(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
24 February 2011 (24.02.2011)

PCT

(10) International Publication Number
WO 2011/022667 A2

(51) International Patent Classification:
*C12N 9/02* (2006.01) *C12N 15/63* (2006.01)
*C07H 21/00* (2006.01) *C07H 21/04* (2006.01)

(21) International Application Number:
PCT/US2010/046192

(22) International Filing Date:
20 August 2010 (20.08.2010)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/235,776 21 August 2009 (21.08.2009) US

(71) Applicant *(for all designated States except US)*: **ARRESTO BIOSCIENCES, INC** [US/US]; 3183 Porter Drive, Palo Alto, CA 94304 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **MCCAULEY, Scott** [US/US]; 265 San Benito Road, Brisbane, CA 94005 (US). **SMITH, Victoria** [AU/US]; 19 Dwight Road, Burlingame, CA 94010 (US).

(74) Agent: **FRANCIS, Carol L.**; 1900 University Avenue, Suite 200, East Palo Alto, CA 94303 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

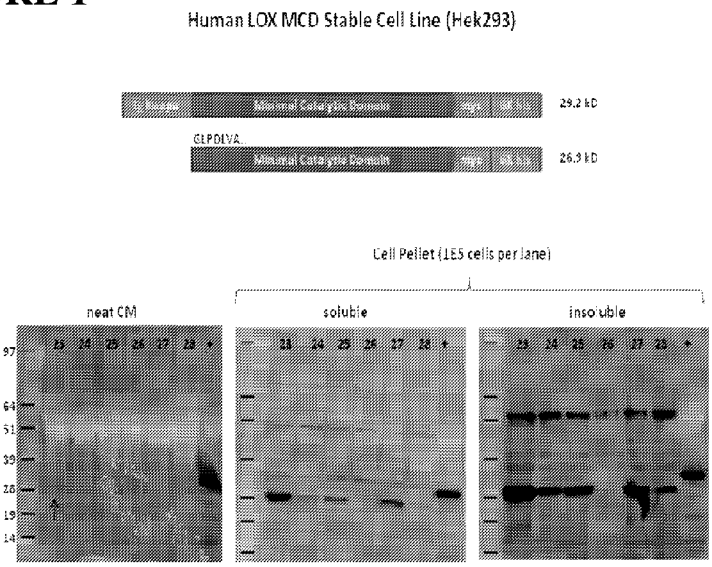
(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

**Published**:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

(54) **Title**: CATALYTIC DOMAINS FROM LYSYL OXIDASE AND LOXL2

**FIGURE 1**




(57) **Abstract**: Disclosed herein are amino acid sequences, and encoding nucleotide sequences, of isolated catalytic domains of the LOX and LOXL2 proteins from human and mouse. Methods for the preparation and use of these isolated catalytic domains are also provided.

WO 2011/022667 A2

# CATALYTIC DOMAINS FROM LYSYL OXIDASE AND LOXL2

## CROSS REFERENCE TO RELATED APPLICATIONS

This application claims benefit of United States provisional application No. 61/235,776 filed on August 21, 2009, the disclosure of which is hereby incorporated by reference in its entirety for all purposes.

## STATEMENT REGARDING FEDERAL SUPPORT

Not applicable.

## FIELD

The present application is in the fields of enzymology and molecular biology.

## BACKGROUND

Connective tissue provides a framework in which the cells and organs of the body reside. A primary component of connective tissue in vertebrates is the extracellular matrix. The two main structural constituents of the extracellular matrix are polysaccharides, which form a gel-like ground substance, and fibrous proteins embedded in the ground substance. Two of the most common of these fibrous proteins are collagen and elastin. Collagen fibers are formed by self-association of collagen fibrils, which are themselves assembled by the cross-linking of triple-helical collagen molecules. This cross-linking is catalyzed by lysyl oxidase (LOX) and related enzymes ("lysyl oxidase-like" or "LOXL"), all of which contain a catalytic domain capable of deaminating the ε-amino groups of lysine and hydroxylysine residues, resulting in conversion of peptidyl lysine to peptidyl-α-aminoadipic-δ-semialdehyde (allysine). Allysine residues are able to condense spontaneously with each other, resulting in crosslinking of collagen molecules.

The involvement of the extracellular matrix in various pathologies (including, for example, fibrosis and metastasis) has become increasingly apparent. See, for example, WO 01/83702 (Nov. 8, 2001); WO 2004/047720 (June 10, 2004); WO 2007/126457 (Aug. 11, 2007); US 2006/0127402 (June 15, 2006); US2007/0225242 (Sept. 27, 2007); US 2009/0053224 (Feb. 26, 2009); US 2009/0104201 (Apr. 23, 2009); Csiszar (2001)

*Prog. Nucleic Acid Res. and Molec. Biol.* **70:**1-32; Kirschmann *et al.* (2002) *Cancer Research* **62:**4478-4483. Since lysyl oxidase and lysyl oxidase-like enzymes play a key role in the formation of the extracellular matrix, by crosslinking collagen, they represent important therapeutic targets. Hence, methods to screen for inhibitors of these collagen-crosslinking enzymes, methods for identifying molecules that bind to these enzymes, and sources of collagen-crosslinking activity for various therapeutic uses (*e.g.*, wound healing) would all be desirable.

## SUMMARY

The present disclosure provides isolated catalytic domains of the lysyl oxidase (LOX) and lysyl oxidase-like-2 (LOXL2) enzymes from humans and mice; along with nucleic acids encoding these catalytic domains. Thus, the following peptides, and nucleic acids encoding these peptides, are provided: human LOX catalytic domain, human LOXL2 catalytic domain, murine LOX catalytic domain and murine LOXL2 catalytic domain. Accordingly, the present disclosure provides:

1. A polypeptide comprising the amino acid sequence of the catalytic domain of human lysyl oxidase (LOX). (SEQ ID NO:1)

2. A polynucleotide comprising a nucleotide sequence encoding the catalytic domain of human lysyl oxidase (LOX). (SEQ ID NO:2)

3. A polypeptide comprising the amino acid sequence of the catalytic domain of human lysyl oxidase-like 2 (LOXL2). (SEQ ID NO:3)

4. A polynucleotide comprising a nucleotide sequence encoding the catalytic domain of human lysyl oxidase-like 2 (LOXL2). (SEQ ID NO:4)

5. A polypeptide comprising the amino acid sequence of the catalytic domain of murine lysyl oxidase (LOX). (SEQ ID NO:5)

6. A polynucleotide comprising a nucleotide sequence encoding the catalytic domain of murine lysyl oxidase (LOX). (SEQ ID NO:6)

7. A polypeptide comprising the amino acid sequence of the catalytic domain of murine lysyl oxidase-like 2 (LOXL2). (SEQ ID NO:7)

8. A polynucleotide comprising a nucleotide sequence encoding the catalytic domain of murine lysyl oxidase-like 2 (LOXL2). (SEQ ID NO:8)

Also provided are:

1a. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of human lysyl oxidase (LOX) as set forth herein (SEQ ID NO:1), that does not contain sequences of human LOX outside of its catalytic domain.

2a. A polynucleotide comprising a nucleotide sequence encoding all or part of the catalytic domain of human lysyl oxidase (LOX) as set forth herein (SEQ ID NO:2), that does not encode sequences of human LOX outside of its catalytic domain.

3a. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of human lysyl oxidase-like 2 (LOXL2) as set forth herein (SEQ ID NO:3), that does not contain sequences of human LOXL2 outside of its catalytic domain.

4a. A polynucleotide comprising a nucleotide sequence encoding all or part of the catalytic domain of human lysyl oxidase-like 2 (LOXL2) as set forth herein (SEQ ID NO:4), that does not encode sequences of human LOXL2 outside of its catalytic domain.

5a. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of murine lysyl oxidase (LOX) as set forth herein (SEQ ID NO:5), that does not contain sequences of murine LOX outside of its catalytic domain.

6a. A polynucleotide comprising a nucleotide sequence encoding all or part of the catalytic domain of murine lysyl oxidase (LOX) as set forth herein (SEQ ID NO:6), that does not encode sequences of murine LOX outside of its catalytic domain.

7a. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of murine lysyl oxidase-like 2 (LOXL2) as set forth herein (SEQ ID NO:7), that does not contain sequences of murine LOXL2 outside of its catalytic domain.

8a. A polynucleotide comprising a nucleotide sequence encoding all or part of the catalytic domain of murine lysyl oxidase-like 2 (LOXL2) as set forth herein (SEQ ID NO:8), that does not encode sequences of murine LOXL2 outside of its catalytic domain.

Also provided are expression vectors comprising the aforementioned nucleic acids and/or polynucleotides. Such expression vectors optionally contain promoters (*e.g.*, T7 promoter, T3 promoter, SP6 promoter, *E. coli* RNA polymerase promoter, CMV promoter, SV40 promoter, PGK promoter, EF-1alpha promoter), transcription termination signals (*e.g.*, SV40 termination signal), splice sites (*e.g.*, SV40 splice sites, beta-globin splice site), ribosome binding sites, signal sequences (*e.g.*, immunoglobulin kappa signal sequence), epitopes tags (*e.g.*, *myc*), purification tags (*e.g.*, $His_6$), replication origins and drug selection markers. Linker sequences, encoding linker amino acids and/or comprising restriction enzyme recognition sites, or any other type of linker sequence, can also be present in the expression vectors disclosed herein.

Accordingly, the present disclosure also provides:

9. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of human LOX that does not contain human LOX amino acid sequences outside of its catalytic domain, further comprising one or more of a signal sequence, an epitope tag and a $His_6$ purification tag; for example, a polypeptide comprising a signal sequence, the catalytic domain of human LOX, a *myc* epitope tag and a $His_6$ purification tag (e.g., SEQ ID NO:9).

10. A polynucleotide encoding a polypeptide according to embodiment 9; for example, a polynucleotide comprising sequences encoding a signal sequence, the catalytic domain of human LOX, a *myc* epitope tag and a $His_6$ purification tag (*e.g.*, SEQ ID NO:10).

11. An expression vector comprising the polynucleotide of embodiment 10.

12. The expression vector of embodiment 11, further comprising any one of, any combination of, or all of a promoter, a drug selection marker and an origin of replication.

13. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of human LOXL2 that does not contain human LOXL2 amino acid sequences outside of its catalytic domain, further comprising one or more of a signal sequence, an epitope tag and a $His_6$ purification tag; for example, a polypeptide comprising a signal sequence, the catalytic domain of human LOXL2, a *myc* epitope tag and a $His_6$ purification tag (e.g., SEQ ID NO:11).

14. A polynucleotide encoding a polypeptide according to embodiment 13; for example, a polynucleotide comprising sequences encoding a signal sequence, the catalytic domain of human LOXL2, a *myc* epitope tag and a $His_6$ purification tag (*e.g.*, SEQ ID NO:12).

15. An expression vector comprising the polynucleotide of embodiment 14.

16. The expression vector of embodiment 15, further comprising any one of, any combination of, or all of a promoter, a drug selection marker and an origin of replication.

17. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of murine LOX that does not contain murine LOX amino acid sequences outside of its catalytic domain, further comprising one or more of a signal sequence, an epitope tag and a $His_6$ purification tag; for example, a polypeptide comprising a signal sequence, the catalytic domain of murine LOX, a *myc* epitope tag and a $His_6$ purification tag (e.g., SEQ ID NO:13).

18. A polynucleotide encoding a polypeptide according to embodiment 17; for example, a polynucleotide comprising sequences encoding a signal sequence, the catalytic domain of murine LOX, a *myc* epitope tag and a $His_6$ purification tag (*e.g.*, SEQ ID NO:14).

19. An expression vector comprising the polynucleotide of embodiment 18.

20. The expression vector of embodiment 19, further comprising any one of, any combination of, or all of a promoter, a drug selection marker and an origin of replication.

21. A polypeptide comprising the amino acid sequence of all or part of the catalytic domain of murine LOXL2 that does not contain murine LOXL2 amino acid sequences outside of its catalytic domain, further comprising one or more of a signal sequence, an epitope tag and a $His_6$ purification tag; for example, a polypeptide comprising a signal sequence, the catalytic domain of murine LOXL2, a *myc* epitope tag and a $His_6$ purification tag (e.g., SEQ ID NO:15).

22. A polynucleotide encoding a polypeptide according to embodiment 21; for example, a polynucleotide comprising sequences encoding a signal sequence, the catalytic domain of murine LOXL2, a *myc* epitope tag and a $His_6$ purification tag (*e.g.*, SEQ ID NO:16).

23. An expression vector comprising the polynucleotide of embodiment 22.

24. The expression vector of embodiment 23, further comprising any one of, any combination of, or all of a promoter, a drug selection marker and an origin of replication.

## BRIEF DESCRIPTION OF THE DRAWINGS

**Figure 1** shows expression of the catalytic domain of the human lysyl oxidase (hLOX) protein by HEK293 cells transfected with the phLOXMCD expression vector. Analysis of six stably transfected cell lines (numbered 23 through 28) by immunoblotting is shown. The left panel shows an immunoblot of a polyacrylamide gel containing samples (15 ul) of undiluted growth medium (neat CM) from each of the six cell lines. The middle panel shows analysis of soluble intracellular material, and the right panel shown analysis of insoluble intracellular material. For each of these panels, each lane contains material from approximately $10^5$ cells. All blots were probed with a primary mouse anti-$His_5$ antibody, then reacted with a secondary HRP conjugated donkey-anti-mouse antibody. HRP activity was revealed using the Chemi-Glow® reagent (Alpha Innotech, San Leandro, CA). The processed catalytic domain has a predicted molecular weight of 26.9 kD.

The lane labeled "+" in each panel contained a protein containing a $His_6$ sequence, to serve as a positive control for the anti-$His_5$ antibody.

**Figure 2** shows expression of the catalytic domain of the human lysyl oxidase-like 2 (hLOXL2) protein by HEK293 cells transfected with the phLOXL2MCD expression vector. The left panel shows an immunoblot of whole cell lysates from a number of stably transfected cell lines (indicated by a number at the top of each lane), with each lane containing material from approximately 1 x $10^5$ cells. The right panel shows an immunoblot of a polyacrylamide gel containing samples of undiluted growth medium (15 µl Neat CM) from each of six cell lines (indicated by numbers). All blots were probed with a primary mouse anti-$His_5$ antibody, then reacted with a secondary HRP conjugated donkey-anti-mouse antibody. HRP activity was revealed using the Chemi-Glow® reagent (Alpha Innotech, San Leandro, CA). The processed catalytic domain has a predicted molecular weight of 31 kD.

The lane labeled "+" in the left panel contained a protein containing a $His_6$ sequence, to serve as a positive control for the anti-$His_5$ antibody.

**Figure 3** shows expression of the catalytic domain of the murine lysyl oxidase (mLOX) protein by HEK293 cells transfected with the pmLOXMCD expression vector. Analysis of five stably transfected cell lines (numbered 4, 9, 12, 18 and 19) by immunoblotting is shown. The left panel shows an immunoblot of a polyacrylamide gel containing samples (15 ul) of undiluted growth medium (neat CM) from each of six cell lines. The right panel shows analysis of soluble and insoluble intracellular fractions from five of those six lines, with each lane containing material from approximately $10^5$ cells.

All blots were probed with a primary mouse anti-His$_5$ antibody, then reacted with a secondary HRP conjugated donkey-anti-mouse antibody. HRP activity was revealed using the Chemi-Glow® reagent (Alpha Innotech, San Leandro, CA). The processed catalytic domain has a predicted molecular weight of 27 kD.

**Figure 4** shows differences in secretion and amino acid sequence between the human and murine LOX catalytic domains. See Example 10 for details.

**Figure 5** shows a time-course of resorufin production (measured by absorbance at 590 nm) in an Amplex® Red assay of an isolated human LOXL2 catalytic domain. See example 12 for details.

**Figure 6** shows an alignment of amino acid sequences of various polypeptides in the present disclosure, including those that derive from human (hLOX, hLOXL1, hLOXL2, etc.) and mouse (mLOX and mLOXL2). The numbering of the amino acid residues starts with "one" at the most N-terminal residue shown and is not necessarily in accordance with convention in the art. Asterisks indicate amino acid identity at the position among all the polypeptides shown, while colons indicate conservative amino acid substitutions and single dots indicate semi-conservative amino acid substitutions, in accordance with the ClustalW2 program provided by the European Bioinformatics Institute (EMBL-EBI).

**Figure 7** shows an alignment of the amino acid sequences of various polypeptides in the present disclosure, including only those that derive from human. Numbering and legends are the same as those used in Fig. 6.

