: $\alpha=1$, $K_i=0.067$ and $\beta=0.5$ (see FIG. 10).

Example 5

Kinetic Measurement of AB0023 Antibody Binding to LOXL2 by Surface Plasmon Resonance

[0582] Binding affinity and off-rate of AB0023 were assessed via Surface Plasmon Resonance (SPR).

[0583] Binding affinities were measured using a Bio-Rad ProteOn instrument thermostated to 25° C. The binding affinities were determined using two methods, using amine coupling; one in which the antibody was immobilized and the antigen (LOXL2) was added, and another in which the antigen (LOXL2) was immobilized and antibody was added. Antibody or antigen was immobilized on a GLC chip using at 1:1 ratio of NHS to EDC provided with the ProteOn immobilization kit. Chip was first activated with NHS/EDC a mixture and then antigen or antibody at 1 µg/mL in acetate buffer pH 4.5 was flowed over activated surface to couple. This typically yielded a coupling of about 500 RU's. The activated chip surface was then capped with the addition of 1M etha-

nolamine. Coupled chips were stored at 4° C. and regenerated with 50 mM sodium hydroxide.

[0584] Dissociation constants were determined by probing the coupled chip with a dilution series of antibody or antigen in PBST (0.05% Tween-20). Data was acquired on all six channels available on the ProteOn using a non-coupled channel as a reference. Collected data was analyzed using ProteOn manager software from Bio-Rad.

[0585] AB0023 was found to bind tightly to LOXL2 and release slowly. K_d was estimated to be 0.1-1.0 nM. Furthermore, AB0023 was found to have the following characteristics: $k_{on}=1.68 \times 10^6 \text{ M}^{-1}\text{s}^{-1}$, $k_{off}=1.17 \times 10^{-4} \text{ s}^{-1}$, $K_D=0.69 \text{ nM}$ and $t_{1/2}=98.7$ minutes. See FIG. 11.

Example 6

[0586] Domain mapping was conducted and AB0023 was found to bind to the SRCR3-4 domain.

Materials and Methods

[0587] All plates were obtained from Corning. Secondary antibody and Pico substrate were obtained from Pierce. Horse radish peroxidase (HRP) was obtained from Sigma. All ProteOn reagents were obtained from Bio-Rad. LOXL2 was obtained from R&D systems. Antibodies used in this study were produced at Antibody Solution or via ascites from Aragen Biosciences. All other reagents were of the highest quality possible.

Binding via ELISA

[0588] Binding of antibody to LOXL2 was determined using a luminescence based ELISA. White Corning plates were coated with 0.1 µg/mL of LOXL2 or antigen of interest in 50 mM borate buffer (pH 8.0) overnight at 4° C. Plates were washed using BioTek plate washer and blocked with 5% skim milk in PBST (0.05% tween-20) for 1 hour at room temperature. Plates were washed with PBST (0.05% tween-20) and then used immediately or stored at 4° C. in dessicator for future use. The antibody body to be tested was serially diluted in PBST (0.01% tween-20) and 100 µL of each dilution was added per well. Plates were incubated with test article for 1 hour at room temperature and then washed with PBST (0.05% Tween-20). Detection antibody (anti-mouse HRP conjugate) was diluted 16,000 fold in 5% skim milk in PBST (0.05% Tween-20) and 100 µL was applied per well. Plates were incubated for 1 hour with detection antibody and then washed with PBST (0.05% PBST). Signal was detected using the SuperSignal ELISA pico chemiluminescent substrate from Pierce following the manufacturer's instructions. Luminescence was measure using a Molecular Devices M5 plate reader with an integration time of 500 ms capturing all wavelengths. Data was background corrected and the dependence of luminescence signal to antibody concentration was fit using the Langmuir isotherm equation using the GraFit program. In instances where the antigen concentration was similar to the dissociation constant the quadratic equation of tight binding was used. Reported dissociation values were obtained from the fits to these equations; were PL represents the signal of the bound complex, B_{max} is that maximal binding, K_D is the dissociation constant and L is the ligand concentration.

[0589] Langmuir Isotherm equation:

$$[PL] = \frac{B_{max} * [L]}{K_D * [L]}$$

[0590] Tight binding equation:

$$[PL] = B_{max} * \frac{([P]_T + [L]_T + K_D) - \sqrt{([P]_T + [L]_T + K_D)^2 - 4[P]_T[L]_T}}{2[P]_T}$$

[0591] AB0023 was tested against MCD-LOXL2, LOXL2 (R&D), SRCR1-2 and SRCR 1-4. AB0023 was found to bind to the SRCR3-4 domain (see FIG. 12).

Example 7

Inhibition of Migration/Invasion in Collagen I and Collagen IV and Inhibition of Cell Growth

[0592] Cell based assays were conducted to assess binding of AB0023 to bind substrate (i.e., collagen).

[0593] Briefly, AB0023 was scaled up from various samples prior to testing.

[0594] Cultrex 96-well collagen I and collagen IV cell invasion kits (Trevigen, Gaithersburg, Md.) were used for anti-sera/antibody supernatant screenings. MDA MB 231 cells were serum-deprived 24 hours prior to assay set up. On day of set up, collagen I and collagen IV coated plates were made at least 4 hours prior to invasion assay set up (not longer than 8 hours prior). Collagen I and collagen IV plates were coated according to manufacturer's instructions. Cells were plated at 20,000 cells per well in 95 μ l serum-free media in the upper chamber of the plate. One hundred fifty (150) μ l of media containing 10% FBS and 1 $\times$ L-glutamine was aliquoted into the lower chambers of the plate. Using a multi-channel pipette, 5 μ l of each anti-sera was placed in the upper chambers of the plate. The anti-sera and cell mixture was carefully mixed up and down once with the pipette. Plates were incubated at 37° C. with 5% CO₂ for 48 hours.

[0595] After 48 hours, the plates were ready to be read. The cell dissociation solution containing calcein AM was made according to manufacturer's instructions. The plates were also washed and disassembled according to manufacturer's instructions. 125 μ l of cell dissociation solution containing calcein AM was added to the lower chambered wells and the plates were placed at 37° C. for 30 minutes. After 30 minutes the sides of the plates were tapped to loosen the cells, and the plates were placed in incubator for another 30 minutes at 37° C. The plates were then disassembled and the lower plate was placed into the plate reader (SpectraMax M5, Molecular Devices, Sunnyvale, Calif.) with settings: Fluorescence, 485-520 emission, top read, black opaque plate, sensitivity at 30.

[0596] Consistent inhibition of migration/invasion was observed in collagen I (FIG. 13) and collagen IV, from supernatants through 10 mL preparation material and scaled up 100 mL preparations and ascites.

Cell Adhesion Assays

[0597] MDA-MB231 cells were plated in 15 cm² plates and grown in 4.5 g/L glucose containing DMEM (10% FBS and 2 mM L-Glutamine) so that they were confluent on the day of

the assay. The media was aspirated and the cells were washed 2 times with 10 ml 1 mM EDTA PBS per plate. Cells were removed from plates by incubating with another 10 ml 1 mM EDTA PBS for 5 minutes at 37° C. in a biosafety cabinet and subsequently pipetting the cells off of the plate in the EDTA PBS solution. Cell concentration was determined and enough cells for assay (50 k/well plus extra for pipetting) were spun down in 15 ml conical tube. Cell pellet was dispersed in pre-warmed serum-free DMEM to 500K cells/ml and CuCl₂ was added to 1 μ M final concentration. One hundred (100) μ l/well of cell suspension was pipetted into a U-bottom style 96 well tissue culture plate containing 10 μ l of appropriate mAb dilution. The cell suspension/mAb mixture was left to incubate for 10 minutes at room temperature in the dark. One hundred (100) μ l/well of re-suspended cells/mAb mixture was then transferred to collagen IV coated 96 well plates (BD Biocoat, BD Biosciences). Plates were incubated at 37° C. in a biosafety cabinet for 1 hour. Wells were then aspirated and washed gently two times with 200 μ l DPBS (Mediatech) to remove cell that had not adhered. One hundred (100) μ l of 10 μ M final concentration Calcein-AM (BD Biosciences) in DPBS was then added to each well to stain the cells that remained. Plates were incubated at 37° C. in a biosafety cabinet for 1 hour. Plates were read on a Molecular Devices M5 plate reader at 494/517 (excitation/emission). Percent (%) adhesion was calculated by normalizing to PBS or unrelated antibody controls.

[0598] Using this assay, partial inhibition of adhesion was observed upon exposure of cells to AB0023 antibody.

Cell Growth

[0599] Anti-LOXL2 antibodies inhibited cell growth of four cell lines: 231 is a breast cancer cell line, BT549 is a breast cancer cell line, HT1080 is a fibrosarcoma, and BxPC3 is a prostate cancer cell line (FIG. 17). Thus, the antibody is effective in inhibiting growth of cancers of different origins.

Example 8

AB0023 Inhibition of EMT-Like Change

[0600] Epithelial to Mesenchymal changes were assessed using immunohistochemistry.

[0601] To detect whether a cell is in an EMT or mesenchymal-to-epithelial transition (MET) state, cells were stained with antibodies specific to cellular protein markers for epithelial or mesenchymal states such as E-cadherin, vimentin, fibronectin, and phalloidin to detect F-actin.

Rhodamine Phalloidin Staining Protocol

[0602] Cells were seeded 24 hours prior to day of staining; cells were approximately 80% confluent 24 hours later in an 8-chambered slide. The next day, the media was aspirated and the chambers were rinsed with 1 $\times$ PBS. Cells were then fixed with 4% Paraformaldehyde (PFA) for 20 minutes at room temperature and then rinsed once with 1 $\times$ Phosphate Buffered Saline (PBS). For permeabilization, the cells were treated with 0.5 Saponin (JT Baker, Phillipsburg, N.J.) in PBS for 5 minutes at room temperature. The chambers were carefully rinsed once with 1 $\times$ PBS, and a 1:100 dilution of rhodamine phalloidin (Invitrogen, Carlsbad, Calif.) in PBS was added to the cells and incubated for 15 minutes at room temperature.

The chambers were rinsed two times with 1× PBS and the slides were mounted with Vectashield (Vector Laboratories, Burlingame, Calif.).

E-Cadherin Staining Protocol

[0603] Cells were seeded 24 hours prior to day of staining; cells were approximately 80% confluent the next day in an 8-chambered slide. The next day, the media was aspirated and the chambers were rinsed with 1× PBS. Cells were then fixed with ice cold methanol and then incubated for 2 minutes in −20° C. The cells were rinsed once with 1× PBX and 1 µg/ml of E-cadherin Ab (Calbiochem, Gibbstown, N.J.) was added to the slide chambers. The slides were then incubated at 37° C. for 1 hour. After carefully rinsing the chambers one time with 1× PBS, the secondary Ab (anti-mouse IgG cy3 conjugated, Jackson Immuno Research, West Grove, Pa.) was added and incubated at room temperature for 30-45 minutes. The chambers were rinsed two times with 1× PBS and mounted with Vectashield (Vector Laboratories, Burlingame, Calif.).

[0604] Conditioned media from HS-578t cells (LOXL2 high) applied to MCF-7 cells (LOXL2 low/negative). Cells were stained with rhodamine-phalloidin (F-actin, red) and Dapi (nuclei, blue).

[0605] AB0023 was found to inhibit EMT-like changes induced by conditioned media from tumor cells that express LOXL2 (data not shown).

Example 9

[0606] Anti-LOXL2 antibody AB0023 binds matrix-associated LOXL2.

Internalization and Ab Uptake Studies in Hs578t Cells.

[0607] Hs578t cells were cultured in DMEM containing 10% FBS and 1× glutamine. The cells were seeded in an 8 chamber glass slide (BD Falcon, Franklin Lakes, N.J.) and allowed to adhere overnight. For low confluency, cells were seeded at 30-40,000 cells per slide. Low confluency was used for detection of Lox in the cytosol 24 hours later. For high confluency, cells were seeded at 100,000 cells per slide. High confluency was used for detection of Lox associated with the matrix and collagen approximately 48-72 hours later.

[0608] The following day, 1 µg/ml (final concentration in regular growth medium) of anti-Lox M64 or anti-Lox12 M20 monoclonal Ab (mAb) was added to the chambers. For continuous uptake, the mAbs were incubated with cells at different time points: for example, 3 hours, 8 hours, or 24 hours (overnight). After appropriate amount of continuous uptake, the media was removed and the chambers were rinsed with 1× PBS. The cells were fixed in 4% PFA (paraformaldehyde) at room temperature for 20 minutes. After fixation, the cells were washed with IX PBS at room temperature for 5 minutes and then quenched in 50 mM ammonium chloride at room temperature for 10 minutes. The cells were washed again with 1× PBS at room temperature for 5 minutes.

[0609] The cells were permeabilized by adding saponin buffer (0.5% Saponin/1% BSA in PBS) at room temperature for 20 minutes. The secondary detection Ab (Alexa Fluor 488 donkey anti-mouse IgG, Invitrogen, Carlsbad, Calif.) was added at room temperature in saponin buffer and the cells were incubated for 30-45 minutes. The cells were then washed 3× in saponin buffer. The slides were mounted with vectashield (Vector Laboratories, Burlingame, Calif.).

[0610] For detection of collagen detection, cells were incubated with anti-collagen antibody (1:50, Calbiochem anti-collagen type I Rabbit polyclonal, Gibbstown, N.J.), one hour prior to fixing the cells with 4% PFA. Secondary Ab for collagen used is donkey anti-rabbit Cy3 (ImmunoJackson Labs, West Grove, Pa.).

[0611] Analysis by immunoblotting and immunofluorescence (data not shown) indicated that LOXL2 was predominantly intracellular at low density but was secreted at high cell density (confluent cells). LOXL2 was detected in the media of confluent cells and also on the extracellular matrix. Immunofluorescence on live cells indicated that AB0023 bound LOXL2 associated with the collagen matrix.

Example 10

Anti-LOX Antibody M64 Binds LOX

[0612] The activity of anti-LOX antibody M64 was assessed over increasing concentrations of 1.5 DAP and over increasing concentrations of antibody (see FIG. 15).

Materials and Methods

[0613] All plates were obtained from Corning. Secondary antibody and Pico substrate were from Pierce. Amplex red reagent was from Invitrogen. Horse radish peroxidase (HRP), 1,5-diaminopentane, antifoam were from Sigma. All ProteOn reagents were from Bio-Rad. LOX was produced in house at Arresto Biosciences. Antibodies used in this study were produced at Antibody Solution or via ascites (asc) from Aragen Biosciences. All other reagents were of the highest quality possible.

Binding via ELISA

[0614] Binding of antibody to LOX was determined using a luminescence based ELISA. White Corning plates were coated with 0.1 µg/mL of LOX or antigen of interest in 50 mM borate buffer (pH 8.0) overnight at 4° C. Plates were washed using a BioTek plate washer and blocked with 5% skim milk in PBST (0.05% tween-20) for 1 hour at room temperature. Plates were washed with PBST (0.05% tween-20) and then used immediately or stored at 4° C. in a dessicator for future use. The antibody to be tested was serially diluted in PBST (0.01% tween-20) and 100 µL of each dilution was added per well. Plates were incubated with test material for 1 hour at room temperature and then washed with PBST (0.05% tween-20). Detection antibody (anti-mouse HRP conjugate) was diluted 16000 fold in 5% skim milk in PBST (0.05% tween-20) and 100 µL was applied per well. Plates were incubated for 1 hour with detection antibody and then washed with PBST (0.05% PBST). Signal was detected using the SuperSignal ELISA pico chemiluminescent substrate from Pierce following the manufacturer's instructions. Luminescence was measured using a Molecular Devices M5 plate reader with an integration time of 500 ms capturing all wavelengths. Data was background corrected and the dependence of luminescence signal to antibody concentration was fit using the Langmuir isotherm equation using the GraFit program. In instances where the antigen concentration was similar to the dissociation constant the quadratic equation of tight binding was used. Reported dissociation values were obtained from the fits to these equations; were PL represents

the signal of the bound complex, B_{max} is that maximal binding, K_D is the dissociation constant and L is the ligand concentration.