## DETAILED DESCRIPTION

Practice of the present disclosure employs, unless otherwise indicated, standard methods and conventional techniques in the fields of cell biology, toxicology, molecular biology, biochemistry, cell culture, immunology, oncology, recombinant DNA and related fields as are within the skill of the art. Such techniques are described in the literature and thereby available to those of skill in the art. See, for example, Alberts, B. *et al.*, "Molecular Biology of the Cell," 5th edition, Garland Science, New York, NY, 2008; Voet, D. *et al.* "Fundamentals of Biochemistry: Life at the Molecular Level," 3rd edition, John Wiley & Sons, Hoboken, NJ, 2008; Sambrook, J. *et al.*, "Molecular Cloning: A

Laboratory Manual," 3rd edition, Cold Spring Harbor Laboratory Press, 2001; Ausubel, F. *et al.*, "Current Protocols in Molecular Biology," John Wiley & Sons, New York, 1987 and periodic updates; Freshney, R.I., "Culture of Animal Cells: A Manual of Basic Technique," 4th edition, John Wiley & Sons, Somerset, NJ, 2000; and the series "Methods in Enzymology," Academic Press, San Diego, CA.

**Lysyl Oxidase-type Enzymes**

As used herein, the terms "lysyl oxidase-type enzyme" or "lysyl oxidase enzyme" refer to a member of a family of proteins containing a catalytic domain that catalyzes oxidative deamination of ε-amino groups of lysine and hydroxylysine residues, resulting in conversion of peptidyl lysine to peptidyl-α-aminoadipic-δ-semialdehyde (allysine) and the release of stoichiometric quantities of ammonia and hydrogen peroxide:

| | | | |
|---|---|---|---|
| \| | | \| | |
| C=O | | C=O | |
| \| | | \| | |
| $CH\text{-}CH_2\text{-}CH_2\text{-}CH_2\text{-}CH_2\text{-}NH_2$ | $+H_2O$ → | $CH\text{-}CH_2\text{-}CH_2\text{-}CH_2\text{-}CH{=}O$ | $+NH_3$ |
| \| | $+O_2$ | \| | $+H_2O_2$ |
| NH | | NH | |
| \| | | \| | |
| peptidyl lysine | | peptidyl allysine | |

This reaction most often occurs extracellularly, on lysine residues in collagen and elastin. The aldehyde residues of allysine are reactive and can spontaneously condense with other allysine and lysine residues, resulting in crosslinking of collagen molecules to form collagen fibrils.

Lysyl oxidase enzymes have been purified from chicken, rat, mouse, bovines and humans. All lysyl oxidase enzymes contain a common catalytic domain, approximately 205 amino acids in length, located in the carboxy-terminal portion of the protein and containing the active site of the enzyme. The active site contains a copper-binding site which includes a conserved amino acid sequence containing four histidine residues which coordinate a Cu(II) atom. The active site also contains a lysyltyrosyl quinone (LTQ) cofactor, formed by intramolecular covalent linkage between a lysine and a tyrosine residue (corresponding to lys314 and tyr349 in rat lysyl oxidase, and to lys320 and tyr355 in human lysyl oxidase). The sequence surrounding the tyrosine residue that forms the LTQ cofactor is also conserved among lysyl oxidase enzymes. The catalytic domain also contains ten conserved cysteine residues, which participate in the formation of five disulfide bonds. The catalytic domain also includes a fibronectin binding domain. Finally, an amino acid sequence similar to a growth factor and cytokine receptor domain, containing four cysteine residues, is present in the catalytic domain.

Despite the presence of these conserved regions, the different lysyl oxidase-type enzymes can be distinguished from one another, both within and outside their catalytic domains, by virtue of regions of divergent nucleotide and amino acid sequence.

The first member of this family of enzymes to be isolated and characterized was lysyl oxidase (EC 1.4.3.13); also known as protein-lysine 6-oxidase, protein-L-lysine:oxygen 6-oxidoreductase (deaminating), or LOX. *See, e.g.*, Harris *et al., Biochim. Biophys. Acta* (1974) 341:332-344; Rayton *et al.* (1979) *J. Biol. Chem.* 254:621-626; Stassen (1976) *Biophys. Acta* 438:49-60.

Additional lysyl oxidase-type enzymes were subsequently discovered. These proteins have been dubbed “LOX-like,” or “LOXL.” They all contain the common catalytic domain described above and have similar enzymatic activity. Currently, five different lysyl oxidase enzymes are known to exist in both humans and mice: LOX and the four LOX related, or LOX-like proteins LOXL1 (also denoted “lysyl oxidase-like,” “LOXL” or “LOL”), LOXL2 (also denoted “LOR-1”), LOXL3, and LOXL4. Each of the genes encoding the five different lysyl oxidase-type enzymes resides on a different chromosome. See, for example, Molnar *et al.* (2003) *Biochim Biophys Acta.* 1647:220-24; Csiszar (2001) *Prog. Nucl. Acid Res.* 70:1-32*;* WO 01/83702 published on Nov. 8, 2001, and U.S. Patent No. 6,300,092, all of which are incorporated by reference herein. A LOX-like protein termed LOXC, with some similarity to LOXL4 but with a different expression pattern, has been isolated from a murine EC cell line. Ito et al. (2001) *J. Biol. Chem.* 276:24023-24029. Two lysyl oxidase enzymes, DmLOXL-1 and DmLOXL-2, have been isolated from *Drosophila*.

Although all lysyl oxidase-type enzymes share a common catalytic domain, they also differ from one another, particularly within their amino-terminal regions. The four

LOXL proteins have amino-terminal extensions, compared to LOX. Thus, while human preproLOX (e.g., the primary translation product prior to signal sequence cleavage, see below) contains 417 amino acid residues; LOXL1 contains 574, LOXL2 contains 638, LOXL3 contains 753 and LOXL4 contains 756. The convention of numbering full length lysyl oxidase-type enzymes in the art starts from "one" at the most N-terminal amino acid residue which begins with the signal sequence.

Within their amino-terminal regions, LOXL2, LOXL3 and LOXL4 contain four repeats of the scavenger receptor cysteine-rich (SRCR) domain. These domains are not present in LOX or LOXL1. SRCR domains are found in secreted, transmembrane, or extracellular matrix proteins, and are known to mediate ligand binding in a number of secreted and receptor proteins. Hoheneste *et al.* (1999) *Nat. Struct. Biol.* **6:**228-232; Sasaki *et al.* (1998) *EMBO J.* **17:**1606-1613. In addition to its SRCR domains, LOXL3 contains a nuclear localization signal in its amino-terminal region. A proline-rich domain appears to be unique to LOXL1. Molnar *et al.* (2003) *Biochim. Biophys. Acta* 1647:220-224. The various lysyl oxidase-type enzymes also differ in their glycosylation patterns.

Tissue distribution also differs among the lysyl oxidase-type enzymes. Human LOX mRNA is highly expressed in the heart, placenta, testis, lung, kidney and uterus, but marginally in the brain and liver. mRNA for human LOXL1 is expressed in the placenta, kidney, muscle, heart, lung, and pancreas and, similar to LOX, is expressed at much lower levels in the brain and liver. Kim *et al.* (1995) *J. Biol. Chem.* **270:**7176-7182. High levels of LOXL2 mRNA are expressed in the uterus, placenta, and other organs, but as with LOX and LOXL, low levels are expressed in the brain and liver. Jourdan Le-Saux *et al.*(1999) *J. Biol. Chem.* **274:**12939:12944. LOXL3 mRNA is highly expressed in the testis, spleen, and prostate, moderately expressed in placenta, and not expressed in the liver, whereas high levels of LOXL4 mRNA are observed in the liver. Huang *et al.* (2001) *Matrix Biol.* **20:**153-157; Maki and Kivirikko (2001) *Biochem. J.* **355:**381-387; Jourdan Le-Saux *et al.* (2001) *Genomics* **74:**211-218; and Asuncion *et al.* (2001) *Matrix Biol.* **20:**487-491.

The expression and/or involvement of the different lysyl oxidase enzymes in diseases may also vary. See, for example, Kagan (1994) *Pathol. Res. Pract.* **190:**910-919; Murawaki *et al.* (1991) *Hepatology* **14:**1167-1173; Siegel *et al.* (1978) *Proc. Natl. Acad.*

*Sci. USA* **75:**2945-2949; Jourdan Le-Saux *et al.* (1994) *Biochem. Biophys. Res. Comm.* **199:**587-592; and Kim *et al.* (1999) *J. Cell Biochem.* **72:**181-188. Lysyl oxidase-type enzymes have also been implicated in a number of cancers, including head and neck cancer, bladder cancer, colon cancer, esophageal cancer and breast cancer. See, for example, Wu *et al.* (2007) *Cancer Res.* **67:**4123-4129; Gorough *et al.* (2007) *J. Pathol.* **212:**74-82; Csiszar (2001) *Prog. Nucl. Acid Res.* **70:**1-32 and Kirschmann *et al.* (2002) *Cancer Res.* **62:**4478-4483.

Thus, although the lysyl oxidase-type enzymes exhibit some overlap in structure and function, each appears to have distinct functions as well. With respect to structure, for example, certain antibodies raised against the catalytic domain of the human LOX protein do not bind to human LOXL2. With respect to function, it has been reported that targeted deletion of LOX appears to be lethal at parturition in mice, whereas LOXL1 deficiency causes no severe developmental phenotype. Hornstra *et al.* (2003) *J. Biol. Chem.* **278:**14387-14393; Bronson *et al.* (2005) *Neurosci. Lett.* **390:**118-122.

Although the most widely documented activity of lysyl oxidase-type enzymes is the oxidation of specific lysine residues in collagen and elastin outside of the cell, there is evidence that lysyl oxidase-type enzymes also participate in a number of intracellular processes. For example, there are reports that some lysyl oxidase-type enzymes regulate gene expression. Li *et al.* (1997) *Proc. Natl. Acad. Sci. USA* 94:12817-12822; Giampuzzi *et al.* (2000) *J. Biol. Chem.* 275:36341-36349. In addition, LOX has been reported to oxidize lysine residues in histone H1. Additional extracellular activities of LOX include the induction of chemotaxis of monocytes, fibroblasts and smooth muscle cells. Lazarus *et al.* (1995) *Matrix Biol.* 14:727-731; Nelson *et al.* (1988) *Proc. Soc. Exp. Biol. Med.* 188:346-352. Expression of LOX itself is induced by a number of growth factors and steroids such as TGF-β, TNF-α and interferon. Csiszar (2001) *Prog. Nucl. Acid Res.* 70:1-32. Recent studies have attributed other roles to LOX in diverse biological functions such as developmental regulation, tumor suppression, cell motility, and cellular senescence.

Examples of lysyl oxidase (LOX) proteins from various sources include enzymes 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. One embodiment of LOX is human lysyl oxidase (hLOX) preproprotein.

Exemplary disclosures of sequences encoding lysyl oxidase-like enzymes are as follows: LOXL1 is encoded by mRNA deposited at GenBank/EMBL BC015090; AAH15090.1; LOXL2 is encoded by mRNA deposited at GenBank/EMBL U89942; LOXL3 is encoded by mRNA deposited at GenBank/EMBL AF282619; AAK51671.1; and LOXL4 is encoded by mRNA deposited at GenBank/EMBL AF338441; AAK71934.1.

The primary translation product of the LOX protein, known as the prepropeptide, contains a signal sequence extending from amino acids 1-21. This signal sequence is released intracellularly by cleavage between Cys21 and Ala22, in both mouse and human LOX, to generate a 46-48 kDa propeptide form of LOX, also referred to herein as the full-length form. The propeptide is N-glycosylated during passage through the Golgi apparatus to yield a 50 kDa protein, then secreted into the extracellular environment. At this stage, the protein is catalytically inactive. A further cleavage, between Gly168 and Asp169 in mouse LOX, and between Gly174 and Asp175 in human LOX, generates the mature, catalytically active, 30-32 kDA enzyme, releasing a 18 kDa propeptide. This final cleavage event is catalyzed by the metalloendoprotease procollagen C-proteinase, also known as bone morphogenetic protein-1 (BMP-1). Interestingly, this enzyme also functions in the processing of LOX's substrate, collagen. The N-glycosyl units are subsequently removed.

Potential signal peptide cleavage sites have been predicted at the amino termini of LOXL1, LOXL2, LOXL3, and LOXL4. The predicted signal cleavage sites are between Gly25 and Gln26 for LOXL1, between Ala25 and Gln26, for LOXL2, between Gly25 and Ser26 for LOXL3 and between Arg23 and Pro24 for LOXL4.

A BMP-1 cleavage site in the LOXL1 protein has been identified between Ser354 and Asp355. Borel *et al.* (2001) *J. Biol. Chem.*__276:__48944-48949. Potential BMP-1 cleavage sites in other lysyl oxidase-type enzymes have been predicted, based on the consensus sequence for BMP-1 cleavage in procollagens and pro-LOX being at an

Ala/Gly-Asp sequence, often followed by an acidic or charged residue. A predicted BMP-1 cleavage site in LOXL3 is located between Gly447 and Asp448; processing at this site may yield a mature peptide of similar size to mature LOX. A potential cleavage site for BMP-1 was also identified within LOXL4, between residues Ala569 and Asp570. Kim *et al.* (2003) *J. Biol. Chem.* **278:**52071-52074. LOXL2 may also be proteolytically cleaved analogously to the other members of the LOXL family and secreted. Akiri *et al.*(2003) *Cancer Res.* **63:**1657-1666.

Based on the presence of a common catalytic domain in the lysyl oxidase-type enzymes, certain amino acid residues of the C-terminal 30 kDa region of the proenzyme in which the active site is located are highly conserved. A more moderate degree of conservation (approximately 60-70%) is observed in the propeptide domain.

For the purposes of the present disclosure, the term "lysyl oxidase-type enzyme" encompasses all five of the lysine oxidizing enzymes discussed above, *i.e.*, LOX, LOXL1 (also identified as LOXL), LOXL2, LOXL3 and LOXL4; and also encompasses functional fragments and/or derivatives of LOX, LOXL1, LOXL2, LOXL3 and LOXL4 that substantially retain enzymatic activity; *e.g.*, the ability to catalyze deamination of lysyl residues. A "fragment and/or derivative" in the context of an amino acid sequence or polynucleotide sequence (*e.g.*, an amino acid sequence "derived from" LOXL2) is meant to indicate that the polypeptide or nucleic acid contains a contiguous sequence of all or a portion of a naturally-occurring lysyl oxidase-type enzymes protein or its encoding nucleic acid, and is not meant to be limiting as to the source or method in which the protein or nucleic acid is made.

Typically, a functional fragment or derivative retains at least 50% of its lysine oxidation activity. In some embodiments, a functional fragment or derivative retains at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 99% or 100% of its lysine oxidation activity.

It is also intended that a functional fragment of a lysyl oxidase-type enzyme can include conservative amino acid substitutions (with respect to the native polypeptide sequence) that do not substantially alter catalytic activity. The term "conservative amino acid substitution" refers to grouping of amino acids on the basis of certain common structures and/or properties. With respect to common structures, amino acids can be grouped into those with non-polar side chains (glycine, alanine, valine, leucine, isoleucine, methionine, proline, phenylalanine and tryptophan), those with uncharged polar side chains (serine, threonine, asparagine, glutamine, tyrosine and cysteine) and those with charged polar side chains (lysine, arginine, aspartic acid, glutamic acid and histidine). A group of amino acids containing aromatic side chains includes phenylalanine, tryptophan and tyrosine. Heterocyclic side chains are present in proline, tryptophan and histidine. Within the group of amino acids containing non-polar side chains, those with short hydrocarbon side chains (glycine, alanine, valine. leucine, isoleucine) can be distinguished from those with longer, non-hydrocarbon side chains (methionine, proline, phenylalanine, tryptophan). Within the group of amino acids with charged polar side chains, the acidic amino acids (aspartic acid, glutamic acid) can be distinguished from those with basic side chains (lysine, arginine and histidine).

A functional method for defining common properties of 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, 1979). According to such analyses, groups of amino acids can be defined in which amino acids within a group are preferentially substituted for one another in homologous proteins, and therefore have similar impact on overall protein structure (Schulz, G. E. and R. H. Schirmer, Principles of Protein Structure, Springer-Verlag, 1979). According to this type of analysis, conservative amino acid substitution" refers to a substitution of one amino acid residue for another sharing chemical and physical properties of the amino acid side chain (*e.g.*, charge, size, hydrophobicity/hydrophilicity). Following are examples of amino acid residues sharing certain chemical and/or physical properties:

(i) amino acids containing a charged group, consisting of Glu, Asp, Lys, Arg and His,

(ii) amino acids containing a positively-charged group, consisting of Lys, Arg and His,

(iii) amino acids containing a negatively-charged group, consisting of Glu and Asp,

(iv) amino acids containing an aromatic group, consisting of Phe, Tyr and Trp,

(v) amino acids containing a nitrogen ring group, consisting of His and Trp,

(vi) amino acids containing a large aliphatic non-polar group, consisting of Val, Leu and Ile,

(vii) amino acids containing a slightly-polar group, consisting of Met and Cys,

(viii) amino acids containing a small-residue group, consisting of Ser, Thr, Asp, Asn, Gly, Ala, Glu, Gln and Pro,

(ix) amino acids containing an aliphatic group consisting of Val, Leu, Ile, Met and Cys, and

(x) amino acids containing a hydroxyl group consisting of Ser and Thr.

Certain "conservative substitutions" may include substitution within the following groups of amino acid residues: gly, ala; val, ile, leu; asp, glu; asn, gln; ser, thr; lys, arg; and phe, tyr.

Thus, as exemplified above, conservative substitutions of amino acids are known to those of skill in this art and can be made generally without altering the biological activity of the resulting molecule. Those of skill in this art also 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., Menlo Park, CA, p. 224.

For additional information regarding lysyl oxidase enzymes, see, *e.g.*, Rucker *et al.* (1998) *Am. J. Clin. Nutr.* **67:**996S-1002S and Kagan *et al.* (2003) *J. Cell. Biochem* **88:**660-672. See also co-owned United States patent applications US 2009/0053224 (February 26, 2009) and US 2009/0104201 (Apr. 23, 2009); the disclosures of which are incorporated by reference herein for the purposes of describing lysyl oxidase and lysyl oxidase-like enzymes, modulators of these enzymes, and methods for identifying modulators of these enzymes. See also WO 2004/47720 (June 10, 2004); WO 2007/126457 (August 11, 2007); WO 2009/010974 (January 22, 2009); US 2006/0127402 (June 15, 2006); US 2007/0021365 (Jan. 25, 2007) and US 2007/0225242 (Sept. 27, 2007); all of which are incorporated by reference herein for the purposes of describing lysyl oxidase and lysyl oxidase-like enzymes, modulators of these enzymes, and methods for identifying modulators of these enzymes.

**Polypeptides having a catalytic domain of a lysyl oxidase or lysyl oxidase-type enzyme**

The present disclosure provides polypeptides having activity of a lysyl oxidase-type enzyme, such as those belonging to EC 1.4.3.13 in accordance with the nomenclature of International Union of Biochemistry and Molecular Biology, as described above. A full-length protein contains a signal sequence and/or propeptide, both of which may be cleaved before the protein attains full catalytic activity *in vivo*. The full-length lysyl oxidase or lysyl oxidase-like enzyme may be of a length of more than 100, 200, 300, 400, 500, 700, up to 754 or more amino acid residues. The mature full-length protein without the signal sequence and/or propeptide may be of a length of more than 100, 200, 240, 480, 720, 730, up to 740 or more amino acid residues.

The polypeptides of the present disclosure can be derived from the mature full-length LOX or LOXL proteins (*e.g.* without the signal peptide and/or propeptide). Exemplary polypeptides can have any of the amino acid sequences as set forth in Figures 6 and 7.

Figure 6 shows an alignment of amino acid sequences of polypeptides that are derived from human LOX, human LOXL1, human LOXL2, human LOXL3, human LOXL4, murine LOX, and murine LOXL2. Fig. 7 shows an alignment of the sequences of polypeptides that are derived from only human LOX/LOXL proteins. For convenience, the numbering of the amino acid residues starts with “one” at the most N-terminal residue shown in Figs 6 and 7. Polypeptides of the present disclosure thus can be described with reference to the numbering system used for sequences set forth in Figs 6 and 7 or the numbering system used in the art as described previously. Alternatively, the polypeptides may be described with reference to the sequence identifier numbers assigned herein. Asterisks in Figs. 6 and 7 indicate an identical amino acid at the position among all the polypeptides shown, while colons indicate conservative amino acid substitutions and single dots indicate semi-conservative amino acid substitutions, in accordance with the legends used by the ClustalW2 program provided by the European Bioinformatics Institute (EMBL-EBI).

The polypeptides of the present disclosure may encompass a polypeptide having at least about 50, at least about 75, at least about 100, at least about 120, at least about

140, at least about 150, at least about 170, at least about 180, at least about 200, at least about 220, up to at least about 240 or more amino acids of the C-terminal portion of a lysyl oxidase-type enzyme. For example, a polypeptide of the present disclosure may contain the C-terminal 207 amino acid residues as shown by SEQ ID NO: 1, SEQ ID NO: 5, or SEQ ID NO: 17 in Fig. 6. Polypeptides of the present disclosure also encompass those having an amino acid sequence that is less than that of a naturally-occurring full-length lysyl oxidase-type enzyme. Polypeptides can contain up to about 25, up to about 50, up to about 75, up to about 100, up to about 120, up to about 140, up to about 160, up to about 180, up to about 200, up to about 220, up to about 230 or more amino acid residues in a C-terminal portion of a LOX or LOXL-protein, *e.g.* as exemplified by sequences set forth in Figs 6 and 7. The polypeptides may exclude the signal sequence, the propeptide, and/or any of the portions of the LOX or LOXL-protein that are N-terminal to the sequences shown in Figs 6 and 7.

The polypeptides of the present disclosure may also be described with reference to the numbering system used in the art as described above, in which amino acid number "one" denotes the most N-terminal amino acid residue for the full-length LOX or full-length LOXL-proteins containing the signal sequence. According to such numbering, the polypeptides can be described as those encompassing an amino acid sequence starting at residue number between about 190 and 240, about 200 and 230 or between about 210 and 220 in LOX (e.g. SEQ ID NO: 1 or SEQ ID NO:5). The polypeptide may encompass an amino acid sequence starting at residue number between about 350 and 360, between about 340 and 370, or between about 330 and 380 in LOXL1. Alternatively, the polypeptide may encompass an amino acid sequence starting at residue number between about 540 and 550, between about 530 and 560, or between about 520 and 570 in LOXL2 (e.g. SEQ ID NO: 3 or SEQ ID NO:7). The polypeptide may also encompass an amino acid sequence starting at residue number between about 520 and 530, between about 510 and 540, or between about 500 and 550 in LOXL3. The polypeptide may also encompass an amino acid sequence starting at residue number between about 530 and 540, between about 540 and 550, or between about 530 and 560 in LOXL4.

Polypeptides of the present disclosure encompass those having 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more amino acid substitutions, *e.g.*, conservative amino acid substitutions as compared to an amino acid sequence set forth in Figs 6 and 7. Guidance for amino acid substitutions can be obtained from the alignments provided in Figs 6 and 7. Amino acid residues that may be substituted may be located at residue positions that are not highly conserved, such as those not marked by an asterisk, colons, or dots. The ordinarily skilled artisan will appreciate that based on the alignments shown, amino acid residues at certain residue positions may tolerate substitutions, deletions, and/or insertions without changing the physical and chemical property of the overall polypeptide as compared to other residue positions.

Polypeptides of the present disclosure encompass those having an amino acid sequence that is at least 80%, at least 90%, at least 95%, at least 99% or 100% identical to any of the polypeptides shown in Fig. 6. For example, the amino acid sequence of the murine LOX catalytic domain polypeptide shown in Fig. 6 shares 98% amino acid sequence identity with the amino acid sequence of the human LOX catalytic domain polypeptide.

A protein from which a polypeptide of the present disclosure can be derived in accordance with the description above includes LOX (GenBank Accession No. NP_002308), LOXL1 (NP_005567), LOXL2 (NP_002309), LOXL3 (NP_115882), and LOXL4 (NP_115587), in which the aforementioned GenBank Accession numbers denote human sequences. In addition to those found in humans, these LOX or LOXL proteins cam also include those found in mouse or other mammals. For example, a LOX, LOXL1, or LOXL2 protein can be murine in origin (GenBank accession numbers NP_034858, NP_034859, NP_201582, respectively).

The subject polypeptides can include amino acid sequences derived from a lysyl oxidase-type enzyme (*e.g.*, LOX or LOXL2) further comprising heterologous amino acid sequences, *e.g.*, LOX or LOXL2 sequences linked to a polypeptide that is not part of a LOX or LOXL2 protein. Such polypeptides can be fusion proteins, such as a fusion protein containing epitope tags, purification tags, and/or detectable labels. A fusion protein can optionally include a linker sequence between the heterologous sequences and the amino acid sequence derived from the lysyl oxidase-type enzyme. Methods for producing a fusion protein of interest when provided a nucleic acid sequence are well-known in the art. Other heterologous elements and exemplary fusion proteins are described in more detail below.

Exemplary polypeptides containing heterologous elements may include *myc* and/or $His_6$ tags and may optionally include flanking linker sequences, such as those set forth in SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, or SEQ ID NO:15.

Polypeptides of the present disclosure further encompass those that are joined to a reporter polypeptide, *e.g.*, a fluorescent protein, and/or conjugated to a molecule. The molecule conjugated to the polypeptide may be a carrier molecule or an immunogen known to elicit an immune response when present in an animal (*e.g.*, an adjuvant). Other conjugates may include those that facilitate delivery and/or increase the half-life of the subject polypeptide.

The polypeptide of the present disclosure may also contain one or more poly(ethylene glycol) (PEG) moieties. Such polypeptides are referred to as "PEGylated polypeptides." Methods and reagents suitable for PEGylation of polypeptides are well known in the art. In general, PEG suitable for conjugation to a polypeptide is generally soluble in water at room temperature, and has the general formula $R(O\text{-}CH_2\text{-}CH_2)_nO\text{-}R$, where R is hydrogen or a protective group such as an alkyl or an alkanol group, and where n is an integer from 1 to 1000. Where R is a protective group, it generally contains from 1 to 8 carbon atoms.

The PEG may have at least one hydroxyl group modified to generate a functional group that is reactive with an amino group (*e.g.*, an epsilon amino group of a lysine residue or a free amino group at the N-terminus of a polypeptide) or a carboxyl group in the polypeptide.

Additional derivatives of PEG comprises a terminal thiocarboxylic acid group, -COSH, which selectively reacts with amino groups to generate amide derivatives. In other embodiments, the PEG comprises a reactive ester such as an N-hydroxy succinimidate at the end of the PEG chain. Such an N-hydroxysuccinimidate-containing PEG molecule reacts with select amino groups at particular pH conditions such as a neutral pH of around 6.5-7.5.

The PEG can be conjugated directly to an amino acid residue of the polypeptide, or through a linker. In some embodiments, a linker is added to the polypeptide, forming a linker-modified polypeptide. Such linkers provide various functionalities, *e.g.*, reactive groups such as sulfhydryl, amino, or carboxyl groups to couple a PEG reagent to the linker-modified polypeptide.

The PEG that is conjugated to the polypeptide may be linear or branched. Branched PEG derivatives include, but are not limited to, those described in U.S. Pat. No. 5,643,575, "star-PEGs," and multi-armed PEGs such as those described in Shearwater Polymers, Inc. catalog "Polyethylene Glycol Derivatives 1997-1998." Star PEGs are described in the art, *e.g.*, in U.S. Patent No. 6,046,305.

**Polynucleotides encoding polypeptides having a catalytic domain of a lysyl oxidase-type enzyme**

The present disclosure contemplates a polynucleotide comprising a nucleic acid sequence encoding a polypeptide described previously that has an activity of a lysyl oxidase-type enzyme. The nucleic acid contemplated herein has a nucleotide sequence that is at least 70% identical to (*e.g.*, at least 85%, at least 90%, at least 95%, at least 98%, at least 99% or 100%) to a contiguous sequence of a nucleic acid that encodes any of the polypeptides described above. The percentage identity is based on the shorter of the sequences compared. Well known programs such as BLASTN (2.0.8) (Altschul *et al.* (1997) *Nucl. Acids. Res.* **25:**3389-3402) using default parameters and no filter can be employed to make a sequence comparison. Nucleic acid sequence identity (*e.g.* between two different polynucleotides encoding identical amino acid sequences) can be lower than the percent of amino acid sequence identity due to degeneracy of the genetic code.

Examples of nucleic acid sequences in a polynucleotide encoding a polypeptide of the present disclosure include SEQ ID NO:2 (human LOX-derived), SEQ ID NO:4 (human LOX2-derived), SEQ ID NO:6 (murine LOX-derived), and SEQ ID NO:8 (murine LOX2-derived). These nucleic acid sequences can also be provided in an expression vector.

Expression vectors provided herein contain the aforementioned nucleic acids and/or polynucleotides. Such expression vectors can contain promoters (*e.g.*, T7 promoter, T3 promoter, SP6 promoter, *E. coli* RNA polymerase promoter, CMV promoter, SV40 promoter, PGK promoter, EF-1alpha promoter), transcription termination signals (*e.g.*, SV40 termination signal), splice sites (*e.g.*, SV40 splice sites, beta-globin splice site), ribosome binding sites, signal sequences (*e.g.*, immunoglobulin kappa signal sequence), epitopes tags (*e.g.*, *myc*, FLAG), purification tags (*e.g.*, $His_6$), replication origins and drug selection markers. Linker sequences, encoding linker amino acids and/or comprising restriction enzyme recognition sites, or any other type of linker sequence, can also be operably linked to the nucleic acid encoding the subject polypeptide present in the vectors disclosed herein. Further details of vectors and uses thereof are described below.

**Methods of making polypeptides of the present disclosure**

Polypeptides of the present disclosure can be produced by any suitable method, including recombinant and non-recombinant methods (*e.g.*, chemical synthesis). The subject polypeptide can be prepared by solid-phase synthesis methods well-known in the art, (*e.g.*, Fmoc- or t-Boc chemistry), such as those described by Merrifield (1963) *J. Am. Chem. Soc.* **85:**2149 and Methods in Molecular Biology, Vol 35: Peptide Synthesis Protocols.

Where the polypeptide is produced using recombinant techniques, the methods can involve any suitable construct and any suitable host cell, which can be a prokaryotic or eukaryotic cell (*e.g.* a bacterial host cell, a yeast host cell, or a cultured mammalian host cell). Methods for introducing genetic material into host cells include, for example, transformation, electroporation, lipofection, conjugation, calcium phosphate methods and the like. The method for transfer can be selected so as to provide for stable expression of the introduced polypeptide-encoding nucleic acid. The polypeptide-encoding nucleic acid can be provided as an inheritable episomal element (*e.g.*, plasmid) or can be genomically integrated.

Suitable vectors for transferring a polypeptide-encoding nucleic acid can vary in composition. Integrative vectors can be conditionally replicative or suicide plasmids, bacteriophages, and the like. The constructs can include various elements, including for example, promoters, selectable genetic markers (*e.g.,* genes conferring resistance to antibiotics (for instance neomycin, G418, methotrexate, ampicillin kanamycin, erythromycin, chloramphenicol, or gentamycin)), origins of replication (to promote replication in a host cell, *e.g.*, a bacterial host cell), and the like. The choice of vector will depend upon a variety of factors such as the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression of protein in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal. The choice of appropriate vector is well within the skill of the art. Many such vectors are available commercially.

The vector used can be an expression vector based on episomal plasmids containing selectable drug resistance markers and elements that provide for autonomous replication in different host cells. Vectors are amply described in numerous publications well known to those in the art, including, *e.g.*, Short Protocols in Molecular Biology, (1999) F. Ausubel, *et al.*, eds., Wiley & Sons. Vectors may provide for expression of the nucleic acids encoding the subject polypeptide, may provide for propagating the subject nucleic acids, or both.

Constructs can be prepared by, for example, inserting a polynucleotide of interest into a construct backbone, typically by means of DNA ligase attachment to a cleaved restriction enzyme site in the vector. Alternatively, the desired nucleotide sequence can be inserted by homologous recombination or site-specific recombination, or by one or more amplification methods (*e.g.*, PCR). Typically homologous recombination is accomplished by attaching regions of homology to the vector on the flanks of the desired nucleotide sequence, while site-specific recombination can be accomplished through use of sequences that facilitate site-specific recombination (*e.g.*, cre-lox, att sites, *etc.*). Nucleic acid containing such sequences can be added by, for example, ligation of oligonucleotides, or by polymerase chain reaction using primers comprising both the region of homology and a portion of the desired nucleotide sequence.

For expression of the polypeptide of interest, an expression cassette can be employed. Thus, the present disclosure provides a recombinant expression vector comprising a subject nucleic acid. The expression vector can provide transcriptional and translational regulatory sequences, and can also provide for inducible or constitutive expression, wherein the coding region is operably placed under the transcriptional control of a transcriptional initiation region (*e.g.*, a promoter or enhancer), and transcriptional and translational termination regions. These control regions may be native to a lysyl oxidase-type enzyme from which the subject polypeptide is derived, or may be derived from exogenous sources. As such, control regions from exogenous sources can be considered heterologous elements that are operably linked to the nucleic acid encoding the subject polypeptide. In general, the transcriptional and translational regulatory sequences can include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. Promoters can be either constitutive or inducible, and can be a strong constitutive promoter (*e.g.*, T7, and the like).

Expression vectors generally have convenient restriction sites located near the promoter sequence to provide for the insertion of nucleic acid sequences encoding proteins of interest. A selectable marker operative in the expression host can be present to facilitate selection of cells containing the vector. In addition, the expression construct can include additional elements. For example, the expression vector can have one or two replication systems, thus allowing it to be maintained, for example, in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. In addition, the expression construct can contain a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

It should be noted that the polypeptides of the present disclosure can also contain additional elements, such as a detectable label, *e.g.*, a radioactive label, a fluorescent label, a biotin label, an immunologically detectable label (*e.g.*, a hemagglutinin (HA) tag, a poly-Histidine tag) and the like. Additional elements can be provided (*e.g.*, in the form of fusion polypeptides) to facilitate expression (*e.g.* N-terminal methionine and/or a heterologous signal sequence to facilitate expression in host cells), and/or isolation (*e.g.*, biotin tag, immunologically detectable tag) of the polypeptides of the disclosure through various methods. The polypeptides can also optionally be immobilized on a support through covalent or non-covalent attachment. Exemplary nucleic acids encoding the subject polypeptide can contain SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14 or SEQ ID NO:16. The nucleic acid can encode a polypeptide derived from a human or murine lysyl oxidase-type enzyme that has a *myc* tag, a $His_6$ tag, and/or linker sequences.