Langmuir Isotherm Equation

[0615] Langmuir Isotherm equation:

$$[PL] = \frac{B_{max} * [L]}{K_D * [L] + 1}$$

[0616] Tight binding equation:

$$[PL] = B_{max} * \frac{([P]_T + [L]_T + K_D) - \sqrt{([P]_T + [L]_T + K_D)^2 - 4[P]_T[L]_T}}{2[P]_T}$$

[0617] Anti-LOX antibody M64 was tested in three batches and was found to have a K_D of 6.6 nM, 5.0 nM and 5.7 nM for Batch 3, Batch 4 and Batch 5, respectively (FIG. 15).

Example 11

Kinetic Measurement of M64 Antibody Binding to LOX by Surface Plasmon Resonance

[0618] Binding affinity of M64 was assessed via Surface Plasmon Resonance (SPR).

[0619] Binding affinities were measured using a Bio-Rad ProteOn instrument thermostated to 25° C. The binding affinities were determined using two methods, using amine coupling; one in which the antibody was immobilized and the antigen (LOX) was added, and another in which the antigen (LOX) was immobilized and antibody was added. Antibody or antigen was immobilized on a GLC chip using at 1:1 ratio of NHS to EDC provided with the ProteOn immobilization kit. Chip was first activated with NHS/EDC a mixture and then antigen or antibody at 1 µg/mL in acetate buffer pH 4.5 was flowed over activated surface to couple. This typically yielded a coupling of about 500 RU's. The activated chip surface was then capped with the addition of 1M ethanolamine. Coupled chips were stored at 4° C. and regenerated with 50 mM sodium hydroxide.

[0620] Dissociation constants were determined by probing the coupled chip with a dilution series of antibody or antigen in PBST (0.05% tween-20). Data was acquired on all six channels available on the ProteOn using a non-coupled channel as a reference. Collected data was analyzed using ProteOn manager software from Bio-Rad.

[0621] M64 was found to have a K_D of 7 nM (FIG. 16).

Example 12

[0622] Below is a listing of sequences described throughout the specification.

SEQ ID NO	Sequence
1.	MEWSRVFIFLLSVTAGVHSQVQLQQSGAELVRPGTSVKVSCKASGYAFTYYLLEWVKQRPQGQLEWIGVYNPGSGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCARNWMNEDYWGQGTTLTVSS
2.	MRCLAELFGLLVLPWIPGAIGDIVMTQAAPSVSVPGESVSISSCRSSKSLHNSNGNTYLYWFLQRPQSPQFLIYRMSNLASGVPDRFSGSGSGTAFTLRISRVEADVGYYCMQHLEYPTTFGGGKLEIK
3.	MGWSWVFLFLLSVTAGVHSQVQLQQSGAELVKPGASVKLSCKASGYTFRSYDINWVRQRPQGLEWIGNIFPGDGETKYNEKFKGKAILTTDKSSSTAYMQLSRLTSEDSAVYFCARVYAMDYWGQGTSTVTVSS
4.	MKLPVRLVLMFWIPASSSDVLLTQTPLSLPVS LGDQASISCRSSQSI VHSNGNTYLEWYLQKPGQSPKLLIYKVSINRFSGVPDRFSGSGSGTDFTLKINRVEADLGIYYCQSSHIPLTFGAGTKLELKRAD
5.	MKLPVRLVLMFWIPASSSDVLLTQTPLSLPVS LGDQASISCRSSQSI VHSNGNTYLEWYLQKPGQSPKLLIYKVSIRFSGVPDRFSGSGSGTDFTLKINRVEADLGIYYCQSSHIPLTFGAGTKLELKRAD
6.	VRLRGGAYIGRVEVLKNGEWGTVCDKWDLVSAVVCRELGFSGAKEAVTGSRLGGQIGIHLNEIQCTGNEKSIIDCKFNAESQGCNHEEDAGVRCNTPAMGLQKKLRNLNGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVCRLGLGFASNAFQETWYHGDVNSNKVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQYAGVACS
7.	MRFAWTVLLGLPLQLCALVHCAPPAAGQQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSGYQPPQRRRDPGAAPVGAANASAAQQRTPILLIRDNRTAAARTTAGSSGVTAGRPRTARHWFQAGYSTSRAREAGASRAENQTAPGEVPALSNLRPPSRVDGMVGGDDPYNPYKYSDDNPYNYDYTYERPRPGGRYPGYGTGYFQYGLPDLVADPYIIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFLEDTSCDYGHYHRRFACTAHTQGLSPGCYDITYGADIDCQWIDITDVKPGNYILKVS VNP SYLVPESDYTNVVRCDIRYTGHHAYASGCTISPY
8.	ALVHCAPPAAGQQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSGYQPPQRRRDPGAAPVGAANASAAQQRTPILLIRDNRTAAARTTAGSSGVTAGRPRTARHWFQAGYSTSRAREAGASRAENQTAPGEVPALSNLRPPSRVDGMVGGDDPYNPYKYSDDNPYNYDYTYERPRPGGRYPGYGTGYFQYGLPDLVADPYIIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFLEDTSCDYGHYHRRFACTAHTQGLSPGCYDITYGADIDCQWIDITDVKPGNYILKVS VNP SYLVPESDYTNVVRCDIRYTGHHAYASGCTISPY
9.	DDPYNPYKYSDDNPYNYDYTYERPRPGGRYPGYGTGYFQYGLPDLVADPYIIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFLEDTSCDYGHYHRRFACTAHTQGLSPGCYDITYGADIDCQWIDITDVKPGNYILKVS VNP SYLVPESDYTNVVRCDIRYTGHHAYASGCTISPY

-continued

SEQ ID NO	Sequence
	TQRRVAEGHKASFCELEDTSCDYGYHRRFACTAHTQGLSPGICYDTYGADIDCQWIDITDVKPGNYILKVSVN PSYLVPESDYTNNVVRCDIRYTGHHAYASGCTISPY
10.	gggagtgatgttgagccccgtttttattttctgtgagccacgtcctcctcgaggggggtcaatctggcctcaaa ggagtgatgcgcttcgcctggacccgtgctcctgctcgggcctttgcagctctgcgcgctagtgcactgcgc ccctcccgccgcccggcccaacagcagcccccgccgagccgcccggcggtccggcgccctggcgccagcaga tccaatgggagaaacacgggaggtgttcagcttgcctgagcctgggctcacagtagccagcctcagcgccgc cgggacccggcgcccgctcctggtgcagccaaacgcctccgcccagcagcccgactccgatcctgct gatccgcgacaacccgacccgcccgcggaacgcggagcggcggtcatctggagtaccgctggcgcc ccaggcccccgcctcactggttccaagctggctactcgacatctagagcccggaacgtggcgcccg cgccgggagaaacagacagcgcgggagaaagtctcctgcgctcagtaacctcgccgcggccagccgctgga cggcatggtggcgacgaccttacaacccctacaagtagctctgacgacaaccttattacaactactacg atacttatgaaaggccagacctgggggaggtaccggcccgatacggcactggctacttccagtagcgt ctccagacactggtggcgacccctactacatccaggcgtccagctacgtgcagaagatgtccatgtacaa cctgagatgcgcggcgaggagaaactgtctggccagtagacatcacgggcagatgcagagattatgatc acagggtgctgctcagatttccccaaagagtgaacaaacaggagacatcagatttcttaccagccgacca agataattcctgggaatggcacagtgtcatcaacattaccacagtagtgatgagtttagccactatgacct gcttgatgcacaacccagcagtaggagtaggtgctgaaggccacaagcaagtttctgctctgaagacacatcct gtgactatggctaccacaggcgatttgcatgtactgcacacacacagggtatgagtcctggctgttatgat acctatggtgcagacatagactgccagtggtatgataccagatgtaaaacctggaaactatctcctaaa ggtagctgttaaccccccagctacctggttccctgaatctgactataccaaatgttctgctgtgacattc gctacacaggacatcatgctatgctcaggtgcacaatttccacgtatagaaggcaaaagcaaaactcc caatggataaaactcagtcgctggtgtctgaagtgggaaaaaatagactaacctcagtaggatttatgtatt ttgaaaaagagaaacagaaacacaaaagaatttttggctgttttcaataacaaagcacataactg gattttgaacgcttaagtcaateattacttgaaatttntaatgtttattattacatcaactttgtgaat taacacagtggttcaattctgtaatttcatattcgactcttt
11.	MRFAWTVLLGLPLQCALVHCAPPAAGQQPPREPPAAPGAWRQIQWENNGQVFSLLSLGSQYQPQRRRD PGAAPVGAANASAQQPRTPILLIRDNRTAAARTTAGSSGVTAGRPRPTARHWFQAGYSTSRARERASRA ENQTAPGEVPALSNLRPPSRVDGMVGDDPYNPYKYSDDNPIYNYDYTYERPRPGGRYRPGYGTGYFYGLP DLVADPYIYQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQRVKNQGTSDFLPSRPRY SHEWHSCHQHYHSMDBFSHYDLLDANTQRRVAEGHKASFCELEDTSCDYGYHRRFACTAHTQGLSPGICYDTY GADIDCQWIDITDVKPGNYILKVSVNPSYLVPESDYTNNVVRCDIRYTGHHAYASGCTISPY
12.	atgcgcttcgcctggacccgtgctcctgctcgggcctttgcagctctgcgcgctagtgcactgcgccccctcc cgccgcccggcccaacagcagcccccgccgagccgcggcggtccggcgccctggcgccagcagatccaat gggagaaacacgggaggtgttcagcttgcctgagcctgggcccacagcaccagccccagcgcccgccgggac ccggcgccgcgctcctggtgcagccaaacgcctccgcccagcagcccgactccgatcctgcogactccg cgacaacccgaccccgccgcccgcggaacgcggagcggcggtcatctggagtcaaccgctggcgcccccaggc ccaccgcccgtcactggttccaagctggctactcgacatctagagcccggaacgtggcgccctcgcgccgcg gagaaacagacagcgcgggagaaagtctcctgcgctcagtaacctcgccgcggccagccgctggagggcat ggtggcgacgaccttacaacccctacaagtagctctgacgacaaccttattacaactactacgatactt atgaaaggccagacctgggggaggtaccggcccgatacggcactggctacttccagtagcgtctccca gacctggtggcgacccctactacatccaggcgtccagctacgtgcagaagatgtccatgtacaacctgag atgcgcggcgaggaaaaactgtctggccagtacagcatacagggcagatgtcagagattatgatcacaggg tgctgctcagatttccccaaagagtgaacaaacaggagacatcagatttctcaccagccgaccaagatat tccctgggaatggcacagtgtcatcaacattaccacagtagtgatgagtttagccactatgacctgcttga tgccaaacccagagagagtaggtgctgaaggccacaagcaagtttctgcttgaagacacatcctgtgact atggctaccacaggcgatttgcatgtactgcacacacacagggtatgagtcctggctgttatgatacctat ggtgcagacatagactgccagtggtatgacattacagatgtaaaacccggaaactatctcctaaaggtcag tgcaaacccagctacctggttccctgaatctgactacaccaaatgtgtgcccgtgacattcgcgtaca caggacatcatgctatgctcaggctgcacaatttccacgtatag
13.	MRFAWTVLLGLPLQCALVHCAPPAAGQQPPREPPAAPGAWRQIQWENNGQVFSLLSLGSQYQPQRRRD PGAAPVGAANASAQQPRTPILLIRDNRTAAARTTAGSSGVTAGRPRPTARHWFQAGYSTSRARERASRA ENQTAPGEVPALSNLRPPSRVDGMVGDDPYNPYKYSDDNPIYNYDYTYERPRPGGRYRPGYGTGYFYGLP DLVADPYIYQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQRVKNQGTSDFLPSRPRY SHEWHSCHQHYHSMDBFSHYDLLDANTQRRVAEGHKASFCELEDTSCDYGYHRRFACTAHTQGLSPGICYDTY GADIDCQWIDITDVKPGNYILKVSVNPSYLVPESDYTNNVVRCDIRYTGHHAYASGCTISPY
14.	ggggcaggactgagaaaggggaagggaggggtgccacgtccgagcagccgcttgactggggaagggcct gaatcccccccttgccatgtcttggtggagactgagatacccgcgctccgctcgccctccctggttgaagat tctccctccctccagcagctttgagccccgttttactttctgtgagccagctccctcccgagcggggcca atctggcacaagagtgatgcgcttcgctggacccgtgctcctgctcgggcctttgcagctctgcgcgcta gtgcactgcgcctcccgccgcccggcccaacagcagcccccgccgagcccgccggcggtccggggcgctg gcgcagcagatccaatgggagaaacacgggaggtgttcagcttgctgagcctgggctcacagtagccagc ctcagcgcccgccgggacccggcgccgctcctggtgcagccaaacgcctccgcccagcagcccgact ccgatcctgctgactccgcgacaacccgacccgcccggggcggaacggagggcggtcactctggagtca cgctggcgcccccagcccccaccccgctcactggttccaagctggctactcgacatctagagcccggaag ctgggcccctcgccgcccggagaaacagacagcgcgggagaaagtctcctgctctcagtaacctgcggcgccc agccgctggagggcaggtggggcagcagcccttacaacccctacaagtagctctgacgacaaccttatta caactactacgatacttatgaaaggccagacactgggggaggtaccggcccgatacggcactggctact tccagtagcgtctccagacactggtggcgacccctactacatccaggcgtccagctacgtgcagaagatg

-continued

[illegible]

-continued

SEQ ID NO	Sequence
	gaaactatatcctaaggtcagtgtaaacccagctacctggttctggaatctgactataccaacaatggt gtgcgctgtgacattcgctacacaggacatcatgctatgcctcaggctgcacaatttcaccgtattagaa ggcaaaagcaaaactcccaatggataaatcagtgctggtgttct
19.	MRFAWTVLLGLPLCALVHCAPPAAGQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSEQYQPQRRRD PGAAPVPGAANASAQQRTPILLIRDNRATAARTRTAGSSGVTAGRPRTARHWFQAGYSTSRAREAGASRA ENQTAPGEVPALSNLRPPSRVDMGMDPYNPYKYSDNPNYNYDYTYERPRPGGRYRPGYGTGYFYGLP DLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRKNQGTSDLPSRPRY SWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSCDYGYYHRRFACTAHTQGLSPGCTDY GADIDCQWIDITDVKPGNYILKVSVPNSYLVPESDYTNVVRCDIRYTGHHAYASGCTISPY
20.	ggtcaatctggcaaaaggagtgatgcgcttcgctggaccgtgctcctgctcgggcctttgcagctctgcg cgctagtgcactgcgccccctccgcgcgcggcccaacagcagccccgcgcgagccgcggcggtccgggc gctggcgccagcagatccaatgggagaaacaacggcgaggtgttcagcttgcctgagcctgggctcacagta cagccctcagcgccgcgcgggacccggcgccgcgctccctggcgagccaacgcctccgcccagcagcccc gcactccgactcctgctgatccgcgcgaacccgcacccgcgcggcggaacgcggagccgcggctcatctgga gtcaccgctggcgcccccagggccacccgcctcactggttccaagctggctactcgacatctagagcccg cgaagctggcgctcctgcgcgcggagaaacagacagcgccgggagaaagtctctgctcagtaacctgcgcg cgcccagccgcgtggagcgcatggtggcgacgaccccttacaacccctacaagtaactctgacgacaaacct tatacaactactacgatacttatgaaagggccagacctggggggcaggtaccggcccgatagggcactgg ctacttccagtagcgtctccagacctggtggcgacccctactacatccaggcgtccagtaactgacgaga agatgtccatgtacaacctgagatgcgcggcgaggaaaaactgtctggcagtaacagcacaagggcagat gtcagagattatgatcacagggtgctgctcagatttccccaaagatgaaaaaccaagggacatcagattt cttaccagcccgcaagaatattcctgggaatggcacagttgtcatcaacattaccacagtaaggatgagt ttagccactatgacctgcttgatgccaacaccagagagagtggtgaagggcacaagcaagtttctgt cttgaagacacatcctgtgactatggctaccacagggcagtttgcattgactgcacacacacagggattgag tctggctgtttatgatacctatggtgcagacatagactgccagtggttgatattacagatgtaaaacctg gaaactatatcctaaggtcagtgtaaacccagctacctggttctggaatctgactataccaacaatggt gtgcgctgtgacattcgctacacaggacatcatgctatgcctcaggctgcacaatttcaccgtattagaa ggcaaaagcaaaactcccaatggataaatcagtgctggtgttctgaa
21.	MRFAWTVLLGLPLCALVHCAPPAAGQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSEQYQPQRRRD PGAAPVPGAANASAQQRTPILLIRDNRATAARTRTAGSSGVTAGRPRTARHWFQAGYSTSRAREAGASRA ENQTAPGEVPALSNLRPPSRVDMGMDPYNPYKYSDNPNYNYDYTYERPRPGGRYRPGYGTGYFYGLP DLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRKNQGTSDLPSRPRY SWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASECLEDTSCDYGYYHRRFACTAHTQGLSPGCTDY GADIDCQWIDITDVKPGNYILKVSVPNSYLVPESDYTNVVRCDIRYTGHHAYASGCTISPY
22.	Gttcagcttgcagcctgggctcacagtaaccagcctcagcgccgcgggacccggcgccgcgctccctg gtgcagccaacgcctccgcccagcagccccgcactccgactcctgctgatccgcgacaacccgcacccgcgcg gcgcgaacgcggagccggcctcatctggagtcacgcctggcgccccaggccacccgcgcctcactggtt ccaagctggctactcgacatctagagcccgcaagctggcgctcgcgcgcggagaaacagacagcgccgcg gagaagtctctgctcagtaacctgcggcgcccccagccgcgtggacggcatggtggcgacgaccttac aaccctacaagtactctgacgacaacccctattacaactactacgatacttatgaaagggccagacctgg ggcgaggtaccggcccgatagggcactggctacttccagtaaggtaagtaccccaagtcgctggaagc accgctgacactggtcccgactatgtggtctcttctcgactggtgctggcgcgccggggcccggtc ctcgagatccgacccctcccccagcgctgagtgagcgccctggaatccagtgcaaacccgcgctctgg ccctcctgctctcttccacattgcttgcagtcgggggggtccccagttctctgctgctccctccgctcc actctgcagtcgggtggcggaaggtgagggagtaagggacctagaggggtaggagttggagcggggggc gcggggtgtttcactgctgcgcctgctgctgactttaggtctccagacactggtg
23.	FSLLSLGSQYQPQRRRDPGAAPVPGAANASAQQRTPILLIRDNRATAARTRTAGSSGVTAGRPRTARHWF QAGYSTSRAREAGASRAENQTAPGEVPALSNLRPPSRVDMGMDPYNPYKYSDNPNYNYDYTYERPRPG GRYRPGYGTGYFYGLPDLV
24.	MEWSRVFIFLLSVTAGVHSQVQLQQSGAELVRPGTSVKVSKASGYAFTYYLIEWVKQRPQGQLEWIGVIN PGSGGTTNYNEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARNMMNFDYWGQGTTLTVSS
25.	QVQLVQSGAELKPKGASVKVSKASGYAFTYYLIEWVKQAPQGQLEWIGVINPGSGGTTNYNEKFKGRATLT ADKSTSTAYMELSSCRSEDSAVYFCARNMMNFDYWGQGTTLTVSS
26.	QVQLVQSGAELVKKPGASVKVSKASGYAFTYYLIEWVRQAPQGQLEWIGVINPGSGGTTNYNEKFKGRATLT ADKSTSTAYMELSSCRSEDTAVYFCARNMMNFDYWGQGTTLTVSS
27.	QVQLVQSGAELVKKPGASVKVSKASGYAFTYYLIEWVRQAPQGQLEWIGVINPGSGGTTNYNEKFKGRATIT ADKSTSTAYMELSSLRSEDTAVYFCARNMMNFDYWGQGTTLTVSS
28.	QVQLVQSGAELVKKPGASVKVSKASGYAFTYYLIEWVRQAPQGQLEWIGVINPGSGGTTNYNEKFKGRVTIT ADKSTSTAYMELSSLRSEDTAVYFCARNMMNFDYWGQGTTLTVSS
29.	MRCLEFLGLLVLPWIPGAIGDIVMTQAAPSVSVTPGESVSISSKSLHSNGNTYLYWFLQRPQSQPQF LIYRMSNLASGVPRDFSGSGTAFTLRISRVEAEDVGVIYCMOHLFYPYTFGGGTTKLEIK

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SEQ ID NO	Sequence
30.	DIVMTQTPLSLSVTPGQPASISCRSSKSLHLSNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVPDRFSGSG SGTAFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
31.	DIVMTQTPLSLSVTPGQPASISCRSSKSLHLSNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVPDRFSGSG SGTDFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
32.	DIVMTQTPLSLSVTPGQPASISCRSSKSLHLSNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVPDRFSGSG SGTDFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
33.	MEWSRVFIFLLSVTAGVHSQVQLQSGAELVRPGTSVKVSCAS
34.	WVKQRPQGLEWIG
35.	KATLTADKSSSTAYMQLSSLTSDSAVYFCAR
36.	WGQGTTLTVSS
37.	QVQLVQSGAELKPGASVKVSCAS
38.	WVKQAPGQGLEWIG
39.	RATLTADKSTSTAYMELSSLRSEDSAVYFCAR
40.	WGQGTITVTVSS
41.	GYAFTYYLIE
42.	VINPGSGGTNYNEKFKG
43.	NWMNFDY
44.	QVQLVQSGAEVKKPGASVKVSCAS
45.	WVRQAPGQGLEWIG
46.	RATLTADKSTSTAYMELSSLRSEDTAVYFCAR
47.	RATITADKSTSTAYMELSSLRSEDTAVYFCAR
48.	RVTITADKSTSTAYMELSSLRSEDTAVYFCAR
49.	MRCLAFLGLLVLPWIPGAIGDIVMTQAAPSVSVTPGESVSISC
50.	WFLQRPQSPQFLTY
51.	GVPDRFSGSGSGTAFTLRISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
52.	FGGGTKVEIK
53.	DIVMTQTPLSLSVTPGQPASISCRSSKSLHLSNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVPDRFSGSG SGTAFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
54.	WFLQKPGQSPQFLIY
55.	GVPDRFSGSGSGTAFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
56.	FGGGTKVEIK
57.	RSSKSLHLSNGNTYLY
58.	RMSNLAS
59.	MQHLEYPYT
60.	GVPDRFSGSGSGTDFTLKTISRVEAEDVGVIYCMQHLEYPYTFGGGTKVEIK
61.	WFLQKPGQSPQFLIY
62.	Alternative cleavage sites can be between amino acids 21 and 22 of preprotein compared to SEQ ID NO: 8 APPAAGQQQPPREPPAAGAWRQIQWENNGQVFSLLSLGSQYQPRRRDPGAAPGAANASAQPRTPIL LIRDNRATAARTTAGSSGVTAGRPRPTARHWFQAGYSTSRAREAGASRAENQTAPGEVPALSNLRPPSRV DGMVGDDPYNPYKYSDDNPYYNYDTYERPRPGGRYRPGYGTGYFQYGLPDLVADPYIQASTYVQKMSMY NLRCAAEENCLASTAYRADVRDYDHRVLLRFPQVRVKNQGTSDFLPSRPRYSWEWHSCQHYSMDDEFSHYD

-continued

SEQ ID NO	Sequence
	LLDANTQRRVAEGHKASFLEDTS ^{CDYGYHRR} FACTAHTQGLSPG ^{CDY} TYGADIDCQWIDITDVKPGNYILKVS ^{VNP} SVLVPESDYTN ^{NVVR} CDIRYTGHHAYASGCTISPY
63.	Alternative cleavage sites can be between amino acids 27 and 28 of preprotein compared to SEQ ID NO: 8 QQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSQYQPQRRRDPGA ^{AV} PGAANAS ^{AQ} QPRTPILLIRDNR TAAARTRTAGSSGVTAGRPRPTARHWFQAGYSTSRAREAGASRAENQTAPGEVPALSNLRPPSRVDGMVGD DPYNPYKYSDDNPYYNYD ^{TYER} PRPGGRYRPGYGTGYFYGLPDLVADPYYIQASTYVQKMSMYNLRCAA EENCLASTAYRADVRDYDHRVLLRFPQVRKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYD ^{LLDANT} QRRVAEGHKASFLEDTS ^{CDYGYHRR} FACTAHTQGLSPG ^{CDY} TYGADIDCQWIDITDVKPGNYILKVS ^{VNP} SVLVPESDYTN ^{NVVR} CDIRYTGHHAYASGCTISPY
64.	Human LOX mRNA sequence ATGCGCTTCGCTGGACCGTGCCTCCTGCTCGGGCCTTTGACAGCTCTGCGCGCTAGTGCACTGCGCCCTCC CGCCGCGCGCAACAGCAGCAGCCCGCGCGAGCCGCGCGGCTCCGGGCGCCTGGCGCCAGCAGATCCAAT GGGAGAACAAACGGGCAGGTGTTACGCTTGTGAGCCTGGGCTCACAGTACCAGCCTCAGCGCCGCGGGAC CCGGGCGCGCGCTCCCTGGTGACGCAACGCTCCGCCCAGCAGCCCGCACTCCGATCCTGCTGATCCG CGACAACCGCACCCGCGCGCGGCGCAACGCGGACGGCCGGCTCATCTGGAGTCA ^{CCGCTGGCGCGCCAGGC} CCACCGCCCGTCACTGGTTC ^{AAGCTGGCTACTCGACATCTAGAGCCCGGAAGCTGGCGCTCGCGCGCG} GAGAACAGACAGCGCGCGGAGAGTTCCTGCGCTCAGTAACCTGCGGCGCCAGCCGCGTGGACGGCAT GGTGGGCGAGCGACCTTACAACCCCTACAAGTACTCTGACGACAACCCCTTATTACA ^{CTACTACGATACTT} ATGAAAGGCCAGACCTGGGGGAGGTACCGGCCGGATACGGCAGTGGCTACTTCCAGTACGGTCTCCCA GACCTGGTGGCGAGCCCTACTACATCCAGGCGTCCACGTACGTGAGAGATGCCATGTACAACTGAG ATGCGCGCGCGGAGGAAAACCTGTCTGGCCAGTACAGCATA ^{CAGGGCAGATGTGAGAGATTATGATCAGGG} TGCTGCTCAGATTCCCAAGAGTGA ^{AAACCAAGGACATCAGATTCTTACCCAGCCGACCAAGATAT} TCCTGGGAATGGCACAGTTGTCAACATTACCAAGTATGGATGAGTTAGCCACATGACCTGCTTGA TGCCAAACCCAGAGGAGAGTGGCTGAAGGCCACAAGCAAGTTCTGTCTTGAAGACATCCTGTGACT ATGGCTACCAAGCGGATTTGCATGTACTGCACACACAGGGATTGAGTCTGGCTGTTATGATACCTAT GGTGAGACATAGACTGCCAGTGGATTGATATTACAGATGTA ^{AAACCTGGAACATATATCCTAAAGGTCAG} TGTAACCCCGAGCTACCTGGTTCTGAATCTGACTATACCAACAATGTGTGCGCTGTGACATTGCTACAC CAGGACATCATGCGTATGCCTCAGGCTGCACAATTCACCGTAT
65.	Human LOX Protein Sequence MRFAWTVLLGLPLQLCALVHCAPPAAGQQQPPREPPAAPGAWRQQIQWENNGQVFSLLSLGSQYQPQRRRD PGA ^{AV} PGAANAS ^{AQ} QPRTPILLIRDNR ^{TAAARTRTAGSSGVTAGRPRPTARHWFQAGYSTSRAREAGASRA} ENQTAPGEVPALSNLRPPSRVDGMVGD ^{DPYNPYKYSDDNPYYNYD} TYERPRPGGRYRPGYGTGYFYGLP DLVADPYYIQASTYVQKMSMYNLRCAA ^{EENCLASTAYRADVRDYDHRVLLRFPQVRKNQGTSDFLPSRPRYS} WEWHSCHQHYHSMDEFSHYD ^{LLDANTQRRVAEGHKASFLEDTS} CDYGYHRRFACTAHTQGLSPG ^{CDY} TY GADIDCQWIDITDVKPGNYILKVS ^{VNP} SVLVPESDYTN ^{NVVR} CDIRYTGHHAYASGCTISPY

Example 13

Amino Acid Sequence and Encoding Nucleic Acid
Sequence of Humanized Anti-LOXL2 Antibody
Light Chain

[0623] The nucleic acid sequence encoding the light chain of a humanized anti-LOXL2 antibody was determined using standard methods. The amino acid sequence of the light chain, which is also presented in FIG. 19, is as follows:

(SEQ ID NO: 71)
MRVPAQLLGLLLWLPGARCDIVMTQTPLSLSVTPGQPASISCRSSKSLH
SNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVDPDRFSGSGSDFTLKIS
RVEAEDVGVYYCMQHLEYPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLK
SGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSL
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

[0624] This amino acid sequence contains the amino acid sequence of V_K variant 2.pro in FIG. 14. The sequence of the nucleic acid encoding SEQ ID NO:71 is provided in FIG. 19 as SEQ ID NO:72. FIG. 19 further provides the amino acid

sequence and encoding nucleic acid sequence for the signal peptide sequence (indicated by a single underline), the variable region framework (indicated by a dashed underline), the CDR regions (indicated by a double underline); and the constant region framework (provided as unformatted text). It is understood that, due to the degeneracy of the genetic code, nucleic acids that encode all or a portion of SEQ ID NO:71, but that differ in sequence from that shown in FIG. 19 are also contemplated by the present disclosure.

As shown in FIG. 19, the above sequence includes a signal peptide having the amino acid sequence: MRV-PAQLLGLLLLWLPGAR (SEQ ID NO: 73). Thus, the amino acid sequence of the light chain polypeptide without the signal peptide is:

(SEQ ID NO: 74)
DIVMTQTPLSLSVTPGQPASISCRSSKSLH
SNGNTYLYWFLQKPGQSPQFLIYRMSNLASGVDPDRFSGSGSDFTLKIS
RVEAEDVGVYYCMQHLEYPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAK
VQWKVDNALQSGNSQESVTEQDSKDSYSLSTLTLSKADYEKHKVYACE
VTHQGLSSPVTKSFNRGEC.

[0625] The nucleic acid encoding this light chain polypeptide comprises the sequence:

(SEQ ID NO: 75)
 GATATTGTGATGACCCAGACTCCACTCTCTGTCCGTCACCCCTGGACA
 GCCGCCCTCCATCTCCTGAGGCTAGTAAGAGTCTCCTGCATAGTAATG
 GCAACACTTACTTGTATTGGTTCTGCAGAAGCCAGGCGAGTCTCCACAG
 TTCTGATCTATCGGATGTCCAACCTTGCCCTCAGGAGTGCCAGATAGGTT
 CAGTGGCAGCGGGTCAGGACAGACTTCACACTGAAAAATCAGCCGGGTGG
 AGGCTGAGGATGTTGGGGTTTATTACTGCATGCAACATCTAGAATATCCT
 TACACCTTCGGCGAGGGACCAAGGTGGAGATCAAACGAAGTGTGGCTGC
 ACCATCTGTCTTCATCTTCCGCCATCTGATGAGCAGTTGAAATCTGGAA
 CTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCAGAGAGGCCAAA
 GTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCC
 TGACGCTGAGCAAAGCAGACTACGAGAAACAAAGTCTACGCTGCGAA
 GTCAACCATCAGGCGCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGG
 AGAGTGTTAG.

[0626] The variable region of this light chain polypeptide, which includes the CDRs and framework regions, has the amino acid sequence:

(SEQ ID NO: 31)
 DIVMTQTPLSLSVTPGQPASISCRSSKSLLSNGNTYLYWFLQKPGQSPQ
 FLIYRMSNLASGVDPDRFSGSGSDTFTLKI SRVEAEDVGYYCMOHLEYF
 YTFGGGTKVEIK

where the underlining represents the amino acid sequence of CDR1, CDR2, and CDR3 of the light chain variable region which are flanked by framework regions.