Isolation and purification of the subject polypeptides can be accomplished according to methods known in the art. The term "isolated" is intended to mean that a compound (*e.g.* polypeptide or polynucleotide) is separated from all or some of the components that accompany it in nature. "Isolated" also refers to the state of a compound separated from all or some of the components that accompany it during manufacture (*e.g.*, chemical synthesis, recombinant expression, culture medium, and the like).

For example, a polypeptide according to the present disclosure can be isolated from a lysate of cells that have been genetically modified to express the subject polypeptide, from the supernatant of cell culture medium, or from a synthetic reaction mixture. Isolation can additionally be achieved by immunoaffinity purification, which generally involves contacting a sample with an antibody (optionally immobilized) against an epitope of the polypeptide (*e.g.*, a heterologous epitope fused to an amino acid sequence derived from a lysyl oxidase-type enzyme), washing to remove non-specifically bound material, and eluting specifically bound polypeptide. Isolated polypeptide can be further purified by dialysis and other methods normally employed in protein purification, *e.g.* metal chelate chromatography, ion-exchange, and size exclusion.

The present disclosure further contemplates recombinant host cells containing an exogenous polynucleotide encoding one or more of the polypeptides of the present disclosure.

**Screening methods**

The polypeptides of the present disclosure, having lysyl oxidase catalytic activity, are useful in methods to screen for modulators of the activity of a lysyl oxidase-type enzyme. Expressing an adequate amount of a subject polypeptide as described previously can be used to provide substrate for the screening assays described below.

Modulators of the activity of a lysyl oxidase-type enzyme (and candidate compounds to be tested for modulatory activity) can comprise macromolecules such as, for example proteins (*e.g.*, antibodies, transcription factors) and nucleic acids (*e.g.*, triplex-forming oligonucleotides, antisense oligonucleotides, ribozymes, siRNA, shRNA), and small organic molecules, such as are obtained by synthetic organic methods and/or combinatorial chemistry.

Modulators of the activity of lysyl oxidase-type enzymes include both activators (agonists) and inhibitors (antagonists), and can be selected by using a variety of screening assays. In one embodiment, modulators can be identified by determining if a test compound binds to a catalytic domain polypeptide as disclosed herein; wherein, if binding has occurred, the compound is a candidate modulator. Optionally, additional tests can be carried out on such a candidate modulator. Alternatively, a candidate compound can be contacted with a polypeptide as disclosed herein, and a biological activity of the polypeptide is assayed; a compound that alters the biological activity of the polypeptide is a modulator of a lysyl oxidase-type enzyme. Generally, a compound that reduces a biological activity of the polypeptide is an inhibitor of the enzyme.

Other methods of identifying modulators of the activity of lysyl oxidase-type enzymes include incubating a candidate compound in a cell culture in which the cells are expressing one or more of the polypeptides of the disclosure, and assaying one or more biological activities or characteristics of the cells. Compounds that alter the biological activity or characteristic of the cells in the culture are potential modulators of the activity of a lysyl oxidase-type enzyme. Biological activities that can be assayed include, for example, lysine oxidation, peroxide production, ammonia production, levels of lysyl oxidase-type enzyme, levels of mRNA encoding a lysyl oxidase-type enzyme, levels of a polypeptide of the disclosure, levels of mRNA encoding a polypeptide of the disclosure and/or one or more functions specific to a lysyl oxidase-type enzyme.

In additional embodiments of the aforementioned assay, in the absence of contact with the candidate compound, the one or more biological activities or cell characteristics are correlated with levels or activity of one or more lysyl oxidase-type enzymes. For example, the biological activity can be a cellular function such as migration, chemotaxis, epithelial-to-mesenchymal transition (EMT), or mesenchymal-to-epithelial transition (MET), and the change is detected by comparison with one or more control or reference sample(s).

Controls can also be used. As an example, negative control samples can include a culture with decreased levels of a polypeptide of the disclosure (or a culture which does not express a polypeptide of the disclosure), to which a candidate compound is added; or a culture with the same amount of a polypeptide of the disclosure as the test culture, but without addition of candidate compound. A control can include the addition of a mock candidate compound or an agent known to activate or inhibit lysyl oxidase activity. In some embodiments, separate cultures containing different levels of a polypeptide of the disclosure are contacted with a candidate compound. If a change in biological activity is observed, and if the change is greater in the culture having higher levels of the polypeptide, the compound is identified as a modulator of the activity of a lysyl oxidase-type enzyme. Determination of whether the compound is an activator or an inhibitor of a lysyl oxidase-type enzyme may be apparent from the phenotype induced by the compound, or may require further assay, such as a test of the effect of the compound on the enzymatic activity of one or more lysyl oxidase-type enzymes.

Methods for obtaining lysysl oxidase-type enzymes, either biochemically or recombinantly, as well as methods for cell culture and enzymatic assay to identify modulators of the activity of lysyl oxidase-type enzymes as described above, are known in the art.

The enzymatic activity of a lysyl oxidase-type enzyme can be assayed by a number of different methods. For example, lysyl oxidase enzymatic activity can be assessed by detecting and/or quantitating production of hydrogen peroxide, ammonium ion, and/or aldehyde, by assaying lysine oxidation and/or collagen crosslinking, or by measuring cellular invasive capacity, cell adhesion, cell growth or metastatic growth. See, for example, Trackman *et al.* (1981) *Anal. Biochem.* **113:**336-342; Kagan *et al.* (1982) *Meth. Enzymol.* **82A:**637-649; Palamakumbura *et al.* (2002) *Anal. Biochem.* **300:**245-251; Albini *et al.* (1987) *Cancer Res.* **47:**3239-3245; Kamath *et al.* (2001) *Cancer Res.* **61:**5933-5940; U.S. Patent No. 4,997,854 and U.S. patent application publication No. 2004/0248871.

Test compounds include, but are not limited to, small organic compounds (*e.g.*, organic molecules having a molecular weight between about 50 and about 2,500 Da), nucleic acids or proteins, for example. The compound or plurality of compounds can be chemically synthesized or microbiologically produced and/or comprised in, for example, samples, *e.g.*, cell extracts from, *e.g.*, plants, animals or microorganisms. The reaction mixture for assaying for a modulator of a lysyl oxidase-type enzyme can be a cell-free extract or can comprise a cell culture or tissue culture. A plurality of compounds can be, *e.g.*, added to a reaction mixture, added to a culture medium, injected into a cell or administered to a transgenic animal. The cell or tissue employed in the assay can be, for example, a bacterial cell, a fungal cell, an insect cell, a vertebrate cell, a mammalian cell, a primate cell, a human cell or can comprise or be obtained from a non-human transgenic animal.

If a sample containing a compound or a plurality of compounds is identified in the method of the disclosure, then it is either possible to isolate the compound from the original sample identified as containing the compound capable of inhibiting or activating the subject polypeptide, or one can further subdivide the original sample, for example, if it consists of a plurality of different compounds, so as to reduce the number of different substances per sample and repeat the method with the subdivisions of the original sample. Depending on the complexity of the samples, the steps described above can be performed several times (*e.g.*, by limiting dilution), until the sample identified according to the method of the disclosure only comprises a limited number of or only one substance(s). In some embodiments the sample comprises substances of similar chemical and/or physical properties, and in some embodiments, the substances are identical.

Furthermore, the above-mentioned methods can be used for the construction of binding epitopes derived from a lysyl oxidase-type enzyme. A similar approach was successfully described for peptide antigens of the anti-p24 (HIV-1) monoclonal antibody; see Kramer (1997) *Cell* **97:**799-809. A general route to fingerprint analyses of peptide-antibody interactions using the clustered amino acid peptide library was described in Kramer (1995) *Mol. Immunol.* **32:**459-465. In addition, antagonists of lysyl oxidase-type enzymes can be derived and identified from monoclonal antibodies that specifically react with the polypeptide of the disclosure in accordance with the methods as described in Doring (1994) *Mol. Immunol.* **31:**1059-1067.

Several methods are known to the person skilled in the art for producing and screening large libraries to identify compounds having specific affinity for a target, such as a lysyl oxidase-type enzyme or a polypeptide of the disclosure. These methods include phage display method in which randomized peptides are displayed from phage and screened by affinity chromatography using an immobilized receptor. See, *e.g.*, WO 91/17271, WO 92/01047, and U.S. Patent No. 5,223,409. In another approach, combinatorial libraries of polymers immobilized on a solid support (*e.g.*, a “chip”) are synthesized using photolithography. See, *e.g.*, U.S. Patent No. 5,143,854, WO 90/15070 and WO 92/10092. The immobilized polymers are contacted with a labeled polypeptide (*e.g.*, a lysyl oxidase-type enzyme or a polypeptide as disclosed herein) and the support is scanned to determine the location of label, to thereby identify polymers binding to the polypeptide.

The synthesis and screening of peptide libraries on continuous cellulose membrane supports that can be used for identifying binding ligands (*e.g.*, activators or inhibitors) of a polypeptide of interest (*e.g.*, a lysyl oxidase-type enzyme or a polypeptide of the disclosure) is described, for example, in Kramer (1998) *Methods Mol. Biol.* **87:** 25-39. Ligands identified by such an assay are candidate modulators of the protein of interest, and can be selected for further testing. This method can also be used, for example, for determining the binding sites and the recognition motifs in a protein of interest. See, for example Rudiger (1997) *EMBO J.* **16:**1501-1507 and Weiergraber (1996) *FEBS Lett.* **379:**122-126.

WO 98/25146 describes additional methods for screening libraries of complexes for compounds having a desired property, *e.g.*, the capacity to agonize, bind to, or antagonize a polypeptide or its binding partners. The complexes in such libraries comprise a compound under test, a tag recording at least one step in synthesis of the compound, and a tether susceptible to modification by a reporter molecule. Modification of the tether is used to signify that a complex contains a compound having a desired property. The tag can be decoded to reveal at least one step in the synthesis of such a compound. Other methods for identifying compounds which interact with a lysyl oxidase-type enzyme (or with the polypeptides of the disclosure) are, for example, *in vitro* screening with a phage display system, filter binding assays, and "real time" measuring of interaction using, for example, the BIAcore apparatus (Pharmacia).

All these methods can be used in accordance with the present disclosure to identify activators/agonists and inhibitors/antagonists of lysyl oxidase-type enzymes or related polypeptides.

Various sources for the basic structure of such an activator or inhibitor can be employed and comprise, for example, mimetic analogs of the polypeptides of the disclosure. Mimetic analogs of the polypeptide of the disclosure or biologically active fragments thereof can be generated by, for example, substituting the amino acids that are expected to be essential for the biological activity with, *e.g.*, stereoisomers, *i.e.* D-amino acids; see e.g., Tsukida (1997) *J. Med. Chem.* **40:**3534-3541. Furthermore, for cases in which polypeptide fragments are used for the design of biologically active analogues, pro-mimetic components can be incorporated into a peptide to reestablish at least some of the conformational properties that may have been lost upon removal of part of the original polypeptide; see, e.g., Nachman (1995) *Regul. Pept.* **57:**359-370.

Such pseudopeptide analogues of a natural amino acid sequence can very efficiently mimic the parent protein. Benkirane (1996) *J. Biol. Chem.* **271:**33218-33224. For example, incorporation of easily available achiral o-amino acid residues into a polypeptide of the disclosure or a fragment thereof results in the substitution of amide bonds by polymethylene units of an aliphatic chain, thereby providing a convenient strategy for constructing a peptide mimetic. Banerjee (1996) *Biopolymers* **39:**769-777. Superactive peptidomimetic analogues of small peptide hormones in other systems have also been described. Zhang (1996) *Biochem. Biophys. Res. Commun.* **224:**327-331.

Peptide mimetics can also be identified by the synthesis of peptide mimetic combinatorial libraries through successive amide alkylation, followed by testing of the resulting compounds, *e.g.*, for their binding and immunological properties. Methods for the generation and use of peptidomimetic combinatorial libraries have been described. *See*, for example, Ostresh, (1996) *Methods in Enzymology* **267:**220-234 and Dorner (1996) *Bioorg. Med. Chem.* **4:**709-715. Furthermore, a three-dimensional and/or crystallographic structure of a polypeptide of the disclosure can be used for the design of peptide mimetics. Rose (1996) *Biochemistry* **35:**12933-12944; Rutenber (1996) *Bioorg. Med. Chem.* **4:**1545-1558.

The structure-based design and synthesis of low-molecular-weight synthetic molecules that mimic the activity of native biological polypeptides is further described in, *e.g.*, Dowd (1998) *Nature Biotechnol.* **16:**190-195; Kieber-Emmons (1997) *Current Opinion Biotechnol.* **8:**435-441; Moore (1997) *Proc. West Pharmacol. Soc.* **40:**115-119; Mathews (1997) *Proc. West Pharmacol. Soc.* **40:**121-125; and Mukhija (1998) *European J. Biochem.* **254:**433-438.

It is also well known to the person skilled in the art that it is possible to design, synthesize and evaluate mimetics of small organic compounds that, for example, can act as a substrate or ligand of a lysyl oxidase-type enzyme or of a polypeptide of the disclosure. For example, it has been described that D-glucose mimetics of hapalosin exhibited similar efficiency as hapalosin in antagonizing multidrug resistance assistance-associated protein in cytotoxicity. Dinh (1998) *J. Med. Chem.* **41:**981-987.

The structure of the lysyl oxidase-type enzymes, and of the polypeptides disclosed herein, can be investigated to guide the selection of modulators such as, for example, small molecules, peptides, peptide mimetics and antibodies. Structural properties of lysyl oxidase-type enzymes, and of the polypeptides of the disclosure, can help to identify natural or synthetic molecules that bind to, or function as a ligand, substrate, binding partner or the receptor of, a lysyl oxidase-type enzyme. See, *e.g.*, Engleman (1997) *J. Clin. Invest.* **99:**2284-2292. For example, folding simulations and computer redesign of structural motifs of lysyl oxidase-type enzymes can be performed using appropriate computer programs. Olszewski (1996) *Proteins* **25:**286-299; Hoffman (1995) *Comput. Appl. Biosci.* **11:**675-679. Computer modeling of protein folding can be used for the conformational and energetic analyses of detailed peptide and protein structure. Monge (1995) *J. Mol. Biol.* **247:**995-1012; Renouf (1995) *Adv. Exp. Med. Biol.* **376:**37-45. Appropriate programs can be used for the identification of sites, on lysyl oxidase-type enzymes and/or on the polypeptides of the disclosure, that interact with ligands and binding partners, using computer assisted searches for complementary peptide sequences. Fassina (1994) *Immunomethods* **5:**114-120. Additional systems for the design of protein and peptides are described in the art, for example in Berry (1994) *Biochem. Soc. Trans.* **22:**1033-1036; Wodak (1987), *Ann. N.Y. Acad. Sci.* **501:**1-13; and Pabo (1986) *Biochemistry* **25:**5987-5991. The results obtained from the above-described structural analyses can be used for, *e.g.*, the preparation of organic molecules, peptides and peptide mimetics that function as modulators of the activity of one or more lysyl oxidase-type enzymes, and for the preparation of mimetics of the polypeptides of the disclosure.

The inhibitors to be screened herein, such as antibodies, can be competitive inhibitors, uncompetitive inhibitors, mixed inhibitors or non-competitive inhibitors. Competitive inhibitors often bear a structural similarity to substrate, usually bind to the active site and are generally more effective at lower substrate concentrations. The apparent $K_M$ is increased in the presence of a competitive inhibitor. Uncompetitive inhibitors generally bind to the enzyme-substrate complex or to a site that becomes available after substrate is bound at the active site and may distort the active site. Both the apparent $K_M$ and the $V_{\max}$ are decreased in the presence of an uncompetitive inhibitor, and substrate concentration has little or no effect on inhibition. Thus, inhibition by an uncompetitive inhibitor is often most noticeable at high substrate concentration. Mixed inhibitors are capable of binding both to free enzyme and to the enzyme-substrate complex and thus affect both substrate binding and catalytic activity. Non-competitive inhibition is a special case of mixed inhibition in which the inhibitor binds enzyme and enzyme-substrate complex with equal avidity, and inhibition is not affected by substrate concentration. Non-competitive inhibitors generally bind to enzyme at a region outside the active site. For additional details on enzyme inhibition see, for example, Voet *et al.* (2008) *supra*. For enzymes such as the lysyl oxidase-type enzymes, whose natural substrates (*e.g.*, collagen, elastin) are normally present in vast excess *in vivo* (compared to the concentration of any inhibitor that can be achieved *in vivo*), noncompetitive inhibitors are advantageous, since inhibition is independent of substrate concentration.