Example 14

Amino Acid Sequence and Encoding Nucleic Acid Sequence of Humanized Anti-LOXL2 Antibody Heavy Chain Containing (S241P) Modification

[0627] The nucleic acid sequence encoding the heavy chain of a humanized anti-LOXL2 antibody was determined using standard methods. The amino acid sequence of the heavy chain, which is also presented in FIG. 20, is as follows:

(SEQ ID NO: 76)
 MGWSLILLFLVAVATRVHSQVQLVQSGAEVKKPGASVKVSKASGYFTY
 YLIEWVRQAPQGLEWIGVINPGSGGTNYNEKFKGRATITADKSTSTAYM
 ELSSLRSEDNAVYFCARNWMNFDYWGQTTVTVSSASTKGPSVFPLAPCS
 RSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSGLYSL
 SSVVTVPSSSLGKTKYTCNVDHKPSNTKVDKRVESKYGPCCPPAPEFL
 GGPVSFVLPFPKPKDTLMISRTEPVTGVVDVSQEDPEVQFNWYVDGVEVH
 NAKTKPREEQFNSTYRVVSVLTVLHQDNLNGKEYKCKVSNKGLPSSIEKT

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ISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGEYPSDIAVEWESNG
 QPENNYKTPPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNH
 YTQKLSLSLGLK

[0628] This amino acid sequence contains the amino acid sequence of V_H variant 3.pro of FIG. 14. The sequence of the nucleic acid encoding SEQ ID NO:76 is provided in FIG. 20 as SEQ ID NO:77. FIG. 20 further provides the amino acid sequence and encoding nucleic acid sequence for the signal peptide sequence (indicated by a single underline), the variable region framework (indicated by a dashed underline), the CDR regions (indicated by a double underline), the constant region framework (provided as unformatted text), and the modification at the IgG4 hinge to provide for a proline in lieu of a serine. It is understood that, due to the degeneracy of the genetic code, nucleic acids that encode all or a portion of SEQ ID NO:76, but that differ in sequence from that shown in FIG. 20 are also contemplated by the present disclosure.

[0629] As shown in FIG. 20, the above sequence includes a signal peptide having the amino acid sequence: MGWSLILLFLVAVATRVHS (SEQ ID NO:78). Thus, the heavy chain polypeptide without the signal sequence has the amino acid sequence:

(SEQ ID NO: 79)
 QVQLVQSGAEVKKPGASVKVSKASGYFTYLLIEWVRQAPQGLEWIGV
 INPGSGGTNYNEKFKGRATITADKSTSTAYMELSSLRSEDNAVYFCARNW
 MNFDYWGQTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFP
 EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGKTKYTCN
 VDHKPSNTKVDKRVESKYGPCCPPAPEFLGGPSVFLFPPKPKDTLMIS
 RTEPVTGVVDVSQEDPEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVS
 VLTVLHQDNLNGKEYKCKVSNKGLPSSIEKTISKAKGQPREPQVYTLPPS
 QEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSF
 FLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKLSLSLGLK.

[0630] The nucleic acid encoding this heavy chain polypeptide comprises the sequence:

(SEQ ID NO: 80)
 CAGGTGCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGCGCTC
 AGTGAAGGTCTCCTGCAAGGCTTCTGGATACGCTTCACTTATTACTTGA
 TAGAGTGGGTGAGACAGGCCCTGGACAAGGGCTTGAAGTGGATCGGAGTG
 ATTAATCTGGAAGTGGTGGTACTAATACTACAATGAGAAGTTCAAGGGCAG
 AGCCACGATCACCGCGGACAAATCCACGAGCACAGCCTACATGGAGCTGA
 GCAGCCTGAGATCTGAGGACACCGCGGTGATTCTGTGCGAGAACTGG
 ATGAACCTTGACTACTGGGGGCAAGGGACACGGTCACCGTCTCCTCAGC
 TTCCACCAAGGGCCCATCCGTCTTCCCCCTGGCGCCCTGCTCCAGGAGCA
 CCTCCGAGAGCACAGCCGCCCTGGGCTGCTGGTCAAGGACTACTTCCCC
 GAACCGGTGACGGTGTCTGGAAGTCAAGCGCCCTGACAGCGCGCTGCA

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CACCTTCCCGGCTGTCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCG
TGGTGACCGTGCCCTCCAGCAGCTTGGGCACGAAGACCTACACCTGCAAT
GTAGATCACAAAGCCAGCAACACCAAGGTGGACAAGAGAGTTGAGTCCAA
ATATGGTCCCCCATGCCACCATGCCAGCACCTGAGTTCTCGGGGGGAC
CATCAGTCTTCTGTTCCTCCCAACCAAGGACACTCTCATGATCTCC
CGGACCCCTGAGGTACGTGCGTGGTGGTGGACGTGAGCCAGGAAGACCC
CGAGGTCCAGTTCAACTGGTACGTGGATGGCGTGGAGGTGCATAATGCCA
AGACAAAGCCGCGGGAGGAGCAGTTCAACAGCAGCTACCGTGTGGTCAGC
GTCTTACCGTCTGCACCAAGGACTGGCTGAACGGCAAGGAGTACAAGTG
CAAGGTCTCCAACAAAGGCCTCCCGTCTCCATCGAGAAAACCATCTCCA
AAGCCAAAGGGCAGCCCCGAGAGCCACAGGTGTACACCTGCCCCATCC
CAGGAGGAGATGACCAAGAACCAGGTACGCTGACCTGCCCTGGTCAAAGG
CTTCTACCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCCGG
AGAACAACACTACAAGACCACGCTCCCGTGTGGACTCCGACGGCTCCTTC
TTCTCTACAGCAGGCTAACCGTGGAAGAGCAGGTGGCAGGAGGGGAA
TGCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACAC
AGAAGAGCCTCTCCTGTCTCTGGGTAATGA

[0631] The variable region of this heavy chain polypeptide, which includes the CDRs and framework regions, has the amino acid sequence:

(SEQ ID NO: 27)
QVQLVQSGAEVKKPGASVKVSCKASGYAFTYYLIEWVRQAPGQGLEWIGY
INPGSGGTNYNEKFKGRATITADKSTSTAYMELSSLRSED TAVYFCARNM
MNFEDYWGQGT TTVTVSS

where the underlining represents the amino acid sequence of CDR1, CDR2, and CDR3 the heavy chain variable region which are flanked by framework regions.

Example 15

Constructs

[0632] As disclosed above, the present disclosure provides for a variety of constructs that incorporate at least antigen binding portions of an anti-LOXL2 antibody, e.g., an anti-human LOXL2 antibody. In one embodiment, the present disclosure provides light chain polypeptide and heavy chain polypeptides, which may be provided with or without signal peptides, and which may be provided in a variety of constructs. The constant region of the heavy chain polypeptide may be optionally modified to provide for a desired feature. For example, where the heavy chain constant region comprises the amino acid sequence of a human heavy chain constant region polypeptide, it may be modified at the hinge region (e.g., by substitution of a naturally occurring serine with a proline). In one embodiment, a polypeptide is provided that includes, from N- to C-terminus, a first light chain polypeptide, a first heavy chain polypeptide, a second light chain polypeptide, and a second heavy chain polypeptide.

[0633] The amino acid sequences of the light chain polypeptide and of the heavy chain polypeptide can have the amino acid sequence of the CDRs of the light chain and heavy chain variable regions described herein, and further may contain the amino acid sequences of any of the light chain variable regions, light chain constant regions, heavy chain variable regions, and/or heavy chain constant regions as disclosed herein. In one example, the light chain variable region comprises the CDRs of A130023 as set out in FIG. 14. In one example, the heavy chain variable region comprises the CDRs of AB0023 as set out in FIG. 14.

[0634] The present disclosure also provides nucleic acid constructs, such as expression constructs, and recombinant host cells containing such constructs. For example, a nucleic acid comprising a sequence encoding a heavy chain polypeptides disclosed herein (or an antigen binding portion thereof, e.g., SEQ ID NO:79, or antigen binding portion thereof) can be provided in an expression construct where the DNA encoding the heavy chain polypeptide is positioned 3' of a promoter that is capable of facilitating expression of the heavy chain polypeptide. In another example, a nucleic acid comprising a sequence encoding a light chain polypeptide disclosed herein (or an antigen binding portion thereof, e.g., SEQ ID NO:74, or antigen binding portion thereof) can be provided in an expression construct where the DNA encoding the light chain polypeptide is positioned 3' of a promoter that is capable of facilitating expression of the light chain polypeptide. In another example, the expression construct includes a both a heavy chain polypeptide coding sequence (or antigen binding portion thereof, e.g., SEQ ID NO:79, or antigen binding portion thereof) or a light chain polypeptide coding sequence (or antigen binding portion thereof, e.g., SEQ ID NO:74, or antigen binding portion thereof). In such constructs the two coding sequences can be under the control of the same or different promoters. The present disclosure also provides recombinant host cells containing such constructs

[0635] In all constructs contemplated by the present disclosure, the heavy chain and/or light chain coding sequences can include a sequence encoding a signal peptide. Thus, the present disclosure provides, for example, an expression construct containing a coding sequence for a signal peptide and a heavy chain polypeptide disclosed herein (or an antigen binding portion thereof, e.g., SEQ ID NO:78, or antigen binding portion thereof), where the coding sequence is positioned 3' of a promoter that is capable of facilitating expression of the coding sequence. In another example, the present disclosure provides an expression construct containing a coding sequence for a signal peptide and a light chain polypeptide disclosed herein (or an antigen binding portion thereof, e.g., SEQ ID NO:71, or antigen binding portion thereof) where the coding sequence is positioned 3' of a promoter that is capable of facilitating expression of the coding sequence. In another example, the expression construct includes both a heavy chain and a light chain polypeptide coding sequences (or antigen binding portions thereof), each having a signal peptide. In such constructs the two coding sequences can be under the control of the same or different promoters. The present disclosure also provides recombinant host cells containing such constructs.

[0636] The present disclosure provides a polypeptide composed of the light chain polypeptide of Example 14 ("kappa") and a modified heavy chain polypeptide of IgG4 ("IgG4") of

Example 14. The amino acid sequence of the polypeptide is as follows (where the light chain amino acid sequence is underlined):

(SEQ ID NO: 81)

DIVMTOTPLS LSVTPGQPAS ISCRSSKSL L HSNNGNTYLYW
FLQKPGQSPQ FLIYRMSNLA SGVPDRFSGS GSGTDFTLKI
SRVEAEDVGV YYCMOHLEYP YTFGGGTVKE IKRTVAAPSV
FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKVDNALQ
SGNSQESVTE QDSKDYSTSL SSTLTLSKAD YEKHKVYACE
VTHQGLSSPY TKSFNREGCQ VQLVQSGAEV KKPASVSVKVS
 CKASGYARTY YLIEWVRQAP GQGLEWIGVI NPGSGGTNYN
 EKFKGRATIT ADKSTSTAYM ELSSLRSEDY AVYFCARNWM
 NFDYWGQGT VTVSSASTKG PSVFPLAPCS RSTSESTAAL
 GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL
 SSVVTVPSST LGTKYTCNV DHKPSNTKVD KRVESKYGPP
 CPPCPAPEFL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD
 VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV
 LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE
 PQVYTLPPSQ EEMTKNQVSL TCVLKGFYPS DIAVEWESNG
 QPENNYKTTP PVLDSGDSFF LYSRLTVDKS RWQEGNVFSC
 SVMHEALHNH YTQKSLSLSL GK

[0637] In another example, the amino acid sequence of the polypeptide may be composed of two “units” of SEQ ID NO:81 is (where the light chain amino acid sequence is underlined):

(SEQ ID NO: 82)

DIVMTOTPLS LSVTPGQPAS ISCRSSKSL L HSNNGNTYLYW
FLQKPGQSPQ FLIYRMSNLA SGVPDRFSGS GSGTDFTLKI
SRVEAEDVGV YYCMOHLEYP YTFGGGTVKE IKRTVAAPSV
FIFPPSDEQL KSGTASVVCL LNNFYPREAK VQWKVDNALQ
SGNSQESVTE QDSKDYSTSL SSTLTLSKAD YEKHKVYACE
VTHQGLSSPY TKSFNREGCQ VQLVQSGAEV KKPASVSVKVS
 CKASGYARTY YLIEWVRQAP GQGLEWIGVI NPGSGGTNYN
 EKFKGRATIT ADKSTSTAYM ELSSLRSEDY AVYFCARNWM
 NFDYWGQGT VTVSSASTKG PSVFPLAPCS RSTSESTAAL
 GCLVKDYFPE PVTVSWNSGA LTSGVHTFPA VLQSSGLYSL
 SSVVTVPSST LGTKYTCNV DHKPSNTKVD KRVESKYGPP
 CPPCPAPEFL GGPSVFLFPP KPKDTLMISR TPEVTCVVVD
 VSQEDPEVQF NWYVDGVEVH NAKTKPREEQ FNSTYRVVSV
 LTVLHQDWLN GKEYKCKVSN KGLPSSIEKT ISKAKGQPRE
 PQVYTLPPSQ EEMTKNQVSL TCVLKGFYPS DIAVEWESNG

-continued

QPENNYKTTP PVLDSGDSFF LYSRLTVDKS RWQEGNVFSC
 SVMHEALHNH YTQKSLSLSL GKDIVMTOTP LSVTPGQP
ASISCRSSKS LLHSNGNTYL YWFLOKPGQS PQFLIYRMSN
LASGVPDRFS GSGSGTDFTL KISRVEAEDV GYYCMOHLE
YPTTGGGTVK VEIKRTVAAP SVFIFPPSDE QLKSGTASV
CLLNNFYPRE AKVQWKVDNA LQSGNSQESV TEQDSKDY
SLSSTLTLSK ADYEKHKVYA CEVTHQGLSS PVTKSFNRGE
 CQVQLVQSGA EVKPPASVSVKVSCKASGYAF TYLLIEWVRQ
 APGQGLEWIG VINPGSGGTN YNEKPKGRAT ITADKSTSTA
 YMELSSLRSE DTAVYFCARN WMNFDYWGQG TTVTVSSAST
 KGPSVFLAP CSRSTSESTA ALGCLVKDYF PEPVTVSWNS
 GALTSGVHTF PAVLQSSGLY SLSSVVTVPS SSLGKTYTC
 NVDHKPSNTK VDKRVESKYG PPCPPCPAPE FLGGPSVFLF
 PPKPKDTLMI SRTPEVTCVV VDSQEDPEV QFNWYVDGVE
 VHNAKTKPRE EQFNSTYRVV SVTLVLHQDW LNGKEYKCKV
 SNKGLPSSIE KTISKAKGQ REPQVYTLPP SQEEMTKNQV
 SLTCLVKGFY PSDIAVEWES NGQPENNYKT TPVLDSDGS
 FFLYSRLTV DKSRLWQEGNV SCVSMHEALH NHYTQKSLSL SLGK

[0638] The IgG4 heavy chain constant region polypeptide may have the amino acid sequence:

(SEQ ID NO: 84)

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGV
 HTFPAVLQSSGLYSLSSVTVPSSTLGKTYTCNVNVDHKPSNTKVDKRVES
 KYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTEVTCVVVDVSQED
 PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVTLVLHQDWLNGKEYK
 CKVSNKGLPSSIEKTISKAKGQREPQVYTLPPSQEEMTKNQVSLTCLVK
 GFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSRLTVDKSRWQEG
 NVFSCVSMHEALHNHYTQKSLSLSLGK.

[0639] While preferred embodiments of the present invention have been shown and described herein, it will be clear to those skilled in the art that such embodiments are provided by way of example only. Numerous variations, changes, and substitutions will now occur to those skilled in the art without departing from the invention. It should be understood that various alternatives to the embodiments of the invention described herein may be employed in practicing the invention. It is intended that the following claims define the scope of the invention and that methods and structures within the scope of these claims and their equivalents be covered thereby.

 SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 84

<210> SEQ ID NO 1

<211> LENGTH: 135

<212> TYPE: PRT

<213> ORGANISM: Mus sp.