**Antibody Production**

The present disclosure also provides a method of producing antibodies specific for the polypeptides of the disclosure. The antibody can be isolated, *e.g.*, is in an environment other than its naturally-occurring environment. Suitable antibodies specific for the subject polypeptide include antibodies of any isotype; single-chain Fv; Fab; Fab; Fv; $F(ab')_2$; artificial antibodies; humanized antibodies; fragments thereof, and the like.

Suitable antibodies can be obtained by immunizing a host animal with peptides comprising all or a portion of a subject polypeptide. Where an animal is to be immunized, the present disclosure provides an immunogenic composition comprising a subject polypeptide. A subject immunogenic composition may include a subject polypeptide and an adjuvant. Adjuvants are known in the art and may include those suitable for use in humans or other mammals.

Suitable host animals to be immunized include mouse, rat sheep, goat, hamster, rabbit, donkey, *etc.* Methods of immunizing animals, including the adjuvants used, booster schedules, sites of injection, suitable animals, *etc.* are well understood in the art (e.g., Harlow *et al.*, *Antibodies: A Laboratory Manual*, First Edition (1988) Cold Spring Harbor, N.Y.), and administration of living cells to animals has been described for several mammals and birds, *e.g.*, McKenzie *et al.* (1989) *Oncogene* **4:**543-548; Scuderi *et al.* (1985) *Med. Oncol. Tumor Pharmacother* **2:**233-242; Roth *et al.* (1984) *Surgery* **96:**264-272 and Drebin *et al.* (1984) *Nature* **312:**545-548. Subsequent to immunization, a population of antibody producing cells is generated. The population of cells may be produced using hybridoma methods that are well known to one of skill in the art (see, *e.g.*, Harlow, *supra.* Cells expressing antibody are fused to immortalized cells, such as myeloma cells or transformed cells, which are capable of replicating indefinitely in cell culture, thereby producing an immortal, immunoglobulin-secreting cell line. The immortal cell line utilized can be selected to be deficient in enzymes necessary for the utilization of certain nutrients. Many such lines (such as myelomas) are known to those skilled in the art, and include, for example: thymidine kinase (TK)-deficient or hypoxanthine-guanine phosphoriboxyl transferase (HGPRT)-deficient cell lines. These deficiencies allow selection for fused cells according to their ability to grow on, for example, hypoxanthine/aminopterin/thymidine (HAT) medium. In alterative embodiments, populations of cells expressing monoclonal antibodies can be made using phage display methods.

Antibodies against the subject polypeptides can also be produced by genetic engineering. In this technique, as with the standard hybridoma procedure, antibody-producing cells are sensitized to the desired antigen or immunogen. The messenger RNA isolated from the immune spleen cells or hybridomas is used as a template to make cDNA using PCR amplification. A library of vectors, each containing one heavy chain gene and one light chain gene retaining the initial antigen specificity, is produced by insertion of appropriate sections of the amplified immunoglobulin cDNA into the expression vectors. A combinatorial library can be constructed by combining the heavy chain gene library with the light chain gene library. This results in a library of clones which co-express a heavy and light chain (resembling the $F_{ab}$ fragment or antigen binding fragment of an antibody molecule). The vectors that carry these genes are co-transfected into a host (*e.g.* bacteria, insect cells, mammalian cells, or other suitable protein production host cell). When antibody gene synthesis is induced in the transfected host, the heavy and light chain proteins self-assemble to produce active antibodies that can be detected by screening with the antigen or immunogen.

Another method of antibody production involves phage display. Phage display is used for high-throughput screening of protein interactions. In this method, phage are utilized to display antigen-binding domains expressed from a repertoire or combinatorial antibody library (*e.g.*, human or murine). Phage expressing an antigen binding domain that binds the subject polypeptide of interest are selected or identified using the polypeptide target, *e.g.*, using labeled polypeptide or polypeptide bound to or captured on a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13. The binding domains can comprise $F_{ab}$, $F_v$ (individual $F_v$ region from light or heavy chains) or disulfide stabilized $F_v$ antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Exemplary methods are set forth, for example, in EP 368684B1; U.S. Pat. No. 5,969,108, Hoogenboom, H. R. and Chames (2000) *Immunol. Today* **21:**371; Nagy *et al.* (2002) *Nat. Med.* **8:**801; Huie *et al.* (2001) *Proc. Natl. Acad. Sci. USA* **98:**2682; Lui *et al.* (2002) *J. Mol. Biol.* **315:**1063, each of which is incorporated herein by reference. Several publications (*e.g.*, Marks *et al.* (1992) *Bio/Technology* **10:**779-783) have described the production of high-affinity human antibodies by chain shuffling, as well as combinatorial infection and *in vivo* recombination as a strategy for constructing large phage libraries.

In related embodiments, ribosomal display can be used as a display platform. *See*, *e.g.*, Hanes *et al.* (2000) *Nat. Biotechnol.* **18:**1287; Wilson *et al.* (2001) *Proc. Natl. Acad. Sci. USA* **98:**3750; and Irving *et al.* (2001) *J. Immunol. Methods* **248:**31).

Cell surface libraries can be screened for antibodies (Boder *et al.* (2000) *Proc. Natl. Acad. Sci. USA* **97:**10701; Daugherty *et al.* (2000) *J. Immunol. Methods* **243:**211. Such procedures provide alternatives to traditional hybridoma techniques for the isolation and subsequent cloning of monoclonal antibodies.

In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. For example, DNA sequences encoding heavy chain variable ($V_H$) and light chain variable ($V_L$) regions are amplified or otherwise isolated from animal cDNA libraries (*e.g.*, human or murine cDNA libraries of lymphoid tissues) or synthetic cDNA libraries. The DNA encoding the $V_H$ and $V_L$ regions may be joined together by an scFv linker (*e.g.*, by PCR) and cloned into a phagemid vector (*e.g.*, p CANTAB 6 or pComb 3 HSS). The vector is electroporated into *E. coli* and the *E. coli* is infected with helper phage. Sequences encoding the $V_H$ or $V_L$ regions are usually recombinantly fused to either gene III or gene VIII sequences of the phage. Phage expressing an antigen binding domain that binds to an antigen of interest (*i.e.*, a subject polypeptide) can be selected or identified with antigen, *e.g.*, using labeled antigen or antigen bound to or captured on a solid surface or bead.

Additional examples of phage display methods include those disclosed in PCT Application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Pat. Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

**Formulations, kits and routes of administration**

Therapeutic compositions comprising catalytic domains as disclosed herein are also provided. Such compositions typically comprise the catalytic domain (or a nucleic acid encoding the catalytic domain) and a pharmaceutically acceptable carrier. Supplementary active compounds can also be incorporated into the compositions.

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 (*e.g.*, a mammal such as a human or a non-human animal such as a primate, rodent, cow, horse, pig, sheep, *etc.*) 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 full or partial 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. An effective amount of an agent is an amount that, when administered, in one or more doses, results in an at least about 5%, at least about 10%, at least about 15%, at least about 20%, at least about 25%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or more than 90%, reduction in the severity of one or more symptoms associated with a lysyl oxidase-type enzyme in an individual, compared to the severity of the one or more symptoms in the absence of treatment with the agent. Such reduction in severity can be manifested, for example, by improved wound healing or enhanced angiogenesis.

A therapeutically effective amount of a catalytic domain of a lysyl oxidase-type enzyme (*e.g.*, a LOX or LOXL2 catalytic domain) varies with the type of disease or disorder, extensiveness of the disease or disorder, and size of the mammal suffering from the disease or disorder.xx

Various pharmaceutical compositions and techniques for their preparation and use are known to those of skill in the art in light of the present disclosure. For a detailed listing of suitable pharmacological compositions and techniques for their administration one may refer to texts such as Remington's Pharmaceutical Sciences, 17th ed. 1985; Brunton *et al.*, “Goodman and Gilman’s The Pharmacological Basis of Therapeutics,” McGraw-Hill, 2005; University of the Sciences in Philadelphia (eds.), “Remington: The Science and Practice of Pharmacy,” Lippincott Williams & Wilkins, 2005; and University of the Sciences in Philadelphia (eds.), “Remington: The Principles of Pharmacy Practice,” Lippincott Williams & Wilkins, 2008.

The disclosed therapeutic compositions further include pharmaceutically acceptable materials, compositions or vehicle, such as a liquid or solid filler, diluent, excipient, solvent or encapsulating material, *i.e.*, carriers. These carriers are involved in transporting the subject composition from one organ, or region of the body, to another organ, or region of the body. Each carrier should be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not injurious to the patient. Some examples of materials which can serve as pharmaceutically-acceptable carriers include: sugars, such as lactose, glucose and sucrose; starches, such as corn starch and potato starch; cellulose and its derivatives, such as sodium carboxymethyl cellulose, ethyl cellulose and cellulose acetate; powdered tragacanth; malt; gelatin; talc; excipients, such as cocoa butter and suppository waxes; oils, such as peanut oil, cottonseed oil, safflower oil, sesame oil, olive oil, corn oil and soybean oil; glycols, such as propylene glycol; polyols, such as glycerin, sorbitol, mannitol and polyethylene glycol; esters, such as ethyl oleate and ethyl laurate; agar; buffering agents, such as magnesium hydroxide and aluminum hydroxide; alginic acid; pyrogen-free water; isotonic saline; Ringer's solution; ethyl alcohol; phosphate buffer solutions; and other non-toxic compatible substances employed in pharmaceutical formulations. Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives and antioxidants can also be present in the compositions.

Another aspect of the present disclosure relates to kits for carrying out the administration of a catalytic domain of a lysyl oxidase-type enzyme, as disclosed herein, or of a nucleic acid encoding such a catalytic domain, to a subject. In one embodiment, the kit comprises a catalytic domain of a lysyl oxidase-type enzyme (or a nucleic acid encoding a catalytic domain of a lysyl oxidase-type enzyme), formulated in a pharmaceutical carrier.

The formulation and delivery methods are generally adapted according to the site(s) and type of disorder to be treated. Exemplary formulations include, but are not limited to, those suitable for parenteral administration, *e.g.*, intravenous, intra-arterial, intra-ocular, 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 disclosure 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.

In additional embodiments, the compositions described herein are delivered locally. Localized delivery allows for the delivery of the composition non-systemically, for example, to a wound or fibrotic area, reducing the body burden of the composition as compared to systemic delivery. Such local delivery can be achieved, for example, through the use of various medically implanted devices including, but not limited to, stents and catheters, or can be achieved by injection or surgery. Methods for coating, implanting, embedding, and otherwise attaching desired agents to medical devices such as stents and catheters are established in the art and contemplated herein.

Implanted stents have been used to carry medicinal agents, such as thrombolytic agents. U.S. Patent No. 5,163,952 discloses a thermal memoried expanding plastic stent device formulated to carry a medicinal agent in the material of the stent itself. U.S. Patent No. 5,092,877 discloses a stent of a polymeric material which can have a coating associated with the delivery of compounds. Other patents which are directed to devices of the class utilizing bio-degradable and bio-sorbable polymers include U.S. Patent No. 4,916,193 and U.S. Patent No. 4,994,071. By way of example, U.S. Patent No. 5,304,121 discloses a coating applied to a stent consisting of a hydrogel polymer and a preselected compound such as a cell growth inhibitor or heparin. Methods of making a coated intravascular stent carrying a therapeutic material are described in U.S. Patent No. 5,464,650 wherein a polymer coating material is dissolved in a solvent and the therapeutic material dispersed in the solvent. The solvent is then evaporated after contact with the stent.

U.S. Patent No. 6,120,536 describes additional types of coatings for use with a wide variety of prosthetic devices, including stents. Examples of additional medical or prosthetic devices that are useful for administration of the compositions described herein include, but are not limited to, blood exchanging devices, vascular access ports, central venous catheters, cardiovascular catheters, extracorporeal circuits, vascular grafts, pumps, heart valves, and cardiovascular sutures.

The use of devices coated with the compositions described herein, including stents and catheters, allows the compositions to be delivered to specific or localized sites. Such site-specific delivery can provide a means for use of compositions, and/or dosages thereof, that are not otherwise amenable to systemic delivery due to solubility, systemic toxicity concerns, or other issues. By way of example, β-aminopropionitrile (BAPN) is known to be useful as an inhibitor of lysyl oxidase-type enzymes, but this compound is highly toxic, presenting problems for its effective use when administered systemically.

The use of a stent, catheter, or other medical device for delivery of an active agent or compound such as BAPN permits use of the compound at effective dosages in a targeted or localized manner, thus decreasing the systemic toxic effects associated with such compounds.

**Uses**

The polypeptides disclosed herein have a number of uses. For example, they can be used as standards (*e.g.*, positive controls) for assays of lysyl oxidase enzymatic activity (*e.g.*, collagen crosslinking). One use for such an assay is in a mutational analysis of, *e.g.*, a LOX or LOXL2 protein and/or its gene. The polypeptides, comprising catalytic domains with lysyl oxidase activity, can also be used to characterize new and existing antibodies to lysyl oxidase-type enzymes.

The polypeptides disclosed herein can also be used to identify molecules that bind to, *e.g.*, LOX and/or LOXL2 catalytic domains, *e.g.*, small organic molecules or macromolecules (*e.g.*, polypeptides). Certain of these binding molecules may act as modulators (*i.e.*, activators or inhibitors) of catalytic activity.

The subject polypeptides disclosed herein are also useful for generation of antibodies directed specifically to the catalytically active region of human and murine LOX and LOXL2 proteins and other lysyl oxidase-type enzymes. Such antibodies can be used, for example, in medical and/or therapeutic applications for diseases or disorders characterized by pathologically increased levels of lysyl oxidase activity.

In addition, the subject polypeptides are useful in medical and/or therapeutic applications requiring crosslinking of collagen: for example wound healing and treatment of diabetic ulcers. The smaller size of the isolated catalytic domains (compared to the full-length proteins) may facilitate their use as therapeutics, due, for example, to enhanced stability and faster absorption.

## EXAMPLES

**Example 1: Human LOX catalytic domain**

A polypeptide including the catalytic domain of the human LOX protein contains 207 amino acid residues and has the following amino acid sequence:

GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLL
RFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVA
EGHKASFCLEDTSCDYGYHRRFACTAHTQGLSPGCYDTYGADIDCQWIDITDVK
PGNYILKVSVNPSYLVPESDYTNNVVRCDIRYTGHHAYASGCTISPY
(SEQ ID NO:1)

In certain embodiments, a polypeptide including the human LOX catalytic domain does not include the initial glycine and leucine residues ("GL") in the sequence shown above.

The human DNA sequence encoding a subject polypeptide containing the LOX catalytic domain is:

GGTCTCCCAGACCTGGTGGCCGACCCCTACTACATCCAGGCGTCCACGTACG
TGCAGAAGATGTCCATGTACAACCTGAGATGCGCGGCGGAGGAAAACTGTCT
GGCCAGTACAGCATACAGGGCAGATGTCAGAGATTATGATCACAGGGTGCTG
CTCAGATTTCCCCAAAGAGTGAAAAACCAAGGGACATCAGATTTCTTACCCA
GCCGACCAAGATATTCCTGGGAATGGCACAGTTGTCATCAACATTACCACAG
TATGGATGAGTTTAGCCACTATGACCTGCTTGATGCCAACACCCAGAGGAGA
GTGGCTGAAGGCCACAAAGCAAGTTTCTGTCTTGAAGACACATCCTGTGACT
ATGGCTACCACAGGCGATTTGCATGTACTGCACACACACAGGGATTGAGTCC
TGGCTGTTATGATACCTATGGTGCAGACATAGACTGCCAGTGGATTGATATTA
CAGATGTAAAACCTGGAAACTATATCCTAAAGGTCAGTGTAAACCCCAGCTA
CCTGGTTCCTGAATCTGACTATACCAACAATGTTGTGCGCTGTGACATTCGCT
ACACAGGACATCATGCGTATGCCTCAGGCTGCACAATTTCACCGTATTAG
(SEQ ID NO:2)

**Example 2: Human LOXL2 catalytic domain**

A polypeptide including the catalytic domain of the human LOXL2 protein has the following amino acid sequence:

TAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTDPTTGYRRLLR
FSSQIHNNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEG
HKASFCLEDTECEGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVP

PGDYLFQVVINPNFEVAESDYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEK
KFEHFSGLLNNQLSPQ (SEQ ID NO:3)

In certain embodiments, a polypeptide including the human LOXL2 catalytic domain does not include the initial threonine and alanine residues (“TA”) in the sequence shown above.