<400> SEQUENCE: 1

```

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

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<210> SEQ ID NO 2

<211> LENGTH: 132

<212> TYPE: PRT

<213> ORGANISM: Mus sp.

<400> SEQUENCE: 2

```

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

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<210> SEQ ID NO 3

-continued

<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 3

Met Gly Trp Ser Trp Val Phe Leu Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe
35 40 45

Arg Ser Tyr Asp Ile Asn Trp Val Arg Gln Arg Pro Glu Gln Gly Leu
50 55 60

Glu Trp Ile Gly Trp Ile Phe Pro Gly Asp Gly Ser Thr Lys Tyr Asn
65 70 75 80

Glu Lys Phe Lys Gly Lys Ala Ile Leu Thr Thr Asp Lys Ser Ser Ser
85 90 95

Thr Ala Tyr Met Gln Leu Ser Arg Leu Thr Ser Glu Asp Ser Ala Val
100 105 110

Tyr Phe Cys Ala Arg Val Tyr Tyr Ala Met Asp Tyr Trp Gly Gln Gly
115 120 125

Thr Ser Val Thr Val Ser Ser
130 135

<210> SEQ ID NO 4
<211> LENGTH: 133
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 4

Met Lys Leu Pro Val Arg Leu Leu Val Met Phe Trp Ile Pro Ala Ser
1 5 10 15

Ser Ser Asp Val Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
20 25 30

Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val
35 40 45

His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly
50 55 60

Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly
65 70 75 80

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

Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe
100 105 110

Gln Ser Ser His Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115 120 125

Leu Lys Arg Ala Asp
130

<210> SEQ ID NO 5
<211> LENGTH: 133
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 5
Met Lys Leu Pro Val Arg Leu Leu Val Met Phe Trp Ile Pro Ala Ser
1      5      10      15
Ser Ser Asp Val Leu Leu Thr Gln Thr Pro Leu Ser Leu Pro Val Ser
20      25      30
Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Ile Val
35      40      45
His Ser Asn Gly Asn Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly
50      55      60
Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Ile Arg Phe Ser Gly
65      70      75      80
Val Pro Asp Arg Phe Gly Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
85      90      95
Lys Ile Asn Arg Val Glu Ala Glu Asp Leu Gly Ile Tyr Tyr Cys Phe
100     105     110
Gln Ser Ser His Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu
115     120     125
Leu Lys Arg Ala Asp
130

<210> SEQ ID NO 6
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 6
Val Arg Leu Arg Gly Gly Ala Tyr Ile Gly Glu Gly Arg Val Glu Val
1      5      10      15
Leu Lys Asn Gly Glu Trp Gly Thr Val Cys Asp Asp Lys Trp Asp Leu
20      25      30
Val Ser Ala Ser Val Val Cys Arg Glu Leu Gly Phe Gly Ser Ala Lys
35      40      45
Glu Ala Val Thr Gly Ser Arg Leu Gly Gln Gly Ile Gly Pro Ile His
50      55      60
Leu Asn Glu Ile Gln Cys Thr Gly Asn Glu Lys Ser Ile Ile Asp Cys
65      70      75      80
Lys Phe Asn Ala Glu Ser Gln Gly Cys Asn His Glu Glu Asp Ala Gly
85      90      95
Val Arg Cys Asn Leu Arg Leu Asn Gly Gly Arg Asn Pro Tyr Glu Gly
100     105     110
Arg Val Glu Val Leu Val Glu Arg Asn Gly Ser Leu Val Trp Gly Met
115     120     125
Val Cys Gly Gln Asn Trp Gly Ile Val Glu Ala Met Val Val Cys Arg
130     135     140
Gln Leu Gly Leu Gly Phe Ala Ser Asn Ala Phe Gln Glu Thr Trp Tyr
145     150     155     160
Trp His Gly Asp Val Asn Ser Asn Lys Val Val Met Ser Gly Val Lys
165     170     175

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Cys Ser Gly Thr Glu Leu Ser Leu Ala His Cys Arg His Asp Gly Glu
 180 185 190

Asp Val Ala Cys Pro Gln Gly Gly Val Gln Tyr Gly Ala Gly Val Ala
 195 200 205

Cys Ser
 210

<210> SEQ ID NO 7
 <211> LENGTH: 417
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
 1 5 10 15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
 20 25 30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
 35 40 45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
 50 55 60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
 65 70 75 80

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
 85 90 95

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
 100 105 110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
 115 120 125

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn
 130 135 140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
 145 150 155 160

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
 165 170 175

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
 180 185 190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
 195 200 205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
 210 215 220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
 225 230 235 240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
 245 250 255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
 260 265 270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
 275 280 285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
 290 295 300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
 305 310 315 320

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Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
 325 330 335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
 340 345 350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
 355 360 365

Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
 370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
 385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
 405 410 415

Tyr

<210> SEQ ID NO 8
 <211> LENGTH: 401
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
 1 5 10 15

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
 20 25 30

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
 35 40 45

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
 50 55 60

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
 65 70 75 80

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
 85 90 95

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
 100 105 110

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn
 115 120 125

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
 130 135 140

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
 145 150 155 160

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
 165 170 175

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
 180 185 190

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
 195 200 205

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
 210 215 220

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
 225 230 235 240

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
 245 250 255

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

<210> SEQ ID NO 9
 <211> LENGTH: 249
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

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

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Lys Val Ser Val Asn Pro Ser Tyr Leu Val Pro Glu Ser Asp Tyr Thr
 210 215 220

Asn Asn Val Val Arg Cys Asp Ile Arg Tyr Thr Gly His His Ala Tyr
 225 230 235 240

Ala Ser Gly Cys Thr Ile Ser Pro Tyr
 245

<210> SEQ ID NO 10
 <211> LENGTH: 1604
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <220> FEATURE:
 <221> NAME/KEY: modified_base
 <222> LOCATION: (1530)..(1530)
 <223> OTHER INFORMATION: n = a, c, g, t, unknown or other

<400> SEQUENCE: 10

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gggcgtgatt tgagccccgt ttttattttc tgtgagccac gtctctctcg aggggggtcaa    60
tctggccaaa aggagtgatg cgcttcgcct ggaccgtgct cctgctcggg cctttgcagc    120
tctgcgcgct agtgactgc gccctccccg ccgccggcca acagcagccc ccgcgcgagc    180
cgccggcggc tccggggcgcc tggcgccagc agatccaatg ggagaacaac gggcagggtgt    240
tcagcttgct gagcctgggc tcacagtacc agcctcagcg ccgccgggac ccgggcgccg    300
ccgtccctgg tgcagccaac gcctccgccc agcagccccg cactccgac cgtctgatcc    360
gcgacaaccg caccgcgcg gcgcgaacgc ggacggccgg ctcatctgga gtcaccgctg    420
gccgccccag gcccaccgcc cgtcactggt tccaagctgg ctactcgaca tctagagccc    480
gcgaacgtgg cgctcgcgc gcggagaacc agacagcgcc gggagaagtt cctgcgctca    540
gtaacctgcg gccgcccagc cgcgtggacg gcacgtgggg cgacgaccct tacaaccct    600
acaagtactc tgacgacaac ccttattaca actactacga tacttatgaa aggccagac    660
ctgggggcag gtaccggccc ggatacggca ctggctactt ccagtacggg tccccagacc    720
tggtggccga cccctactac atccaggcgt ccacgtacgt gcagaagatg tccatgtaca    780
acctgagatg cgcggcgagg gaaaactgtc tggccagtac agcatacagg gcagatgtca    840
gagattatga tcacaggggtg ctgctcagat ttccccaag agtgaaaaac caagggacat    900
cagatttctt acccagccga ccaagatatt cctgggaatg gcacagttgt catcaacatt    960
accacagtat ggatgagttt agccactatg acctgcttga tgccaacacc cagaggagag   1020
tggtgtaagg ccacaaagca agtttctgtc ttgaagacac atcctgtgac tatggctacc   1080
acaggcgatt tgcattgact gcacacacac agggattgag tcctggctgt tatgatacct   1140
atggtgcaga catagactgc cagtggattg atattacaga tgtaaaacct ggaaactata   1200
tcctaaaggt cagtgtaaac ccagctacc tggttcctga atctgactat accaacaatg   1260
ttgtgcgctg tgacattcgc tacacaggac atcatgcgta tgctcaggc tgcacaattt   1320
cacggtatta gaaggcaaag caaaactccc aatggataaa tcagtgcctg gtgttctgaa   1380
gtgggaaaaa atagactaac ttcagtagga tttatgtatt ttgaaaaaga gaacagaaaa   1440
caacaaaaga atttttgttt ggactgtttt caataacaaa gcacataact ggattttgaa   1500
cgcttaagtc aatcattact tggaaatttn taatgtttat tatttacatc aactttgtga   1560
attaacacag tgtttcaatt ctgtaatttc atatttgact cttt                    1604

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<210> SEQ ID NO 11
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1          5          10          15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
20          25          30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
35          40          45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
50          55          60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
65          70          75          80

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
85          90          95

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
100         105         110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
115         120         125

Tyr Ser Thr Ser Arg Ala Arg Glu Arg Gly Ala Ser Arg Ala Glu Asn
130         135         140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
145         150         155         160

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
165         170         175

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
180         185         190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
195         200         205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
210         215         220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
225         230         235         240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
245         250         255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
260         265         270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
275         280         285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
290         295         300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
305         310         315         320

Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
325         330         335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
340         345         350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
355         360         365

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Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
 370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
 385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
 405 410 415

Tyr

<210> SEQ ID NO 12
 <211> LENGTH: 1254
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

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atgcgcttcg cctggaccgt gctcctgtgc gggcctttgc agctctgcgc gctagtgcac    60
tgcgcccctc ccgcccgcgg ccaacagcag cccccgcgcg agccgcccgc ggtccggggc   120
gcctggcgcc agcagatcca atgggagaaac aacgggcagg tgttcagctt gctgagcctg   180
ggctcacagt accagcctca gcgcgcgcgg gaccgcggcg ccgcgcgtccc tggtgacagcc  240
aacgcctcgc ccagcagacc ccgcactccg atcctgctga tccgcgacaa ccgcaccgcc   300
gcggcgcgaa cgcggacggc cggtcactct ggagtcaccg ctggccgccc caggcccacc   360
gcccgtcact gggtccaagc tggctactcg acatctagag cccgcgaacg tggcgccctcg   420
cgcgcggaga accagacagc gccgggagaa gttcctgcgc tcagtaacct gcggccgccc   480
agccgcgtgg acggcatggt gggcgacgac ccttacaacc cctacaagta ctctgacgac   540
aacccttatt acaactacta cgatacttat gaaaggccca gacctggggg cagggtaccgg   600
cccgatacgc gactgggcta cttccagtac ggtctcccag acctgggtgc cgaccctac   660
tacatccagg cgtccacgta cgtgcagaag atgtccatgt acaacctgag atgcgcggcg   720
gaggaaaaact gtctggccag tacagcatat agggcagatg tcagagatta tgatcacagg   780
gtgtgtctca gattttccca aagagtgaag aaccaaggga catcagattt cttaccacgc   840
cgaccaagat attcctggga atggcacagt tgtcatcaac attaccacag tatggatgag   900
tttagccact atgacctgct tgatgccaac acccagagga gagtggctga aggccacaaa   960
gcaagtttct gtcttgaaga cacatcctgt gactatggct accacaggcg atttgcatgt  1020
actgcacaca cacagggatt gagtccctggc tggtatgata cctatgggtg agacatagac  1080
tgccagtgga ttgatattac agatgtaaaa cctggaaaact atatoctaaa ggtcagtgta  1140
aaccgccagc acctggttcc tgaatctgac tataccaaca atgttgtgcg ctgtgacatt  1200
cgctacacag gacatcatgc gtatgcctca ggctgcacaa ttccaccgta ttag      1254

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<210> SEQ ID NO 13
 <211> LENGTH: 417
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 13

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
 1 5 10 15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
 20 25 30

-continued

Arg	Glu	Pro	Pro	Ala	Ala	Pro	Gly	Ala	Trp	Arg	Gln	Gln	Ile	Gln	Trp
	35						40				45				
Glu	Asn	Asn	Gly	Gln	Val	Phe	Ser	Leu	Leu	Ser	Leu	Gly	Ser	Gln	Tyr
	50					55					60				
Gln	Pro	Gln	Arg	Arg	Arg	Asp	Pro	Gly	Ala	Ala	Val	Pro	Gly	Ala	Ala
	65				70				75					80	
Asn	Ala	Ser	Ala	Gln	Gln	Pro	Arg	Thr	Pro	Ile	Leu	Leu	Ile	Arg	Asp
				85				90						95	
Asn	Arg	Thr	Ala	Ala	Ala	Arg	Thr	Arg	Thr	Ala	Gly	Ser	Ser	Gly	Val
			100					105						110	
Thr	Ala	Gly	Arg	Pro	Arg	Pro	Thr	Ala	Arg	His	Trp	Phe	Gln	Ala	Gly
		115					120					125			
Tyr	Ser	Thr	Ser	Arg	Ala	Arg	Glu	Arg	Gly	Ala	Ser	Arg	Ala	Glu	Asn
	130					135					140				
Gln	Thr	Ala	Pro	Gly	Glu	Val	Pro	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro
	145				150					155				160	
Ser	Arg	Val	Asp	Gly	Met	Val	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	Lys
				165				170						175	
Tyr	Ser	Asp	Asp	Asn	Pro	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Tyr	Glu	Arg
		180						185					190		
Pro	Arg	Pro	Gly	Gly	Arg	Tyr	Arg	Pro	Gly	Tyr	Gly	Thr	Gly	Tyr	Phe
		195					200					205			
Gln	Tyr	Gly	Leu	Pro	Asp	Leu	Val	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala
	210					215				220					
Ser	Thr	Tyr	Val	Gln	Lys	Met	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	Ala
	225				230					235				240	
Glu	Glu	Asn	Cys	Leu	Ala	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	Arg	Asp
			245					250					255		
Tyr	Asp	His	Arg	Val	Leu	Leu	Arg	Phe	Pro	Gln	Arg	Val	Lys	Asn	Gln
		260						265					270		
Gly	Thr	Ser	Asp	Phe	Leu	Pro	Ser	Arg	Pro	Arg	Tyr	Ser	Trp	Glu	Trp
		275					280					285			
His	Ser	Cys	His	Gln	His	Tyr	His	Ser	Met	Asp	Glu	Phe	Ser	His	Tyr
	290					295					300				
Asp	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	His	Lys
	305				310					315				320	
Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg
			325					330					335		
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr
		340					345						350		
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp
		355				360					365				
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr
	370					375					380				
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile
	385				390					395				400	
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro
				405				410					415		