The human DNA sequence encoding the LOXL2 catalytic domain is:
ACCGCCCCTGACCTGGTCCTCAATGCGGAGATGGTGCAGCAGACCACCTACC
TGGAGGACCGGCCCATGTTCATGCTGCAGTGTGCCATGGAGGAGAACTGCCT
CTCGGCCTCAGCCGCGCAGACCGACCCCACCACGGGCTACCGCCGGCTCCTG
CGCTTCTCCTCCCAGATCCACAACAATGGCCAGTCCGACTTCCGGCCCAAGA
ACGGCCGCCACGCGTGGATCTGGCACGACTGTCACAGGCACTACCACAGCAT
GGAGGTGTTCACCCACTATGACCTGCTGAACCTCAATGGCACCAAGGTGGCA
GAGGGCCACAAGGCCAGCTTCTGCTTGGAGGACACAGAATGTGAAGGAGAC
ATCCAGAAGAATTACGAGTGTGCCAACTTCGGCGATCAGGGCATCACCATGG
GCTGCTGGGACATGTACCGCCATGACATCGACTGCCAGTGGGTTGACATCAC
TGACGTGCCCCCTGGAGACTACCTGTTCCAGGTTGTTATTAACCCCAACTTCG
AGGTTGCAGAATCCGATTACTCCAACAACATCATGAAATGCAGGAGCCGCTA
TGACGGCCACCGCATCTGGATGTACAACTGCCACATAGGTGGTTCCTTCAGC
GAAGAGACGGAAAAAAAGTTTGAGCACTTCAGCGGGCTCTTAAACAACCAG
CTGTCCCCGCAGTAA (SEQ ID NO:4)

**Example 3: Murine LOX catalytic domain**

A polypeptide including the catalytic domain of the murine LOX protein has the following amino acid sequence:
GLPDLVPDPYYIQASTYVQKMSMYNLRCAAEENCLASSAYRADVRDYDHRVLL
RFPQRVKNQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVA
EGHKASFCLEDTSCDYGYHRRFACTAHTQGLSPGCYDTYAADIDCQWIDITDVQ
PGNYILKVSVNPSYLVPESDYTNNVVRCDIRYTGHHAYASGCTISPY
(SEQ ID NO:5)

In certain embodiments, a polypeptide including the murine LOX catalytic domain does not include the initial glycine and leucine residues ("GL") in the sequence shown above.

The murine DNA sequence encoding a polypeptide including the LOX catalytic domain is:

GGTCTCCCGGACCTGGTGCCCGACCCCTACTACATCCAGGCTTCCACGTACGT
CCAGAAGATGTCTATGTACAACCTGAGATGCGCTGCGGAAGAAAACTGCCTG
GCCAGTTCAGCATATAGGGCGGATGTCAGAGACTATGACCACAGGGTACTGC
TACGATTTCCGCAAAGAGTGAAGAACCAAGGGACATCGGACTTCTTACCAAG
CCGCCCTCGGTACTCCTGGGAGTGGCACAGCTGTCACCAACATTACCACAGC
ATGGACGAATTCAGCCACTATGACCTGCTTGATGCCAACACACAGAGGAGAG
TGGCTGAAGGCCACAAAGCAAGCTTCTGTCTGGAGGACACGTCCTGTGACTA
TGGGTACCACAGGCGCTTTGCGTGCACTGCACACACACAGGGATTGAGTCCT
GGATGTTATGACACCTATGCGGCAGACATAGACTGCCAGTGGATTGATATTA
CAGATGTACAACCTGGAAACTACATTCTAAAGGTCAGTGTAAACCCCAGCTA
CCTGGTGCCTGAATCAGACTACACTAACAATGTTGTACGCTGTGACATTCGCT
ACACAGGACATCATGCCTATGCCTCAGGCTGCACAATTTCACCGTATTAG
(SEQ ID NO:6)

**Example 4: Murine LOXL2 catalytic domain**

A polypeptide including the catalytic domain of the murine LOXL2 protein has the following amino acid sequence:

TAPDLVLNAEIVQQTAYLEDRPMSLLQCAMEENCLSASAVHTDPTRGHRRLLRF
SSQIHNNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTYYDLLSLNGTKVAEGH
KASFCLEDTECEGDIQKSYECANFGEQGITMGCWDMYRHDIDCQWIDITDVPPG
DYLFQVVINPNYEVPESDFSNNIMKCRSRYDGYRIWMYNCHVGGAFSEETEQKF
EHFSGLLNNQLSVQ (SEQ ID NO:7)

In certain embodiments, a polypeptide including the murine LOXL2 catalytic domain does not include the initial threonine and alanine residues ("TA") in the sequence shown above.

The murine DNA sequence encoding a polypeptide including the LOXL2 catalytic domain is:

ACTGCACCTGACCTGGTGCTTAATGCTGAGATTGTCCAGCAGACTGCCTACCT
GGAGGACAGGCCCATGTCCTTGCTGCAGTGTGCCATGGAGGAGAACTGCCTC
TCCGCCTCCGCTGTGCACACCGACCCCACCAGAGGCCACCGGCGCCTTTTAC
GCTTCTCCTCCCAGATCCACAACAATGGCCAGTCTGACTTCCGCCCCAAGAAT
GGCCGCCATGCGTGGATTTGGCACGACTGCCACAGGCACTACCACAGCATGG
AAGTCTTCACTTACTATGACCTGCTGAGCCTCAACGGCACCAAGGTGGCTGA
GGGCCACAAGGCCAGCTTCTGCCTGGAGGACACTGAGTGTGAGGGAGACATT
CAGAAGAGTTACGAGTGTGCCAACTTTGGAGAACAAGGCATCACCATGGGCT
GCTGGGACATGTACCGTCATGACATTGACTGCCAGTGGATAGACATCACCGA
TGTGCCCCCTGGAGACTACCTGTTCCAGGTTGTCATTAACCCCAACTATGAAG
TGCCAGAATCAGATTTCTCTAACAACATCATGAAGTGCAGGAGCCGCTATGA
TGGCTACCGCATCTGGATGTACAACTGTCACGTAGGTGGAGCCTTCAGTGAG
GAGACAGAACAGAAGTTCGAACACTTCAGTGGACTTCTAAATAACCAGCTCT
CTGTACAGTAA (SEQ ID NO:8)

**Example 5: Expression of human LOX catalytic domain in mammalian cells**

An expression cassette that is used for the expression of a polypeptide including the human LOX catalytic domain was constructed by PCR amplification, using a human LOX cDNA as template (GenBank NM_002317, obtained from Genecopoeia, Germantown, MD). The amplification product, containing sequences encoding the catalytic domain, was cloned into the pSecTag2/Hygro B vector (Invitrogen, Carlsbad, CA), generating the pSecTag2hygro-hLOX MCD (also referred to as phLOXMCD) plasmid. Transcription of this clone with T7 RNA polymerase generates a mRNA encoding a polypeptide containing (in N-terminal to C-terminal order) an Immunoglobulin kappa signal sequence, the human LOX catalytic domain, a *myc* epitope tag and a $His_6$ purification tag. This polypeptide has the following amino acid sequence:

METDTLLLWVLLLWVPGSTGD*AAQPA*GLPDLVADPYYIQASTYVQKMSMYNLR
CAAEENCLASTAYRADVRDYDHRVLLRFPQRVKNQGTSDFLPSRPRYSWEWHS
CHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSCDYGYHRRFACTAH

TQGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVNPSYLVPESDYTNNVVRC
DIRYTGHHAYASGCTISPY*GP*EQKLISEEDL*NSAVD*HHHHHH (SEQ ID NO:9)

The sequences of the signal peptide and *myc* tag are underlined. The italicized sequences represent amino acid sequences encoded in whole or part by vector sequences and restriction sites used in the cloning (AAQP and GP) and a linker sequence (NSAVD).

The DNA sequence encoding this polypeptide (with underlined sequences denoting nucleotides encoding the signal sequence and the *myc* tag, and linker sequences indicated in lower-case type) is:

ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCA
GGTTCCACTGGTGACgcggcccagccggccGGTCTCCCAGACCTGGTGGCCGACCCC
TACTACATCCAGGCGTCCACGTACGTGCAGAAGATGTCCATGTACAACCTGA
GATGCGCGGCGGAGGAAAACTGTCTGGCCAGTACAGCATACAGGGCAGATG
TCAGAGATTATGATCACAGGGTGCTGCTCAGATTTCCCCAAAGAGTGAAAAA
CCAAGGGACATCAGATTTCTTACCCAGCCGACCAAGATATTCCTGGGAATGG
CACAGTTGTCATCAACATTACCACAGTATGGATGAGTTTAGCCACTATGACCT
GCTTGATGCCAACACCCAGAGGAGAGTGGCTGAAGGCCACAAAGCAAGTTTC
TGTCTTGAAGACACATCCTGTGACTATGGCTACCACAGGCGATTTGCATGTAC
TGCACACACACAGGGATTGAGTCCTGGCTGTTATGATACCTATGGTGCAGAC
ATAGACTGCCAGTGGATTGATATTACAGATGTAAAACCTGGAAACTATATCC
TAAAGGTCAGTGTAAACCCCAGCTACCTGGTTCCTGAATCTGACTATACCAAC
AATGTTGTGCGCTGTGACATTCGCTACACAGGACATCATGCGTATGCCTCAGG
CTGCACAATTTCACCGTATgggcccGAACAAAAACTCATCTCAGAAGAGGATCT
GaatagcgccgtcgacCATCATCATCATCATCATTGA (SEQ ID NO:10)

The phLOXMCD expression vector was transfected into HEK293 cells as follows. 7 x $10^5$ cells were plated into a well of a 6-well culture dish and grown at 37°C, 5% $CO_2$ in complete DMEM (Dulbecco's Modified Eagle's Medium + 10% Fetal Bovine Serum+2mM L-glutamine). After overnight growth the cells were transfected with phLOXMCD using Lipofectamine 2000 (Invitrogen, Carlsbad, CA) according to the manufacturer's instructions. Four hours later, the medium was aspirated and replaced with 2 ml complete DMEM, and the transfected cells were grown overnight. Stable cell lines were selected by limiting dilution in complete DMEM (cDMEM) + 0.8 mg/ml Hygromycin B (hygro). Individual clones that survived selection were expanded and screened for expression of the hLOX catalytic domain, as follows. Expansion was achieved by growing cell clones in 6-well culture dishes to 75% confluence. At that point, medium was aspirated and fresh cDMEM + hygro was added. Five days later, the medium was harvested and analyzed directly for the presence of the LOX catalytic domain, as described below. Cells were removed from the surface of the culture dish by adding PBS + 5 mM EDTA to the dish. The detached cell solution was subjected to centrifugation. Approximately 5 x $10^5$ pelleted cells ( out of a total of ~1 x $10^6$) were lysed in 0.1 ml of M-PER mammalian protein extraction reagent (Pierce, Rockford, IL). After a 20 min incubation on ice, the cell lysate was subjected to centrifugation in a table-top centrifuge at 15,000 rpm for 10 min. The soluble fraction (supernatant) was collected and analyzed for the presence of the LOX catalytic domain as described below. The insoluble fraction (pellet) was washed twice in M-PER, resuspended in M-PER and analyzed for the presence of the LOX catalytic domain as described below.

**Example 6: Detection of human LOX catalytic domain by protein immunoblotting**

Samples of medium, soluble fraction, and insoluble fraction from six different clones were assayed by immunoblotting for the presence of the LOX catalytic domain expressed by the phLOXMCD expression vector. For analysis of medium, 150 ul of conditioned medium was mixed with 50 ul of NuPAGE® 4X LDS sample buffer (Invitrogen, Carlsbad, CA), and 20 ul of the resulting mixture was loaded onto a gel (see below). For the soluble and insoluble intracellular fractions, each sample corresponded to 1 x $10^5$ cells. Samples of the intracellular fractions were mixed with NuPAGE® 4X LDS sample buffer (Invitrogen, Carlsbad, CA) and NuPAGE® 10X reducing agent to final concentrations of 1X of both of these reagents, boiled for 5 min, and subjected to electrophoresis on NuPAGE® Novex Bis-Tris gels (4-12% acrylamide). Running buffer was NuPAGE® MOPS buffer (Invitrogen, Carlsbad, CA). At the conclusion of electrophoresis, proteins were transferred out of the gel onto PVDF using an iBlot apparatus (Invitrogen, Carlsbad, CA).

For detection, the blots were blocked with 3% bovine serum albumin (BSA) in PBS + 0.01% Tween for three hours at room temperature. Blots were then incubated for one hour at room temperature with a mouse anti- $His_5$ antibody (Qiagen, Valencia, CA) followed by a one hour incubation at room temperature with a horseradish peroxidase (HRP)-conjugated donkey anti-mouse antibody (Jackson ImmunoResearch, West Grove, PA) and developed with Chemi-Glow® (Alpha Innotech, San Leandro, CA).

The results are shown in Figure 1, for six clones (labeled 23 through 28). The left most panel, showing assays of growth medium, indicates little to no secretion of the catalytic domain, except for a small amount of secreted product in clone 23 (arrow). The secreted protein exhibits an apparent molecular weight of 29 kD, characteristic of unprocessed polypeptide. This could be due to lack of cleavage (or incomplete cleavage) of the signal peptide or to post-translational modification of the secreted polypeptide.

Trichloroacetic acid precipitation of growth medium from HEK293 cells that had been transiently transfected with the phLOXMCD expression vector revealed the presence of insoluble LOX catalytic domain in the growth medium.

Intracellular expression of the catalytic domain was detected in five out of the six clones, in both the soluble and insoluble fractions (Figure 1, center and right panels). In addition, high-molecular weight aggregates were detected in the insoluble intracellular fraction.

Inasmuch as solubility can be an indication of a correctly folded and processed polypeptide, the presence of soluble intracellular polypeptide product indicates the likelihood that properly folded, enzymatically active catalytic domain is being produced in the transfected cells.

In addition to HEK293 cells, expression of the LOX catalytic domain was observed in additional cell types. Transient expression of the phLOXMCD expression vector in CHOk1 cells resulted in intracellular expression of the catalytic domain (detected in a whole-cell lysate), but no secretion of the catalytic domain was detected. Transient transfection of SW620 cells also resulted in intracellular expression without detectable secretion.

**Example 7: Expression of human LOXL2 catalytic domain in mammalian cells**

An expression cassette (Genecopoeia, Germantown, MD) that is used for the expression of a polypeptide including the human LOXL2 catalytic domain was constructed by PCR amplification, using a human LOXL2 cDNA as template. The amplification product, containing sequences encoding the catalytic domain, was cloned into the pSecTag2/Hygro B vector (Invitrogen, Carlsbad, CA), generating the pSecTag2hygro-hLOXL2 MCD (also referred to as phLOXL2MCD) expression vector. Transcription of this clone with T7 RNA polymerase generates a mRNA encoding a polypeptide containing (in N-terminal to C-terminal order) an Immunoglobulin kappa signal sequence, the human LOXL2 catalytic domain, a *myc* epitope tag and a $His_6$ purification tag. This polypeptide has the following amino acid sequence:

METDTLLLWVLLLWVPGSTGD*AAQPARRARRTKL*TAPDLVLNAEMVQQTTYLED
RPMFMLQCAMEENCLSASAAQTDPTTGYRRLLRFSSQIHNNGQSDFRPKNGRHA
WIWHDCHRHYHSMEVFTHYDLLNLNGTKVAEGHKASFCLEDTECEGDIQKNYE
CANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVINPNFEVAESDY
SNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ*SRGGP*E
QKLISEEDL*NSAVD*HHHHHH. (SEQ ID NO: 11)

The sequences of the signal peptide and *myc* tag are underlined. The italicized sequences represent amino acid sequences encoded in whole or part by vector sequences and restriction sites used in the cloning (AAQPARRARRTKL and SRGGP) and a linker sequence (NSAVD).

The DNA sequence encoding this polypeptide (with underlined sequences denoting those encoding the leader and the *myc* tag, and linker sequences indicated in lower-case type) is:

ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTC
CACTGGTGACgcggcccagccggccaggcgcgcgcgccgtacgaagcttACCGCCCCTGACCTGGT
CCTCAATGCGGAGATGGTGCAGCAGACCACCTACCTGGAGGACCGGCCCATG
TTCATGCTGCAGTGTGCCATGGAGGAGAACTGCCTCTCGGCCTCAGCCGCGC
AGACCGACCCCACCACGGGCTACCGCCGGCTCCTGCGCTTCTCCTCCCAGATC
CACAACAATGGCCAGTCCGACTTCCGGCCCAAGAACGGCCGCCACGCGTGGA

TCTGGCACGACTGTCACAGGCACTACCACAGCATGGAGGTGTTCACCCACTA TGACCTGCTGAACCTCAATGGCACCAAGGTGGCAGAGGGCCACAAGGCCAG CTTCTGCTTGGAGGACACAGAATGTGAAGGAGACATCCAGAAGAATTACGAG TGTGCCAACTTCGGCGATCAGGGCATCACCATGGGCTGCTGGGACATGTACC GCCATGACATCGACTGCCAGTGGGTTGACATCACTGACGTGCCCCCTGGAGA CTACCTGTTCCAGGTTGTTATTAACCCCAACTTCGAGGTTGCAGAATCCGATT ACTCCAACAACATCATGAAATGCAGGAGCCGCTATGACGGCCACCGCATCTG GATGTACAACTGCCACATAGGTGGTTCCTTCAGCGAAGAGACGGAAAAAAAG TTTGAGCACTTCAGCGGGCTCTTAAACAACCAGCTGTCCCCGCAGtctcgaggaggg cccGAACAAAAACTCATCTCAGAAGAGGATCTGaatagcgccgtcgacCATCATCATC ATCATCATTGA (SEQ ID NO: 12)

HEK293 cells were transfected with the phLOXL2MCD expression vector, stable cell lines were selected by limiting dilution, and clones were expanded using the same methods as described in Example 5 for the phLOXMCD vector. Medium was collected for analysis, and cells were detached and pelleted as described in Example 5.

**Example 8: Detection of human LOXL2 catalytic domain by protein immunoblotting**

Samples of pelleted cells containing approximately 5 x $10^5$ cells, obtained as described in Example 7, were analyzed by immunoblotting. Cell suspension containing approximately 5 x $10^5$ cells was subjected to centrifugation at 6,000 rpm for 10 min and the supernatant was aspirated. The pellet was resuspended in 100 ul of M-PER lysis buffer, followed by incubation on ice for 20 min. Insoluble cell debris was removed by centrifugation at 15,000 rpm for 20 min, and 75 ul of the supernatant (cleared cell lysate) was removed and mixed with 30 ul of NuPAGE® 4X LDS sample buffer (Invitrogen, Carlsbad, CA) and 10 ul of NuPAGE® 10X reducing agent. The mixture was boiled for 5 min, then placed on ice until application to the gel. Typically, 20 ul of each sample (corresponding to ~1 x $10^5$ cells) was subjected to electrophoresis on NuPAGE® Novex Bis-Tris gels (4-12% acrylamide). Running buffer was NuPAGE® MOPS buffer (Invitrogen, Carlsbad, CA). At the conclusion of electrophoresis, proteins were transferred out of the gel onto PVDF using an iBlot apparatus (Invitrogen, Carlsbad, CA).

For detection, the blots were processed as described in Example 6 for the phLOXMCD expression products.

The results, shown in the left panel of Figure 2, indicate intracellular expression of the LOXL2 catalytic domain in nine different clones. Both monomeric and aggregated forms of the protein were detected, with monomeric forms predominating.

To determine whether the human LOXL2 catalytic domain was secreted, cell clones, obtained as described in Example 7 for the phLOXMCD-transfected cells, were grown in cDMEM + hygro for 90 hours, at which point 15 ul of medium was removed and mixed with 5 ul of 4X LDS sample buffer + reducing agent (NuPAGE®, Invitrogen, Carlsbad, CA), boiled for 5 min, subjected to polyacrylamide gel electrophoresis and analyzed as described above for whole cell lysates. The results, shown in the right panel of Figure 2 show that , in contrast to the human LOX catalytic domain, the human LOXL2 catalytic domain is secreted by HEK293 cells in quantities that are detectable in unconcentrated growth medium.

**Example 9: Expression of murine LOX catalytic domain in mammalian cells**

An expression cassette that is used for the expression of a polypeptide including the murine LOX catalytic domain was constructed by PCR amplification, using a mouse LOX cDNA as template (GenBank BC018439, obtained from Invitrogen, Carlsbad, CA). The amplification product, containing sequences encoding the catalytic domain, was cloned into the pSecTag2/Hygro B vector (Invitrogen, Carlsbad, CA), generating the pSecTag2hygro-mLOX MCD (also referred to as pmLOXMCD) expression vector. Transcription of this clone with T7 RNA polymerase generates a mRNA encoding a polypeptide containing (in N-terminal to C-terminal order) an Immunoglobulin kappa signal sequence, the murine LOX catalytic domain, a *myc* epitope tag and a $His_6$ purification tag. This polypeptide has the following amino acid sequence:

METDTLLLWVLLLWVPGSTGD*AAQPA*GLPDLVPDPYYIQASTYVQKMSMYNLR
CAAEENCLASSAYRADVRDYDHRVLLRFPQRVKNQGTSDFLPSRPRYSWEWHS
CHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSCDYGYHRRFACTAH
TQGLSPGCYDTYAADIDCQWIDITDVQPGNYILKVSVNPSYLVPESDYTNNVVRC
DIRYTGHHAYASGCTISPY*GP*EQKLISEEDL*NSAVD*HHHHHH (SEQ ID NO:13)

The sequences of the signal peptide and *myc* tag are underlined. The italicized sequences represent amino acid sequences encoded in whole or part by vector sequences or restriction sites used in the cloning (AAQP and GP) and a linker sequence (NSAVD).

The DNA sequence encoding this polypeptide (with underlined sequences denoting those encoding the leader and the *myc* tag, and linker sequences indicated in lower-case type) is:

ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTCCACTGGTGACgcggcccagccggccGGTCTCCCGGACCTGGTGCCCGACCCCTACTACATCCAGGCTTCCACGTACGTCCAGAAGATGTCTATGTACAACCTGAGATGCGCTGCGGAAGAAAACTGCCTGGCCAGTTCAGCATATAGGGCGGATGTCAGAGACTATGACCACAGGGTACTGCTACGATTTCCGCAAAGAGTGAAGAACCAAGGGACATCGGACTTCTTACCAAGCCGCCCTCGGTACTCCTGGGAGTGGCACAGCTGTCACCAACATTACCACAGCATGGACGAATTCAGCCACTATGACCTGCTTGATGCCAACACACAGAGGAGAGTGGCTGAAGGCCACAAAGCAAGCTTCTGTCTGGAGGACACGTCCTGTGACTATGGGTACCACAGGCGCTTTGCGTGCACTGCACACACACAGGGATTGAGTCCTGGATGTTATGACACCTATGCGGCAGACATAGACTGCCAGTGGATTGATATTACAGATGTACAACCTGGAAACTACATTCTAAAGGTCAGTGTAAACCCCAGCTACCTGGTGCCTGAATCAGACTACACTAACAATGTTGTACGCTGTGACATTCGCTACACAGGACATCATGCCTATGCCTCAGGCTGCACAATTTCACCGTATgggcccGAACAAAAACTCATCTCAGAAGAGGATCTGaatagcgccgtcgacCATCATCATCATCATCATTGA (SEQ ID NO:14)

HEK293 cells were transfected with the pmLOXMCD expression vector, stable cell lines were selected by limiting dilution, and clones were expanded using the same methods as described in Example 5 for the phLOXMCD vector. Medium was collected for analysis, and cells were detached, pelleted and fractionated into soluble and insoluble fractions, as described in Example 5.

Expression of the murine LOX catalytic domain was assayed by immunoblotting, using the same methods described in Example 6 for the analysis of the human catalytic domain. The results, shown in Figure 3, indicate that the murine LOX catalytic domain is secreted in detectable quantities (left panel), in contrast to the human LOX catalytic domain. The intracellular expression profile of the mLOX catalytic domain is similar to that of the hLOX catalytic domain, with monomeric protein present in both the soluble and insoluble fractions, and aggregates present in the insoluble fraction.

**Example 10: Secretion of human LOX catalytic domain from mammalian cells**

Figure 4 contains a schematic diagram showing the differences in the amino acid sequences of the human (top) and murine (bottom) LOX catalytic domains. As can be seen, the two sequences differ at only four positions. As shown above, and as confirmed in the left panel of Figure 4, using ten-fold concentrated conditioned growth medium (10X CM), the murine LOX catalytic domain (M) was secreted from cells transfected with a vector encoding it; while the human LOX catalytic domain (H) was not secreted. Therefore, if secretion of a human LOX catalytic domain is desired, one can alter any of residues 7, 38, 146, or 160 (numbers refer to the position in the amino acid sequence of the catalytic domain expressed in the phLOXMCD and pmLOXMCD expression vectors disclosed herein), or any combination of these residues, or all four of these residues, from the human sequence to the murine sequence. For example, any, or all, or any combination, of the following amino acid sequence changes can be made: A7P, T38S, G146A, K160Q.

Conversely, if one desires to reduce secretion of a murine LOX catalytic domain, thereby retaining more of this polypeptide intracellularly, changes at residues 7, 38, 146 and 160, from the murine sequence to the human sequence, can be made. Thus, for example, any, or all, or any combination of the following amino acid sequence changes can be made: P7A, S38T, A146G, Q160K.

**Example 11: Expression of murine LOXL2 catalytic domain in mammalian cells**

An expression cassette that is used for the expression of a polypeptide including the murine LOXL2 catalytic domain is constructed by PCR amplification, using a mouse LOXL2 cDNA as template (commercially synthesized based on GenBank NM033325). The amplification product, containing sequences encoding the catalytic domain, is cloned into the pSecTag2/Hygro B vector (Invitrogen, Carlsbad, CA), generating the pSecTag2hygro-mLOXL2 MCD (also referred to as pmLOXL2MCD) expression vector. Transcription of this clone with T7 RNA polymerase generates a mRNA encoding a polypeptide containing (in N-terminal to C-terminal order) an Immunoglobulin kappa signal sequence, the murine LOXL2 catalytic domain, a *myc* epitope tag and a $His_6$ purification tag. This polypeptide has the following amino acid sequence (with the leader sequence and the *myc* tag underlined):

METDTLLLWVLLLWVPGSTGD*AAQPA*TAPDLVLNAEIVQQTAYLEDRPMSLLQC
AMEENCLSASAVHTDPTRGHRRLLRFSSQIHNNGQSDFRPKNGRHAWIWHDCH
RHYHSMEVFTYYDLLSLNGTKVAEGHKASFCLEDTECEGDIQKSYECANFGEQG
ITMGCWDMYRHDIDCQWIDITDVPPGDYLFQVVINPNYEVPESDFSNNIMKCRSR
YDGYRIWMYNCHVGGAFSEETEQKFEHFSGLLNNQLSVQ*GP*EQKLISEEDL*NSAV*
*D*HHHHHH (SEQ ID NO:15)

The sequences of the signal peptide and *myc* tag are underlined. The italicized sequences represent amino acid sequences encoded in whole or part by vector sequences and restriction sites used in the cloning (AAQP and GP) and a linker sequence (NSAVD).

The DNA sequence encoding this polypeptide (with underlined sequences denoting those encoding the leader and the myc tag, and linker sequences indicated in lower-case type) is:

ATGGAGACAGACACACTCCTGCTATGGGTACTGCTGCTCTGGGTTCCAGGTTC
CACTGGTGACgcggcccagccggccACTGCACCTGACCTGGTGCTTAATGCTGAGAT
TGTCCAGCAGACTGCCTACCTGGAGGACAGGCCCATGTCCTTGCTGCAGTGT
GCCATGGAGGAGAACTGCCTCTCCGCCTCCGCTGTGCACACCGACCCCACCA
GAGGCCACCGGCGCCTTTTACGCTTCTCCTCCCAGATCCACAACAATGGCCA
GTCTGACTTCCGCCCCAAGAATGGCCGCCATGCGTGGATTTGGCACGACTGC
CACAGGCACTACCACAGCATGGAAGTCTTCACTTACTATGACCTGCTGAGCC
TCAACGGCACCAAGGTGGCTGAGGGCCACAAGGCCAGCTTCTGCCTGGAGGA
CACTGAGTGTGAGGGAGACATTCAGAAGAGTTACGAGTGTGCCAACTTTGGA
GAACAAGGCATCACCATGGGCTGCTGGGACATGTACCGTCATGACATTGACT
GCCAGTGGATAGACATCACCGATGTGCCCCCTGGAGACTACCTGTTCCAGGT
TGTCATTAACCCCAACTATGAAGTGCCAGAATCAGATTTCTCTAACAACATCA
TGAAGTGCAGGAGCCGCTATGATGGCTACCGCATCTGGATGTACAACTGTCA

CGTAGGTGGAGCCTTCAGTGAGGAGACAGAACAGAAGTTCGAACACTTCAGT
GGACTTCTAAATAACCAGCTCTCTGTACAGgggcccGAACAAAAACTCATCTCA
GAAGAGGATCTGaatagcgccgtcgacCATCATCATCATCATCATTGA
(SEQ ID NO: 16)

HEK293 cells are transfected with the pmLOXL2MCD expression vector, stable cell lines are selected by limiting dilution, and clones are expanded using the same methods as described in Example 5 for the phLOXMCD vector. Medium is collected for analysis, and cells are detached, pelleted and fractionated into soluble and insoluble fractions, as described in Example 5.

Expression of the murine LOXL2-derived polypeptide is assayed by immunoblotting, using the same methods described in Example 6 for the analysis of the human catalytic domain.

**Example 12: Generation of enzymatically active human LOXL2 catalytic domain from transiently transfected cells**

293F cells (a subclone of the HEK293 cell line adapted for growth in suspension culture, Invitrogen, Carlsbad, CA) were grown in spinner flasks, according to the manufacturer's protocol. Once the culture had reached a density of 0.8 - 1.2 x $10^6$ cells/ml, the cell culture was transferred to a CB22 Bag (WAVE, GE Health, Piscataway, NJ). Eight liters of cell culture was transfected with 8 mg of the phLOXL2 vector, using the 293fectin reagent (Invitrogen, Carlsbad, CA). Transfected cells were grown in the CB22 bag for three days, after which the cell culture was subjected to centrifugation in an Allegra 6R benchtop centrifuge (Beckman Coulter) in a swinging bucket rotor at 3,000 rpm for 10 min. The supernatant was collected and filtered through a 0.22 mm PES membrane.

The LOXL2-derived polypeptide was purified from the cell culture supernatant on a Ni-Sepharose resin (GE Healthcare, Piscataway, NJ). The resin was equilibrated with 0.1 M Tris-Cl, pH 8.0. Conditioned medium (*i.e.*, the cell culture supernatant) was loaded onto the equilibrated resin; then the column was washed with 10 column volumes of 0.1 M Tris-Cl, pH 8.0, 0.25 M NaCl, 0.02 M imidazole. His-tagged catalytic domain was eluted with five column volumes of 0.1 M Tris-Cl, pH 8.0, 0.15 M NaCl, 0.3 M imidazole. The eluate was concentrated on an Amicon Ultra 15 10kD MWCL (Millipore, Billerica, MA) and the concentrated material was dialyzed against 0.05 M borate, pH 8.0 overnight at 4°C. Samples were analyzed on SDS polyacrylamide gels (4-12% gradient Bis-Tris gels, Invitrogen, Carlsbad, CA) under reducing conditions.

**Example 13: Enzymatic activity of the catalytic domain of human LOXL2**

A polypeptide containing the catalytic domain of human LOXL2 was produced as described in Example 12 above. Enzymatic activity was assessed using a biochemical assay that couples the production of peroxide (liberated by LOXL2 after deamination of 1,5-diaminopentane) to the HRP-catalyzed conversion of Amplex® red to a fluorescent product (resorufin). Palamakumbura et *al.* (2002) *Anal. Biochem.* **300:**245-251. Reaction plates were obtained from Corning. Amplex® Red reagent was from Invitrogen (Carlsbad, CA). Horseradish peroxidase (HRP), 1,5-diaminopentane, and antifoam were from Sigma (St. Louis, MO). All other reagents were of the highest quality available.

Enzyme mixture was assembled by adding 10 uL of pooled peak fractions (see Example 12) to 40 uL assay solution (62.5 mM sodium borate pH 8.0, 5 units/mL HRP, 10 ppm antifoam). Substrate solution contained 50 mM sodium borate, 100 uM Amplex® red reagent, 20 mM 1,5-diaminopentane, 10 ppm antifoam. The reaction was started by mixing 50 ul of enzyme mixture with 50 ul of substrate solution. One reaction also contained 2 mM of βAPN (beta-aminoproprionitrile, an inhibitor of the catalytic activity of lysyl oxidase and LOXL2). Reaction mixtures were incubated, at 37°C, in a Molecular Devices M5 plate reader configured to measure fluorescence (ex=544 nm, em=590 nm) in kinetics mode for 1 hour. Data were recorded as the slope of the fluorescence response to time.

Figure 5 shows the results of this assay, in the form of a time course of resorufin production, expressed in relative fluorescent units (RFU). The human LOXL2-derived polypeptide exhibited measurable enzymatic activity, and the activity was inhibited by βAPN. Accordingly, the polypeptide comprises an enzymatically active catalytic domain of LOXL2.

## CLAIMS

That which is claimed is:

**1.** A polypeptide comprising the amino acid sequence of the catalytic domain of human LOX (SEQ ID NO:1), wherein the polypeptide does not contain sequences from human LOX that lie outside its catalytic domain.

**2.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 1.

**3.** The polynucleotide of claim 2 having a nucleotide sequence as set forth in SEQ ID NO:2.

**4.** A polypeptide comprising the amino acid sequence of the catalytic domain of human LOXL2 (SEQ ID NO:3), wherein the polypeptide does not contain sequences from human LOX2 that lie outside its catalytic domain.

**5.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 4.

**6.** The polynucleotide of claim 5 having a nucleotide sequence as set forth in SEQ ID NO:4.

**7.** A polypeptide comprising the amino acid sequence of the catalytic domain of murine LOX (SEQ ID NO:5), wherein the polypeptide does not contain sequences from murine LOX that lie outside its catalytic domain.

**8.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 7.

**9.** The polynucleotide of claim 8 having a nucleotide sequence as set forth in SEQ ID NO:6.

**10.** A polypeptide comprising the amino acid sequence of the catalytic domain of murine LOXL2 (SEQ ID NO:7), wherein the polypeptide does not contain sequences from murine LOXL2 that lie outside its catalytic domain.