Tyr

-continued

<211> LENGTH: 1780

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 14

```

gggccaggac tgagaaagg gaaaggaag ggtgccacgt ccgagcagcc gccttgactg      60
gggaagggtc tgaatccac ccttggcatt gcttgggtga gactgagata cccgtgctcc     120
gctcgctccc ttggttgaag atttctcctt ccctcacgtg atttgagccc cgtttttatt     180
ttctgtgagc cacgtcctcc tcgagcgggg tcaatctggc aaaaggagtg atgcgcttcg     240
cctggaccgt gctcctgctc gggcctttgc agctctgcgc gctagtgcac tgcgcccctc     300
ccgcgcgccg ccaacagcag ccccgcgcg agccgcgggc ggctccgggc gcctggcgcc     360
agcagatcca atgggagaac aacgggcagg tgttcagctt gctgagcctg ggctcacagt     420
accagcctca gcgcgcgccg gacccgggcg ccgcgcgtccc tgggtgcagcc aacgcctccg     480
cccagcagcc ccgactccg atcctgctga tccgcgacaa ccgcaccgcc gcggggcgaa     540
cgcgacgggc cggtcctatc ggagtcaccg ctggccgccc caggcccacc gcccgctact     600
ggttccaagc tggctactcg acatctagag cccgcgaagc tgggccctcg cgcgcggaga     660
accagacagc gccgggagaa gttcctgctc tcagtaacct gcggccgccc agccgcgtgg     720
acggcatggt gggcgacgac cttacaacc cttacaagta ctctgacgac aaccttatt      780
acaactacta cgatacttat gaaaggccca gacctggggg caggtaccgg cccggatacg     840
gcactggcta cttccagtac ggtctcccag acctgggtggc cgacccctac tacatccagg     900
cgtcacagta cgtgcagaag atgtccatgt acaacctgag atgcgcggcg gaggaaaaact    960
gtctggccag tacagcatac agggcagatg tcagagatta tgatcacagg gtgctgctca    1020
gatttcccca aagagtgaag aaccaaggga catcagattt cttaccagc cgaccaagat    1080
attcctggga atggcacagt tgtcatcaac attaccacag tatggatgag tttagccact    1140
tgtacctgct tgatgccaac acccagagga gatgggctga aggccacaaa gcaagtttct    1200
gtcttgaaag cacatcctgt gactatggct accacaggcg atttgcattg actgcacaca    1260
cacagggatt gagtcttgcc tggtatgata cctatggtgc agacatagac tgccagtggg    1320
ttgatattac agatgtaaaa cctggaaact atatcctaaa ggtcagtgtg aaccccagct    1380
acctggttcc tgaatctgac tataccaaca atgttgtgcg ctgtgacatt cgctacacag    1440
gacatcatgc gtatgcctca ggctgcacaa tttcacgta ttagaaggca aagcaaaact    1500
cccaatggat aaatcagtgc ctggtgttct gaagtgggaa aaaatagact aacttcagta    1560
ggatttatgt attttgaaaa agagaacaga aaacaacaaa agaatttttg tttggactgt    1620
tttcaataac aaagcacata actggatttt gaacgcttaa gtcatcatta cttgggaaat    1680
ttttaatggt tattatttac atcactttgt gaattaacac agtgtttcaa ttctgtaatt    1740
acatatttga ctctttcaaa aaaaaaaaaa aaaaaaaaaa

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<210> SEQ ID NO 15

<211> LENGTH: 417

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 15

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Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1           5           10           15

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Ala	Leu	Val	His	Cys	Ala	Pro	Pro	Ala	Ala	Gly	Gln	Gln	Gln	Pro	Pro	20	25	30
Arg	Glu	Pro	Pro	Ala	Ala	Pro	Gly	Ala	Trp	Arg	Gln	Gln	Ile	Gln	Trp	35	40	45
Glu	Asn	Asn	Gly	Gln	Val	Phe	Ser	Leu	Leu	Ser	Leu	Gly	Ser	Gln	Tyr	50	55	60
Gln	Pro	Gln	Arg	Arg	Arg	Asp	Pro	Gly	Ala	Ala	Val	Pro	Gly	Ala	Ala	65	70	75
Asn	Ala	Ser	Ala	Gln	Gln	Pro	Arg	Thr	Pro	Ile	Leu	Leu	Ile	Arg	Asp	85	90	95
Asn	Arg	Thr	Ala	Ala	Gly	Arg	Thr	Arg	Thr	Ala	Gly	Ser	Ser	Gly	Val	100	105	110
Thr	Ala	Gly	Arg	Pro	Arg	Pro	Thr	Ala	Arg	His	Trp	Phe	Gln	Ala	Gly	115	120	125
Tyr	Ser	Thr	Ser	Arg	Ala	Arg	Glu	Ala	Gly	Pro	Ser	Arg	Ala	Glu	Asn	130	135	140
Gln	Thr	Ala	Pro	Gly	Glu	Val	Pro	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro	145	150	155
Ser	Arg	Val	Asp	Gly	Met	Val	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	Lys	165	170	175
Tyr	Ser	Asp	Asp	Asn	Pro	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Tyr	Glu	Arg	180	185	190
Pro	Arg	Pro	Gly	Gly	Arg	Tyr	Arg	Pro	Gly	Tyr	Gly	Thr	Gly	Tyr	Phe	195	200	205
Gln	Tyr	Gly	Leu	Pro	Asp	Leu	Val	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala	210	215	220
Ser	Thr	Tyr	Val	Gln	Lys	Met	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	Ala	225	230	235
Glu	Glu	Asn	Cys	Leu	Ala	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	Arg	Asp	245	250	255
Tyr	Asp	His	Arg	Val	Leu	Leu	Arg	Phe	Pro	Gln	Arg	Val	Lys	Asn	Gln	260	265	270
Gly	Thr	Ser	Asp	Phe	Leu	Pro	Ser	Arg	Pro	Arg	Tyr	Ser	Trp	Glu	Trp	275	280	285
His	Ser	Cys	His	Gln	His	Tyr	His	Ser	Met	Asp	Glu	Phe	Ser	His	Leu	290	295	300
Tyr	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Trp	Ala	Glu	Gly	His	Lys	305	310	315
Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg	325	330	335
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr	340	345	350
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp	355	360	365
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr	370	375	380
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile	385	390	395
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro	405	410	415

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Tyr

<210> SEQ ID NO 16

<211> LENGTH: 1935

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 16

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ccgcgcgcgt ccccggttgc ttccaggact gagaaagggg aaaggggaagg gtgccacgtc      60
cgagcagccg ccttgactgg ggaagggctc gaatcccacc cttggcattg cctggtggag    120
actgagatac cegtgtcccg ctgcctcctc tgggtgaaga tttctccttc cctcacgtga    180
tttgagcccc gtttttattt tctgtgagcc acgtcctcct cgagcggggg caatctggca    240
aaaggagtga tgcgtctcgc ctggaccgtg ctctgtctcg ggcctttgca gctctgcgcg    300
ctagtgcact gcgccccctc cgccgcgggc caacagcagc ccccgcgcca gccgcggcg    360
gtcccgggcg cctggcgcca gcagatccaa tgggagaaca acgggcaggt gtccagcttg    420
ctgagcctgg gctcacagta ccagcctcag cgccgcgggg acccgggcgc cgccgtccct    480
gggtgcagcca acgcctccgc ccagcagccc cgcaactcga tcctgtgat ccgcgacaac    540
cgcacccgcg cggcgcgaa cgggacggcc ggctcatctg gagtaccgc tggccgcccc    600
agggccaccg cccgtcactg gttccaagct ggctactcga catctagagc ccgcgaagct    660
ggcgctcgc gcgcggagaa ccagacagcg ccgggagaag ttctgtcgtc cagtaacctg    720
cggccgcccc gccgcgtgga cggcatggtg ggcgacgacc cttacaaccc ctacaagtac    780
tctgacgaca acccttatta caactactac gatacttatg aaaggcccag acctgggggc    840
aggtaccggc ccgatacagg cactggctac ttccagtacg gtctcccaga cctggtggcc    900
gacccctact acatccaggc gtccacgtac gtgcagaaga tgtccatgta caacctgaga    960
tgcgcggcgg aggaaaaactg tctggccagt acagcataca gggcagatgt cagagattat   1020
gatcacaggg tgetgtctag atttcccaa agagtgaaaa accaaggga c atcagatttc   1080
ttaccagcc gcccaagata ttctgggaa tggcacagtt gtcatacaaa ttaccacagt   1140
atggatgagt ttagcacta tgacctgctt gatgccaaca ccagaggag agtggctgaa   1200
ggccacaaag caagtttctg tcttgaagac acatcctgtg actatggcta ccacaggcga   1260
tttgcatgta ctgcacacac acagggattg agtcctggct gttatgatac ctatggtgca   1320
gacatagact gccagtggat tgatattaca gatgtaaaac ctggaaacta taccctaaag   1380
gtcagtgtaa accccagcta cctggttcct gaatctgact ataccaacaa tgttgtgcgc   1440
tgtgacattc gctacacagg acatcatgcg tatgcctcag gctgcacaat ttcaccgtat   1500
tagaaggcaa agcaaaactc ccaatggata aatcagtgcc tgggtgtctg aagtgggaaa   1560
aaatagacta acttcagtag gatttatgta ttttgaaaaa gagaacagaa aacaacaaaa   1620
gaatttttgt ttgactgtt ttcaataaca aagcacataa ctggattttg aacgcttaag   1680
tcatcattac ttgggaatt tttaatgtt attatttaca tcaactttgtg aattaacaca   1740
gtgtttcaat tctgtaatta catatttgac tctttcaaag aaatccaaat ttctcatgtt   1800
ccttttgaaa ttgtagtgca aaatggctcag tattatctaa atgaatgagc caaaatgact   1860
ttgaactgaa acttttctaa agtgctggaa ctttagtgaa acataataat aatgggttta   1920
tacgacagca acgga                                     1935

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<210> SEQ ID NO 17
<211> LENGTH: 417
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 17

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
1          5          10          15

Ala Leu Val His Cys Ala Pro Pro Ala Ala Gly Gln Gln Gln Pro Pro
20          25          30

Arg Glu Pro Pro Ala Ala Pro Gly Ala Trp Arg Gln Gln Ile Gln Trp
35          40          45

Glu Asn Asn Gly Gln Val Phe Ser Leu Leu Ser Leu Gly Ser Gln Tyr
50          55          60

Gln Pro Gln Arg Arg Arg Asp Pro Gly Ala Ala Val Pro Gly Ala Ala
65          70          75          80

Asn Ala Ser Ala Gln Gln Pro Arg Thr Pro Ile Leu Leu Ile Arg Asp
85          90          95

Asn Arg Thr Ala Ala Ala Arg Thr Arg Thr Ala Gly Ser Ser Gly Val
100         105         110

Thr Ala Gly Arg Pro Arg Pro Thr Ala Arg His Trp Phe Gln Ala Gly
115         120         125

Tyr Ser Thr Ser Arg Ala Arg Glu Ala Gly Ala Ser Arg Ala Glu Asn
130         135         140

Gln Thr Ala Pro Gly Glu Val Pro Ala Leu Ser Asn Leu Arg Pro Pro
145         150         155         160

Ser Arg Val Asp Gly Met Val Gly Asp Asp Pro Tyr Asn Pro Tyr Lys
165         170         175

Tyr Ser Asp Asp Asn Pro Tyr Tyr Asn Tyr Tyr Asp Thr Tyr Glu Arg
180         185         190

Pro Arg Pro Gly Gly Arg Tyr Arg Pro Gly Tyr Gly Thr Gly Tyr Phe
195         200         205

Gln Tyr Gly Leu Pro Asp Leu Val Ala Asp Pro Tyr Tyr Ile Gln Ala
210         215         220

Ser Thr Tyr Val Gln Lys Met Ser Met Tyr Asn Leu Arg Cys Ala Ala
225         230         235         240

Glu Glu Asn Cys Leu Ala Ser Thr Ala Tyr Arg Ala Asp Val Arg Asp
245         250         255

Tyr Asp His Arg Val Leu Leu Arg Phe Pro Gln Arg Val Lys Asn Gln
260         265         270

Gly Thr Ser Asp Phe Leu Pro Ser Arg Pro Arg Tyr Ser Trp Glu Trp
275         280         285

His Ser Cys His Gln His Tyr His Ser Met Asp Glu Phe Ser His Tyr
290         295         300

Asp Leu Leu Asp Ala Asn Thr Gln Arg Arg Val Ala Glu Gly His Lys
305         310         315         320

Ala Ser Phe Cys Leu Glu Asp Thr Ser Cys Asp Tyr Gly Tyr His Arg
325         330         335

Arg Phe Ala Cys Thr Ala His Thr Gln Gly Leu Ser Pro Gly Cys Tyr
340         345         350

Asp Thr Tyr Gly Ala Asp Ile Asp Cys Gln Trp Ile Asp Ile Thr Asp
355         360         365

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-continued

Val Lys Pro Gly Asn Tyr Ile Leu Lys Val Ser Val Asn Pro Ser Tyr
 370 375 380

Leu Val Pro Glu Ser Asp Tyr Thr Asn Asn Val Val Arg Cys Asp Ile
 385 390 395 400

Arg Tyr Thr Gly His His Ala Tyr Ala Ser Gly Cys Thr Ile Ser Pro
 405 410 415

Tyr

<210> SEQ ID NO 18
 <211> LENGTH: 1322
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 18

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ggccaatctg gcaaaaggag tgatgcgctt cgcctggacc gtgctcctgc tcgggccttt    60
gcagctctgc gcgctagtgc actgcgcccc tcccgcgcgc ggccaacagc agcccccgcg    120
cgagccgccc gcggctccgg gcgcctggcg ccagcagatc caatgggaga acaacgggca    180
gggtgttcagc ttgctgagcc tgggtcaca gtaccagcct cagcgccgccc gggaccgggg    240
cgccgcgcgc cctgggtgcag ccaacgcctc cgcccagcag ccccgccactc cgatcctgct    300
gatccgcgac aaccgcaccg ccgcgggcgc aacgcggacg gccgggtcat ctggagtcac    360
cgctggccgc cccaggccca ccgcccgtca ctggttccaa gctgggtact cgacatctag    420
agcccgcgaa gctggcgctt cgcgcgcgga gaaccagaca gcgccgggag aagttcctgc    480
gctcagtaac ctgcccgcgc ccagccgcgt ggacggcatg gtggggcgacg acccttaciaa    540
cccttacaag tactctgacg acaaccctta ttacaactac tacgatactt atgaaaggcc    600
cagacctggg ggcaggtacc ggcccggata cggcactggc tacttccagt acggtctccc    660
agacctgggt gccgaccctt actacatcca ggcgtccacg tacgtgcaga agatgtccat    720
gtacaacctg agatgcgcgg cggaggaaaa ctgtctggcc agtacagcat acagggcaga    780
tgtcagagat tatgatcaca ggggtgctgt cagatttccc caaagagtga aaaaccaag    840
gacatcagat ttcttaccga gccgaccaag atattcctgg gaatggcaca gttgtcatca    900
acattaccac agtatggatg agtttagcca ctatgacctg cttgatgcca acaccagag    960
gagagtgggt gaaggccaca aagcaagttt ctgtcttgaa gacacatcct gtgactatgg    1020
ctaccacagg cgatttgcac gtactgcaca cacacaggga ttgagtcctg gctgttatga    1080
tacctatggt gcagacatag actgccagtg gattgatatt acagatgtaa aacctggaaa    1140
ctatatccta aaggtcagtg taaaccccag ctacctggtt cctgaatctg actataccaa    1200
caatgttgtg cgctgtgaca ttcgtacac aggacatcat gcgtatgctt caggctgcac    1260
aatttcaccg tattagaagg caaagcaaaa ctcccaatgg ataaatcagt gcctgggtgtt    1320
ct                                                                    1322

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<210> SEQ ID NO 19
 <211> LENGTH: 417
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 19

Met Arg Phe Ala Trp Thr Val Leu Leu Leu Gly Pro Leu Gln Leu Cys
 1 5 10 15

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Ala	Leu	Val	His	Cys	Ala	Pro	Pro	Ala	Ala	Gly	Gln	Gln	Gln	Pro	Pro	20	25	30
Arg	Glu	Pro	Pro	Ala	Ala	Pro	Gly	Ala	Trp	Arg	Gln	Gln	Ile	Gln	Trp	35	40	45
Glu	Asn	Asn	Gly	Gln	Val	Phe	Ser	Leu	Leu	Ser	Leu	Gly	Ser	Gln	Tyr	50	55	60
Gln	Pro	Gln	Arg	Arg	Arg	Asp	Pro	Gly	Ala	Ala	Val	Pro	Gly	Ala	Ala	65	70	75
Asn	Ala	Ser	Ala	Gln	Gln	Pro	Arg	Thr	Pro	Ile	Leu	Leu	Ile	Arg	Asp	85	90	95
Asn	Arg	Thr	Ala	Ala	Ala	Arg	Thr	Arg	Thr	Ala	Gly	Ser	Ser	Gly	Val	100	105	110
Thr	Ala	Gly	Arg	Pro	Arg	Pro	Thr	Ala	Arg	His	Trp	Phe	Gln	Ala	Gly	115	120	125
Tyr	Ser	Thr	Ser	Arg	Ala	Arg	Glu	Ala	Gly	Ala	Ser	Arg	Ala	Glu	Asn	130	135	140
Gln	Thr	Ala	Pro	Gly	Glu	Val	Pro	Ala	Leu	Ser	Asn	Leu	Arg	Pro	Pro	145	150	155
Ser	Arg	Val	Asp	Gly	Met	Val	Gly	Asp	Asp	Pro	Tyr	Asn	Pro	Tyr	Lys	165	170	175
Tyr	Ser	Asp	Asp	Asn	Pro	Tyr	Tyr	Asn	Tyr	Tyr	Asp	Thr	Tyr	Glu	Arg	180	185	190
Pro	Arg	Pro	Gly	Gly	Arg	Tyr	Arg	Pro	Gly	Tyr	Gly	Thr	Gly	Tyr	Phe	195	200	205
Gln	Tyr	Gly	Leu	Pro	Asp	Leu	Val	Ala	Asp	Pro	Tyr	Tyr	Ile	Gln	Ala	210	215	220
Ser	Thr	Tyr	Val	Gln	Lys	Met	Ser	Met	Tyr	Asn	Leu	Arg	Cys	Ala	Ala	225	230	235
Glu	Glu	Asn	Cys	Leu	Ala	Ser	Thr	Ala	Tyr	Arg	Ala	Asp	Val	Arg	Asp	245	250	255
Tyr	Asp	His	Arg	Val	Leu	Leu	Arg	Phe	Pro	Gln	Arg	Val	Lys	Asn	Gln	260	265	270
Gly	Thr	Ser	Asp	Phe	Leu	Pro	Ser	Arg	Pro	Arg	Tyr	Ser	Trp	Glu	Trp	275	280	285
His	Ser	Cys	His	Gln	His	Tyr	His	Ser	Met	Asp	Glu	Phe	Ser	His	Tyr	290	295	300
Asp	Leu	Leu	Asp	Ala	Asn	Thr	Gln	Arg	Arg	Val	Ala	Glu	Gly	His	Lys	305	310	315
Ala	Ser	Phe	Cys	Leu	Glu	Asp	Thr	Ser	Cys	Asp	Tyr	Gly	Tyr	His	Arg	325	330	335
Arg	Phe	Ala	Cys	Thr	Ala	His	Thr	Gln	Gly	Leu	Ser	Pro	Gly	Cys	Tyr	340	345	350
Asp	Thr	Tyr	Gly	Ala	Asp	Ile	Asp	Cys	Gln	Trp	Ile	Asp	Ile	Thr	Asp	355	360	365
Val	Lys	Pro	Gly	Asn	Tyr	Ile	Leu	Lys	Val	Ser	Val	Asn	Pro	Ser	Tyr	370	375	380
Leu	Val	Pro	Glu	Ser	Asp	Tyr	Thr	Asn	Asn	Val	Val	Arg	Cys	Asp	Ile	385	390	395
Arg	Tyr	Thr	Gly	His	His	Ala	Tyr	Ala	Ser	Gly	Cys	Thr	Ile	Ser	Pro	405	410	415

-continued

Tyr

<210> SEQ ID NO 20
 <211> LENGTH: 1325
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 20

```

ggccaatctg gcaaaaggag tgatgcgctt cgccctggacc gtgctcctgc tcgggccttt    60
gcagctctgc gcgctagtgc actgcgcccc tcccgcgcgc ggccaacagc agcccccgcg    120
cgagccgcgc ggggctccgc gcgcctggcg ccagcagatc caatgggaga acaacgggca    180
ggtgttcagc ttgctgagcc tgggctcaca gtaccagcct cagcgccgcc gggaccgggg    240
cgccgcgcgc cctggtgcag ccaacgcctc cgcccagcag ccccgcactc cgatcctgct    300
gatccgcgac aaccgcaccg ccgcggcgcg aacgcggacg gccggctcat ctggagtcac    360
cgctggccgc cccaggccca ccgccgtca ctggttccaa gctggctact cgacatctag    420
agcccgcgaa gctggcgctt cgcgcgcgga gaaccagaca gcgccgggag aagtctctgc    480
gctcagtaac ctgcggccgc ccagccgcgt ggacggcatg gtgggcgacg acccttaca    540
cccttacaag tactctgagc acaaccctta ttacaactac tacgatactt atgaaaggcc    600
cagacctggg ggcaggtacc ggcccgata cggcactggc tacttccagt acggtctccc    660
agacctggtg gccgaccctt actacatcca ggcgtccacg tacgtgcaga agatgtccat    720
gtacaacctg agatgcgcgc cggaggaaaa ctgtctggcc agtacagcat acagggcaga    780
tgtcagagat tatgatcaca ggggtctgct cagatttccc caaagagtga aaaaccaagg    840
gacatcagat ttcttaccga gccgaccaag atattcctgg gaatggcaca gttgtcatca    900
acattaccac agtatggatg agtttagcca ctatgacctg cttgatgcca acaccagag    960
gagagtggct gaaggccaca aagcaagttt ctgtcttgaa gacacatcct gtgactatgg   1020
ctaccacagg cgatttgcac gtactgcaca cacacaggga ttgagtcctg gctgttatga   1080
tacctatggt gcagacatag actgccagtg gattgatatt acagatgtaa aacctggaaa   1140
ctatatccta aaggtcagtg taaaccccag ctacctggtt cctgaatctg actataccaa   1200
caatgttgtg cgctgtgaca ttcgctacac aggacatcat gcgtatgctt caggctgcac   1260
aatttcaccg tattagaagg caaagcaaaa ctcccaatgg ataaatcagt gectggtggt   1320
ctgaa                                           1325

```

<210> SEQ ID NO 21
 <211> LENGTH: 407
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 21

```

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

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

<210> SEQ ID NO 22

<211> LENGTH: 842

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

gttcagcttg ctgagcctgg gctcacagta ccagcctcag cgccgcggg acccgggcgc

60

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cgccgtccct ggtgcagcca acgcctccgc ccagcagccc cgcactccga tctgtctgat   120
ccgcgacaac cgcaccgccg cggcgcgaaac gcggacggcc ggctcatctg gagtcaccgc   180
tggcgccccc aggccccaccg cccgtcactg gttccaagct ggctactcga catctagagc   240
cccggaagct ggcgcctcgc gcgcggagaa ccagacagcg ccgggagaag ttctgcgct   300
cagtaacctg cggccgcccc gccgcgtgga cggcatggtg ggcgacgacc cttacaaccc   360
ctacaagtac tctgacgaca acccttatta caactactac gatacttatg aaaggcccag   420
acctgggggc aggtaccggc ccggatacgg cactggctac ttccagtacg gtaagtaccc   480
ccaagtccgc tggaagcacc cgtgcacctg gtccccagct atgtggcttc ttctcgacgt   540
ggctgcctgg gcgcggcggg ccccggtcct cgcagatccg acccctcccc acgcgcctgc   600
agtggcagcc ctggaatcca gtgcaaacgg cgcgtctggc ccctcctgct tctttttcac   660
attgctttgc agtcccgggg gtccccagtt ctcttctgtg cctccgctcc actctgcagt   720
cccgggtggg gaagggtgag gagtaaggga cctagagggg tagggagtgt gagcgggggg   780
cgccgggttg ttctactgct gcgccgctcg cctgctgacg tttaggtctc ccagacctgg   840
tg                                                                    842

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<210> SEQ ID NO 23

<211> LENGTH: 162

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 23

```

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

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<210> SEQ ID NO 24

<211> LENGTH: 135

<212> TYPE: PRT

<213> ORGANISM: Mus sp.

<400> SEQUENCE: 24

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

```

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<210> SEQ ID NO 25
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

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<400> SEQUENCE: 25

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

```

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<210> SEQ ID NO 26
<211> LENGTH: 116
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

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<400> SEQUENCE: 26

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```

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1          5          10          15
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Tyr Tyr
          20          25          30

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-continued

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg 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

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

Thr Val Ser Ser
 115

<210> SEQ ID NO 27
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 27

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

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

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Ala 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

Ala Arg Asn Trp Met Asn Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110

Thr Val Ser Ser
 115

<210> SEQ ID NO 28
 <211> LENGTH: 116
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 28

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

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

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys 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	
Ala	Arg	Asn	Trp	Met	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val
			100					105					110		
Thr	Val	Ser	Ser												
			115												

<210> SEQ ID NO 29
 <211> LENGTH: 132
 <212> TYPE: PRT
 <213> ORGANISM: Mus sp.

<400> SEQUENCE: 29

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

<210> SEQ ID NO 30
 <211> LENGTH: 112
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 30

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

-continued

<210> SEQ ID NO 31
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 31

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

<210> SEQ ID NO 32
<211> LENGTH: 112
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed polypeptide

<400> SEQUENCE: 32

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

<210> SEQ ID NO 33
<211> LENGTH: 44
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 33

Met Glu Trp Ser Arg Val Phe Ile Phe Leu Leu Ser Val Thr Ala Gly
1 5 10 15

-continued

Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
20 25 30

Pro Gly Thr Ser Val Lys Val Ser Cys Lys Ala Ser
35 40

<210> SEQ ID NO 34
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 34

Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10

<210> SEQ ID NO 35
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 35

Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln
1 5 10 15

Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> SEQ ID NO 36
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 36

Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
1 5 10

<210> SEQ ID NO 37
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 37

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> SEQ ID NO 38
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 38

Trp Val Lys Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10

-continued

<210> SEQ ID NO 39
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 39

Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15
Leu Ser Ser Leu Arg Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> SEQ ID NO 40
<211> LENGTH: 11
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 40

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> SEQ ID NO 41
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 41

Gly Tyr Ala Phe Thr Tyr Tyr Leu Ile Glu
1 5 10

<210> SEQ ID NO 42
<211> LENGTH: 17
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 42

Val Ile Asn Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe Lys
1 5 10 15

Gly

<210> SEQ ID NO 43
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 43

Asn Trp Asn Met Phe Asp Tyr
1 5

<210> SEQ ID NO 44
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 44

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

Ser Val Lys Val Ser Cys Lys Ala Ser
20 25

<210> SEQ ID NO 45
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 45

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly
1 5 10

<210> SEQ ID NO 46
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 46

Arg Ala Thr Leu Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> SEQ ID NO 47
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 47

Arg Ala Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys Ala Arg
20 25 30

<210> SEQ ID NO 48
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 48

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

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

<210> SEQ ID NO 49
<211> LENGTH: 43
<212> TYPE: PRT

-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 49
Met Arg Cys Leu Ala Glu Phe Leu Gly Leu Leu Val Leu Trp Ile Pro
1 5 10 15
Gly Ala Ile Gly Asp Ile Val Met Thr Gln Ala Ala Pro Ser Val Ser
20 25 30
Val Thr Pro Gly Glu Ser Val Ser Ile Ser Cys
35 40

<210> SEQ ID NO 50
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 50

Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro Gln Phe Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 51
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 51

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Ala Phe Thr
1 5 10 15
Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 52
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 52

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
1 5 10

<210> SEQ ID NO 53
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 53

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

<210> SEQ ID NO 54
<211> LENGTH: 15

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<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 54

Trp Phe Leu Gln Lys Pro Gly Gln Ser Pro Gln Phe Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 55
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 55

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

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

<210> SEQ ID NO 56
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 56

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> SEQ ID NO 57
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 57

Arg Ser Ser Lys Ser Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr
1 5 10 15

<210> SEQ ID NO 58
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 58

Arg Met Ser Asn Leu Ala Ser
1 5

<210> SEQ ID NO 59
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 59

Met Gln His Leu Glu Tyr Pro Tyr Thr

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1 5

<210> SEQ ID NO 60
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 60

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15
Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
20 25 30

<210> SEQ ID NO 61
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 61

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Phe Leu Ile Tyr
1 5 10 15

<210> SEQ ID NO 62
<211> LENGTH: 396
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 62

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

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

<210> SEQ ID NO 63

<211> LENGTH: 390

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 63

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

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

<210> SEQ ID NO 64

<211> LENGTH: 1251

<212> TYPE: DNA

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 64

atgcgcttcg cctggaccgt gctcctgctc gggcctttgc agctctgcgc gctagtgcac	60
tgcgcccctc ccgcccgcgg ccaacagcag cccccgcgcg agccgcgcgc ggtccggggc	120
gcctggcgcc agcagatcca atgggagaac aacgggcagg tggtcagctt gctgagcctg	180
gggtcacagt accagcctca gcgccgcggg gaccggggcg ccgcgcgtccc tgggtgcagcc	240
aaagcctccg cccagcagcc ccgcactccg atcctgctga tccgcgacaa ccgcaccgcc	300
gcggcgcgaa cgcggacggc cggtcatctt ggagtcaccg ctggccgccc caggcccacc	360
gcccgctcact gggtccaagc tggctactcg acatctagag cccgcgaagc tggcgccctcg	420
cgcgcggaga accagacagc gccgggagaa gttcctgcgc tcagtaacct gcggccgccc	480
agccgcgtgg acggcatggt gggcgacgac cctacaacc cctacaagta ctctgacgac	540
aacccttatt acaactacta cgatacttat gaaaggccca gacctggggg cagggtaccg	600
cccgatacgc gcaactggcta cttccagtac ggtctcccag acctggtggc cgaccctac	660
tacatccagg cgtccacgta cgtgcagaag atgtccatgt acaacctgag atgcgcggcg	720

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gaggaaaact gtctggccag tacagcatac agggcagatg tcagagatta tgatcacagg 780
gtgtgtgtca gatttcccca aagagtgaag aaccaaggga catcagattt cttaccacag 840
cgaccaagat attcctggga atggcacagt tgtcatcaac attaccacag tatggatgag 900
tttagccact atgacctgct tgatgccaac acccagagga gaggggctga aggccacaaa 960
gcaagtttct gtcttgaaga cacatcctgt gactatggct accacaggcg atttgcattg 1020
actgcacaca cacagggatt gaggcctggc tggttatgata cctatggtgc agacatagac 1080
tgccagtgga ttgatattac agatgtaaaa cctggaaaact ataccctaaa ggtcagtgta 1140
aaccaccagt acctggttcc tgaatctgac tataccaaca atgttgtgag ctgtgacatt 1200
cgctacacag gacatcatgc gtatgcctca ggctgcacaa tttcacgta t 1251

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<210> SEQ ID NO 65

<211> LENGTH: 417

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 65

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

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

Tyr

<210> SEQ ID NO 66
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 66

Trp	Glu	Trp	His	Ser	Cys	His	Gln	His	Tyr	His
1			5						10	

<210> SEQ ID NO 67
 <211> LENGTH: 11
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 67

Trp	Ile	Trp	His	Asp	Cys	His	Arg	His	Tyr	His
1			5						10	

<210> SEQ ID NO 68
 <211> LENGTH: 18
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Synthetically constructed peptide
 <220> FEATURE:
 <221> NAME/KEY: MOD_RES
 <222> LOCATION: (14)..(14)
 <223> OTHER INFORMATION: Any amino acid

<400> SEQUENCE: 68

Asp	Ile	Asp	Cys	Gln	Trp	Trp	Ile	Asp	Ile	Thr	Asp	Val	Xaa	Pro	Gly
1			5						10					15	

Asn Tyr

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<210> SEQ ID NO 69
<211> LENGTH: 18
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 69

Asp Ile Asp Cys Gln Trp Val Asp Ile Thr Asp Val Pro Pro Pro Gly
1 5 10 15

Asp Tyr

<210> SEQ ID NO 70
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetically constructed peptide

<400> SEQUENCE: 70

Asn Trp Met Asn Phe Asp Tyr
1 5

<210> SEQ ID NO 71
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)...(239)
<223> OTHER INFORMATION: VK2 kappa light chain

<400> SEQUENCE: 71

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

Gly Ala Arg Cys Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser
20 25 30

Val Thr Pro Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser
35 40 45

Leu Leu His Ser Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Lys
50 55 60

Pro Gly Gln Ser Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala
65 70 75 80

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

Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
100 105 110

Cys Met Gln His Leu Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys
115 120 125

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

Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
145 150 155 160

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

Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp

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180	185	190	
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
195	200	205	
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
210	215	220	
Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys			
225	230	235	

<210> SEQ ID NO 72
 <211> LENGTH: 720
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)...(720)
 <223> OTHER INFORMATION: VK2 kappa DNA sequence encoding light chain sequence

<400> SEQUENCE: 72

atgaggggtcc ccgctcagct cctgggggtc ctgctgctct ggctcccagg cgcgcgatgt	60
gatattgtga tgaccagac tccactctct ctgtccgtca cccttgaca gccggcctcc	120
atctcctgca ggtctagtaa gagtctcctg catagtaatg gcaacactta cttgtattgg	180
ttcctgcaga agccagggca gtctccacag ttcctgatct atcggatgtc caaccttgcc	240
tcaggagtgc cagatagggt cagtggcagc gggtcaggga cagacttcac actgaaaatc	300
agccgggtgg aggetgagga tgttgggtt tattactgca tgcaacatct agaatacct	360
tacaccttcg gcggagggac caaggtggag atcaaacgaa ctgtggctgc accatctgtc	420
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgctg	480
ctgaataact tctatcccag agaggccaaa gtacagtgga aggtggataa cgccctccaa	540
tcgggtaact ccagagagag tgtcacagag caggacagca aggacagcac ctacagcctc	600
agcagcacc tgacgtgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa	660
gtcaccatc agggcctgag ctgcgccgtc acaaagagct tcaacagggg agagtgttag	720

<210> SEQ ID NO 73
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic construct
 <220> FEATURE:
 <221> NAME/KEY: PEPTIDE
 <222> LOCATION: (1)...(20)
 <223> OTHER INFORMATION: VK2 kappa signal peptide

<400> SEQUENCE: 73

Met Arg Val Pro Ala Gln Leu Leu Gly Leu Leu Leu Trp Leu Pro
1 5 10 15
Gly Ala Arg Cys
20

<210> SEQ ID NO 74
 <211> LENGTH: 219
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:

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<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)...(219)
<223> OTHER INFORMATION: VK2 kappa light chain polypeptide
        without signal peptide

<400> SEQUENCE: 74
Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Ser Val Thr Pro Gly
1          5          10         15
Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20         25         30
Asn Gly Asn Thr Tyr Leu Tyr Trp Phe Leu Gln Lys Pro Gly Gln Ser
35         40         45
Pro Gln Phe Leu Ile Tyr Arg Met Ser Asn Leu Ala 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 Met Gln His
85         90         95
Leu Glu Tyr Pro Tyr 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 75
<211> LENGTH: 660
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(660)
<223> OTHER INFORMATION: nucleic acid encoding VK2 kappa light chain
        polypeptide without signal peptide

<400> SEQUENCE: 75
gatattgtga tgaccagac tccactctct ctgtccgtca cccctggaca gccggcctcc      60
atctcctgca ggtctagtaa gagtctctcg catagtaatg gcaacactta cttgtattgg      120
ttcctgcaga agccagggca gtctccacag ttctgatctc atcggatgtc caaccttgcc      180
tcaggagtgc cagataggtt cagtggcagc gggtcaggga cagacttcac actgaaaatc      240
agccgggtgg aggctgagga tgttgggggtt tattactgca tgcaacatct agaatacct      300

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tacaccttcg gcggaggagc caaggtggag atcaaacgaa ctgtggctgc accatctgtc   360
ttcatcttcc cgccatctga tgagcagttg aaatctggaa ctgcctctgt tgtgtgcctg   420
ctgaataact tctatcccag agaggccaaa gtacagtggg aggtgggataa cgccctccaa   480
tcgggtaact cccaggagag tgtcacagag caggacagca aggacagcac ctacagcctc   540
agcagcaccg tgacgctgag caaagcagac tacgagaaac acaaagtcta cgctgcgaa   600
gtcaccatc agggcctgag ctgcccgtc acaaagagct tcaacagggg agagtgttag   660

```

```

<210> SEQ ID NO 76
<211> LENGTH: 462
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: CHAIN
<222> LOCATION: (1)...(462)
<223> OTHER INFORMATION: VH3 IgG4 S241P heavy chain

```

```

<400> SEQUENCE: 76

```

```

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

```

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

<210> SEQ ID NO 77
 <211> LENGTH: 1389
 <212> TYPE: DNA
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: synthetic construct
 <220> FEATURE:
 <221> NAME/KEY: misc_feature
 <222> LOCATION: (1)...(1389)
 <223> OTHER INFORMATION: VH3 IgG4 S241P nucleic acid encoding
 heavy chain sequence

<400> SEQUENCE: 77

```

atgggttgga gcctcatctt gctcttcctt gtcgtgttg ctacgcgtgt ccactcccag    60
gtgcagctgg tgcagctcgg ggctgaggtg aagaagcctg gggcctcagt gaaggtctcc    120
tgcaaggcct ctggatacgc cttcacttat tacttgatag agtgggtgag acaggcccct    180
ggacaagggc ttgagtggat cggagtgatt aatcctggaa gtggtgttac taactacaat    240
gagaagttca agggcagagc cacgatcacc gcggacaaat ccacgagcac agcctacatg    300
gagctgagca gcctgagatc tgaggacacc gccgtgtatt tctgtgcgag aaactggatg    360
aactttgact actgggggca agggaccacg gtcaccgtct cctcagcttc caccaagggc    420
ccatccgtct tccccctggc gccctgctcc aggagcacct ccgagagcac agccgccttg    480
ggctgcctgg tcaaggacta cttccccgaa cgggtgacgg tgcgtggaa ctcaggcgcc    540
ctgaccagcg gcgtgcacac ctcccggtc gtcctacagt cctcaggact ctactccctc    600
agcagcgtgg tgaccgtgcc ctccagcagc ttgggcacga agacctacac ctgcaatgta    660
gatcacaagc ccagcaaac caaggtggac aagagagttg agtccaaata tggcccccca    720
  
```

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

```
<210> SEQ ID NO 80
<211> LENGTH: 1332
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1)...(1332)
```

-continued

<223> OTHER INFORMATION: nucleic acid encoding VH3
IgG4 S241P heavy chain
polypeptide without signal peptide

<400> SEQUENCE: 80

```

cagggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc      60
tcctgcaagg cttctggata cgccttcaact tattacttga tagagtgggt gagacaggcc      120
cctggacaag ggcttgagtg gatcggagtg attaactctg gaagtgggtg tactaactac      180
aatgagaagt tcaagggcag agccacgata accgcggaca aatccacgag cacagcctac      240
atggagctga gcagcctgag atctgaggac accgccgtgt atttctgtgc gagaaactgg      300
atgaactttt actactgggg gcaagggacc acggtcaccg tctcctcagc ttccaccaag      360
ggcccatccg tcttccccct ggccgcttgc tccaggagca cctccgagag cacagccgcc      420
ctgggctgcc tgggtcaagga ctacttcccc gaaccggtga cgggtgtcgtg gaactcaggc      480
gccctgacca gcggcggtga caccttcccg gctgtcctac agtcctcagg actctactcc      540
ctcagcagcg tgggtaccgt gccctccagc agcttgggca cgaagaccta cacctgcaat      600
gtagatcaca agcccagcaa caccaagggtg gacaagagag ttgagtccaa atatggtccc      660
ccatgccccac catgcccagc acctgagttc ctggggggac catcagtcct cctggttcccc      720
ccaaaaccca aggacactct catgatctcc cggacccctg aggtcacgtg cgtgggtggtg      780
gacgtgagcc aggaagaccc cgagggtccag ttcaactggt acgtggatgg cgtggaggtg      840
cataatgcca agacaagacc gcgggaggag cagttcaaca gcacgtaccg tgtggtcagc      900
gtcctcaccg tcctgcacca ggactggctg aacggcaagg agtacaagtg caaggtctcc      960
aacaaggcc tcccgctctc catcgagaaa accatctcca aagccaaagg gcagccccga      1020
gagccacagg tgtacacctt gcccccatcc caggaggaga tgaccaagaa ccaggtcagc      1080
ctgacctgcc tgggtcaaagg cttctacccc agcgacatcg ccgtggagtg ggagagcaat      1140
gggcagccgg agaacaacta caagaccacg cctcccgtgc tggactccga cggtccttc      1200
ttcctctaca gcaggctaac cgtggacaag agcaggtggc aggaggggaa tgtcttctca      1260
tgctccgtga tgcatgagcg tctgcacaac cactacacac agaagagcct ctccctgtct      1320
ctgggtaaat ga                                          1332

```

<210> SEQ ID NO 81

<211> LENGTH: 662

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct

<220> FEATURE:

<221> NAME/KEY: PEPTIDE

<222> LOCATION: (1)...(662)

<223> OTHER INFORMATION: VK2 kappa light chain polypeptide
and VH3 IgG4 S241P
heavy chain polypeptide

<220> FEATURE:

<221> NAME/KEY: PEPTIDE

<222> LOCATION: (1)...(219)

<223> OTHER INFORMATION: VK2 kappa light chain polypeptide

<400> SEQUENCE: 81

```

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

```

```

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser

```

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20						25						30					
Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Trp	Phe	Leu	Gln	Lys	Pro	Gly	Gln	Ser		
		35					40					45					
Pro	Gln	Phe	Leu	Ile	Tyr	Arg	Met	Ser	Asn	Leu	Ala	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	Met	Gln	His		
				85					90					95			
Leu	Glu	Tyr	Pro	Tyr	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		
						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	Gln	Val	Gln	Leu	Val		
						215					220						
Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser		
225					230					235					240		
Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Tyr	Tyr	Leu	Ile	Glu	Trp	Val		
				245					250					255			
Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Val	Ile	Asn	Pro		
				260					265					270			
Gly	Ser	Gly	Gly	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Arg	Ala	Thr		
				275					280					285			
Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser		
						295					300						
Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Asn	Trp	Met		
305					310					315					320		
Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala		
				325					330					335			
Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser		
				340					345					350			
Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe		
				355					360					365			
Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly		
						375					380						
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu		
385					390					395					400		
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr		
				405					410					415			
Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg		
				420					425					430			

-continued

Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu
435 440 445

Phe Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
450 455 460

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
465 470 475 480

Val Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly
485 490 495

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn
500 505 510

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
515 520 525

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro
530 535 540

Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
545 550 555 560

Pro Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn
565 570 575

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
580 585 590

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
595 600 605

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg
610 615 620

Leu Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys
625 630 635 640

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
645 650 655

Ser Leu Ser Leu Gly Lys
660

<210> SEQ ID NO 82
<211> LENGTH: 1324
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: synthetic construct
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (1)...(1324)
<223> OTHER INFORMATION: VK2 kappa light chain polypeptide
and VH3 IgG4 S241P
heavy chain polypeptide
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (1)...(219)
<223> OTHER INFORMATION: light chain polypeptide VK2 kappa
<220> FEATURE:
<221> NAME/KEY: PEPTIDE
<222> LOCATION: (663)...(881)
<223> OTHER INFORMATION: light chain polypeptide VK2 kappa

<400> SEQUENCE: 82

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

Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20 25 30

-continued

Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Trp	Phe	Leu	Gln	Lys	Pro	Gly	Gln	Ser
	35						40					45			
Pro	Gln	Phe	Leu	Ile	Tyr	Arg	Met	Ser	Asn	Leu	Ala	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	Met	Gln	His
			85						90					95	
Leu	Glu	Tyr	Pro	Tyr	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	Gln	Val	Gln	Leu	Val
	210						215				220				
Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ala	Ser	Val	Lys	Val	Ser
225					230					235					240
Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Tyr	Tyr	Leu	Ile	Glu	Trp	Val
				245					250					255	
Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Ile	Gly	Val	Ile	Asn	Pro
			260					265						270	
Gly	Ser	Gly	Gly	Thr	Asn	Tyr	Asn	Glu	Lys	Phe	Lys	Gly	Arg	Ala	Thr
		275					280					285			
Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser
		290					295				300				
Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	Cys	Ala	Arg	Asn	Trp	Met
305					310					315					320
Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Ala
				325					330					335	
Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Cys	Ser	Arg	Ser
			340					345					350		
Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe
		355					360					365			
Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly
	370						375				380				
Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu
385					390					395					400
Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Lys	Thr	Tyr
				405					410					415	
Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg
			420					425					430		
Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu

-continued

435					440					445					
Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
450						455					460				
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
465					470					475					480
Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	Asn	Trp	Tyr	Val	Asp	Gly
				485					490					495	
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Phe	Asn
			500					505					510		
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
		515					520					525			
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Gly	Leu	Pro
530						535					540				
Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
545					550					555					560
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	Glu	Glu	Met	Thr	Lys	Asn
				565					570					575	
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
			580					585					590		
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
		595					600					605			
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Arg
610						615					620				
Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Glu	Gly	Asn	Val	Phe	Ser	Cys
625					630					635					640
Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu
				645					650					655	
Ser	Leu	Ser	Leu	Gly	Lys	Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser
			660					665					670		
Leu	Ser	Val	Thr	Pro	Gly	Gln	Pro	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser
		675					680					685			
Lys	Ser	Leu	Leu	His	Ser	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Trp	Phe	Leu
690						695					700				
Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	Phe	Leu	Ile	Tyr	Arg	Met	Ser	Asn
705					710					715					720
Leu	Ala	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr
				725					730					735	
Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val
			740					745					750		
Tyr	Tyr	Cys	Met	Gln	His	Leu	Glu	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly
		755					760					765			
Thr	Lys	Val	Glu	Ile	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile
		770				775						780			
Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val
785					790					795					800
Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys
				805					810					815	
Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu
			820					825					830		
Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu
		835					840						845		

-continued

Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	850	855	860
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	865	870	875
Cys	Gln	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	885	890	895
Ala	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Tyr	900	905	910
Tyr	Leu	Ile	Glu	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	915	920	925
Ile	Gly	Val	Ile	Asn	Pro	Gly	Ser	Gly	Gly	Thr	Asn	Tyr	Asn	Glu	Lys	930	935	940
Phe	Lys	Gly	Arg	Ala	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	945	950	955
Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Phe	965	970	975
Cys	Ala	Arg	Asn	Trp	Met	Asn	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr	Thr	980	985	990
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	995	1000	1005
Ala	Pro	Cys	Ser	Arg	Ser	Thr	Ser	Glu	Ser	Thr	Ala	Ala	Leu	Gly	Cys	1010	1015	1020
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	1025	1030	1035
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	1045	1050	1055
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	1060	1065	1070
Leu	Gly	Thr	Lys	Thr	Tyr	Thr	Cys	Asn	Val	Asp	His	Lys	Pro	Ser	Asn	1075	1080	1085
Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Ser	Lys	Tyr	Gly	Pro	Pro	Cys	Pro	1090	1095	1100
Pro	Cys	Pro	Ala	Pro	Glu	Phe	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	1105	1110	1115
Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	1125	1130	1135
Thr	Cys	Val	Val	Val	Asp	Val	Ser	Gln	Glu	Asp	Pro	Glu	Val	Gln	Phe	1140	1145	1150
Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	1155	1160	1165
Arg	Glu	Glu	Gln	Phe	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	1170	1175	1180
Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	1185	1190	1195
Ser	Asn	Lys	Gly	Leu	Pro	Ser	Ser	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	1205	1210	1215
Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Gln	1220	1225	1230
Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	1235	1240	1245

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Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 1250                1255                1260

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
1265                1270                1275                1280

Phe Phe Leu Tyr Ser Arg Leu Thr Val Asp Lys Ser Arg Trp Gln Glu
                1285                1290                1295

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
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Tyr Thr Gln Lys Ser Leu Ser Leu Ser Leu Gly Lys
 1315                1320

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<210> SEQ ID NO 83

<400> SEQUENCE: 83

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<210> SEQ ID NO 84

<211> LENGTH: 327

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: synthetic construct

<220> FEATURE:

<221> NAME/KEY: PEPTIDE

<222> LOCATION: (1)...(327)

<223> OTHER INFORMATION: IgG4 heavy chain constant region polypeptide

<400> SEQUENCE: 84

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Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg
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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 Leu 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

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

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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	

1-65. (canceled)

66. A light chain polypeptide comprising the amino acid sequence of SEQ ID NO: 74.

67. The light chain polypeptide of claim 66, comprising the amino acid sequence of SEQ ID NO:71.

68. A nucleic acid comprising a coding sequence for the light chain polypeptide of claim 66.

69-70. (canceled)

71. An antibody comprising the light chain polypeptide of claim 66.

72. A heavy chain polypeptide comprising the amino acid sequence of SEQ ID NO: 79.

73. The heavy chain polypeptide of claim 72, comprising the amino acid sequence of SEQ ID NO:76.

74. A nucleic acid comprising a sequence coding for the heavy chain polypeptide of claim 72.

75-76. (canceled)

77. An antibody comprising the heavy chain polypeptide of claim 72.

78. An antibody comprising:

a light chain polypeptide comprising the amino acid sequence of SEQ ID NO: 74; and

a heavy chain polypeptide comprising the amino acid sequence of SEQ ID NO: 79.

79. A polypeptide comprising the amino acid sequence of SEQ ID NO:82.

80. A cell expressing a polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NOs: 71, 74, 76, and 79.

81. A method of reducing growth of a tumor in a subject, the method comprising:

administering to the subject an antibody comprising the amino acid sequences of SEQ ID NOs: 74 and 79.

82. A method of inhibiting angiogenesis in a subject, comprising: administering to the subject an antibody comprising the amino acid sequences of SEQ ID NOs: 74 and 79.

83. A method of inhibiting a fibrotic disease in a subject, comprising:

administering to the subject an antibody comprising the amino acid sequences of SEQ ID NOs: 74 and 79.

84. A diagnostic method, comprising: determining a level of LOX and/or LOXL2 in a sample from a subject by contacting said sample with an antibody comprising the amino acid sequences of SEQ ID NOs: 74 and 79, wherein a difference in level of LOX and/or LOXL2 in the sample in comparison with a reference sample indicates the presence or increase of a tumor or metastasis.

85. A composition, comprising: an antibody comprising the amino acid sequences of SEQ ID NOs: 74 and 79 and a pharmaceutically acceptable carrier or excipient.

86. A kit for treating a condition associated with LOX or LOXL2, comprising:
the composition of claim 85.

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