**11.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 10.

**12.** The polynucleotide of claim 11 having a nucleotide sequence as set forth in SEQ ID NO:8.

**13.** A polypeptide comprising a signal sequence, the catalytic domain of human LOX, an epitope tag and a purification tag, wherein the polypeptide does not contain sequences from human LOX that lie outside its catalytic domain.

**14.** The polypeptide of claim 13, wherein the signal sequence is an immunoglobulin kappa signal sequence.

**15.** The polypeptide of claim 13, wherein the epitope tag is a *myc* tag.

**16.** The polypeptide of claim 13, wherein the purification tag is a $His_6$ tag.

**17.** The polypeptide of claim 13 having an amino acid sequence as set forth in SEQ ID NO:9.

**18.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 13.

**19.** The polynucleotide of claim 18 having a nucleotide sequence as set forth in SEQ ID NO:10.

**20.** An expression vector comprising the polynucleotide of claim 18.

**21.** An expression vector comprising the polynucleotide of claim 19.

**22.** A polypeptide comprising a signal sequence, the catalytic domain of human LOXL2, an epitope tag and a purification tag, wherein the polypeptide does not contain sequences from human LOXL2 that lie outside its catalytic domain.

**23.** The polypeptide of claim 22, wherein the signal sequence is an immunoglobulin kappa signal sequence.

**24.** The polypeptide of claim 22, wherein the epitope tag is a *myc* tag.

**25.** The polypeptide of claim 22, wherein the purification tag is a $His_6$ tag.

**26.** The polypeptide of claim 22 having an amino acid sequence as set forth in SEQ ID NO:11.

**27.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 22.

**28.** The polynucleotide of claim 27 having a nucleotide sequence as set forth in SEQ ID NO:12.

**29.** An expression vector comprising the polynucleotide of claim 27.

**30.** An expression vector comprising the polynucleotide of claim 28.

**31.** A polypeptide comprising a signal sequence, the catalytic domain of murine LOX, an epitope tag and a purification tag, wherein the polypeptide does not contain sequences from murine LOX that lie outside its catalytic domain.

**32.** The polypeptide of claim 31, wherein the signal sequence is an immunoglobulin kappa signal sequence.

**33.** The polypeptide of claim 31, wherein the epitope tag is a *myc* tag.

**34.** The polypeptide of claim 31, wherein the purification tag is a $His_6$ tag.

**35.** The polypeptide of claim 31 having an amino acid sequence as set forth in SEQ ID NO:13.

**36.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 31.

**37.** The polynucleotide of claim 36 having a nucleotide sequence as set forth in SEQ ID NO:14.

**38.** An expression vector comprising the polynucleotide of claim 36.

**39.** An expression vector comprising the polynucleotide of claim 37.

**40.** A polypeptide comprising a signal sequence, the catalytic domain of murine LOXL2, an epitope tag and a purification tag, wherein the polypeptide does not contain sequences from murine LOXL2 that lie outside its catalytic domain.

**41.** The polypeptide of claim 40, wherein the signal sequence is an immunoglobulin kappa signal sequence.

**42.** The polypeptide of claim 40, wherein the epitope tag is a *myc* tag.

**43.** The polypeptide of claim 40, wherein the purification tag is a $His_6$ tag.

**44.** The polypeptide of claim 40 having an amino acid sequence as set forth in SEQ ID NO:15.

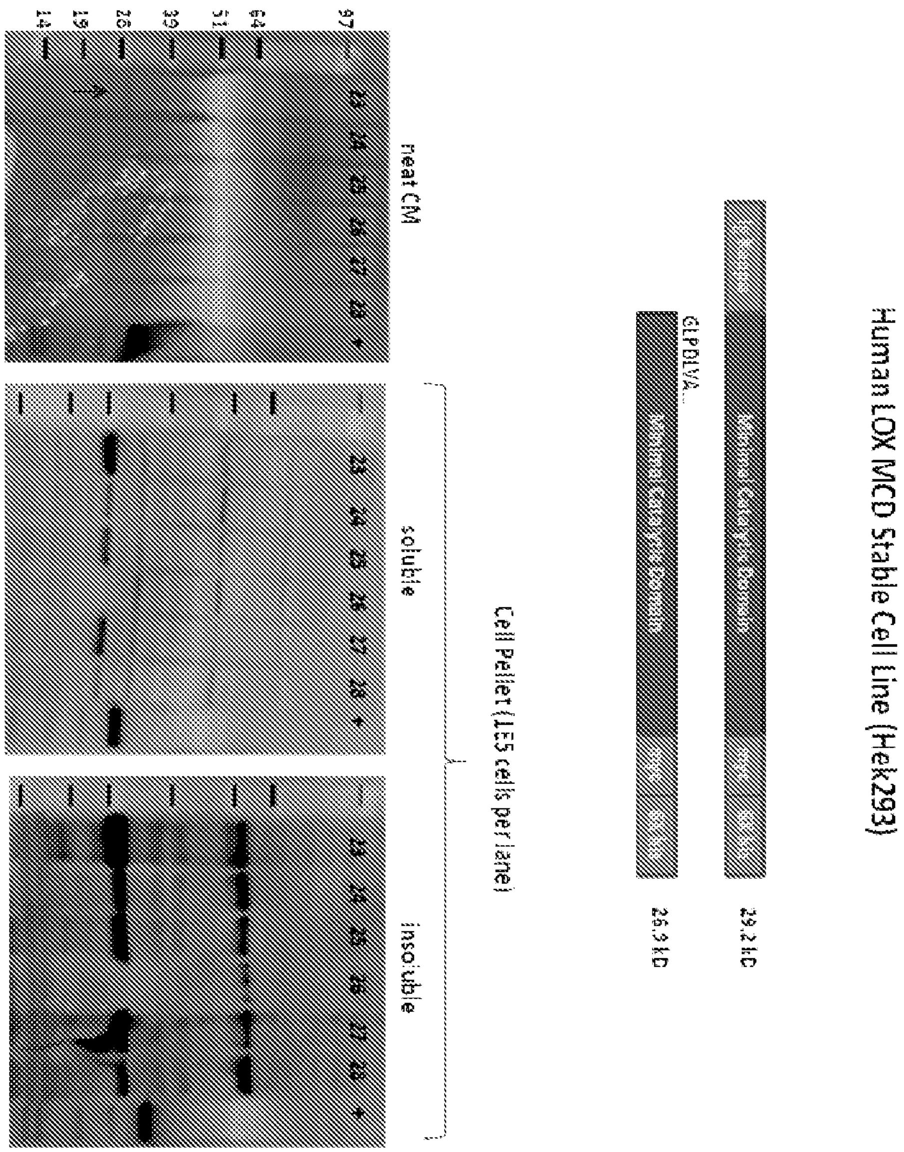
**45.** A polynucleotide comprising a nucleotide sequence encoding the polypeptide of claim 40.

**46.** The polynucleotide of claim 45 having a nucleotide sequence as set forth in SEQ ID NO:16.

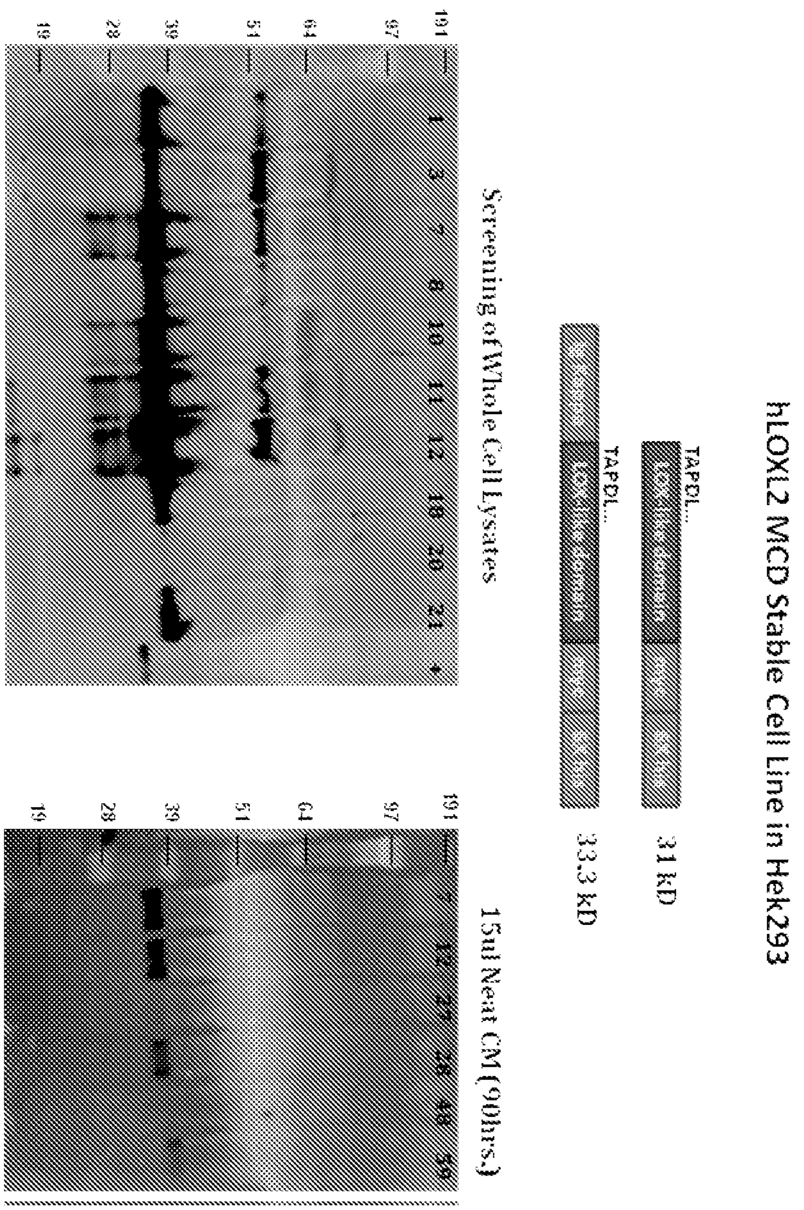
**47.** An expression vector comprising the polynucleotide of claim 45.

**48.** An expression vector comprising the polynucleotide of claim 46.

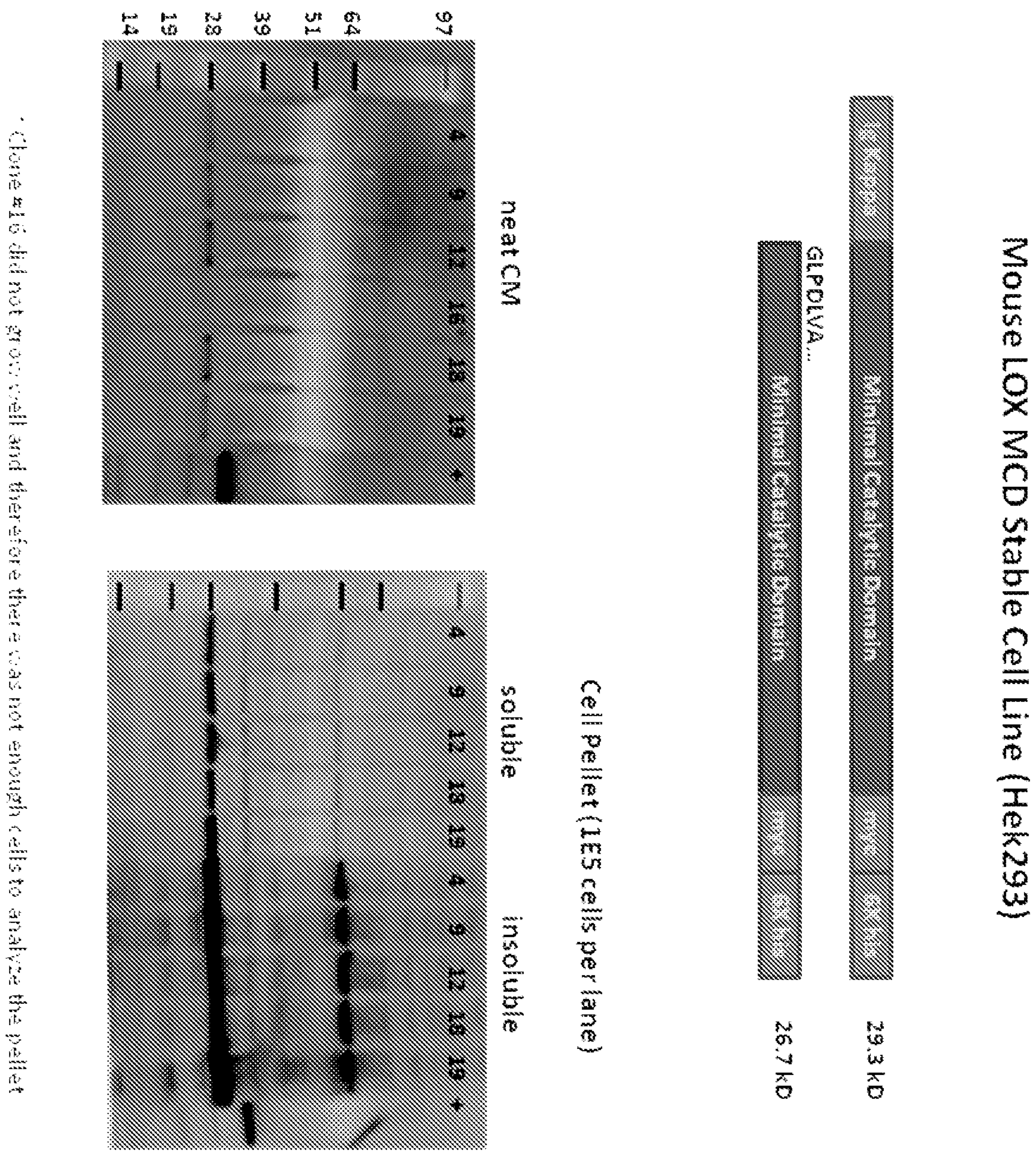
# FIGURE 1


Human LOX MCD Stable Cell Line (Hek293)
neat CM
soluble
insoluble
Cell Pellet (1E5 cells per lane)
97
64
51
39
28
19
14
23 24 25 26 27 28 +
GLPDLVA...
29.2kD
26.3kD

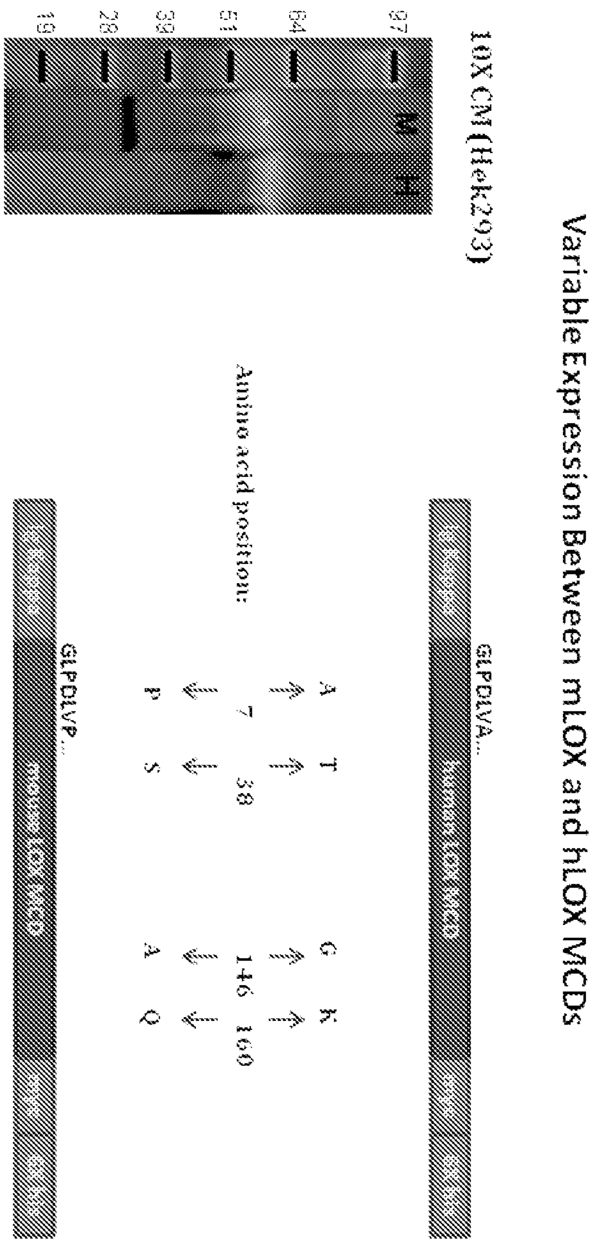
# FIGURE 2


hLOXL2 MCD Stable Cell Line in Hek293
TAPDL...
TAPDL...
31 kD
33.3 kD
Screening of Whole Cell Lysates
1 3 7 8 10 11 12 18 20 21 +
191 97 64 51 39 28 19
15ul Neat CM (90hrs.)
7 12 27 28 48 59
191 97 64 51 39 28 19

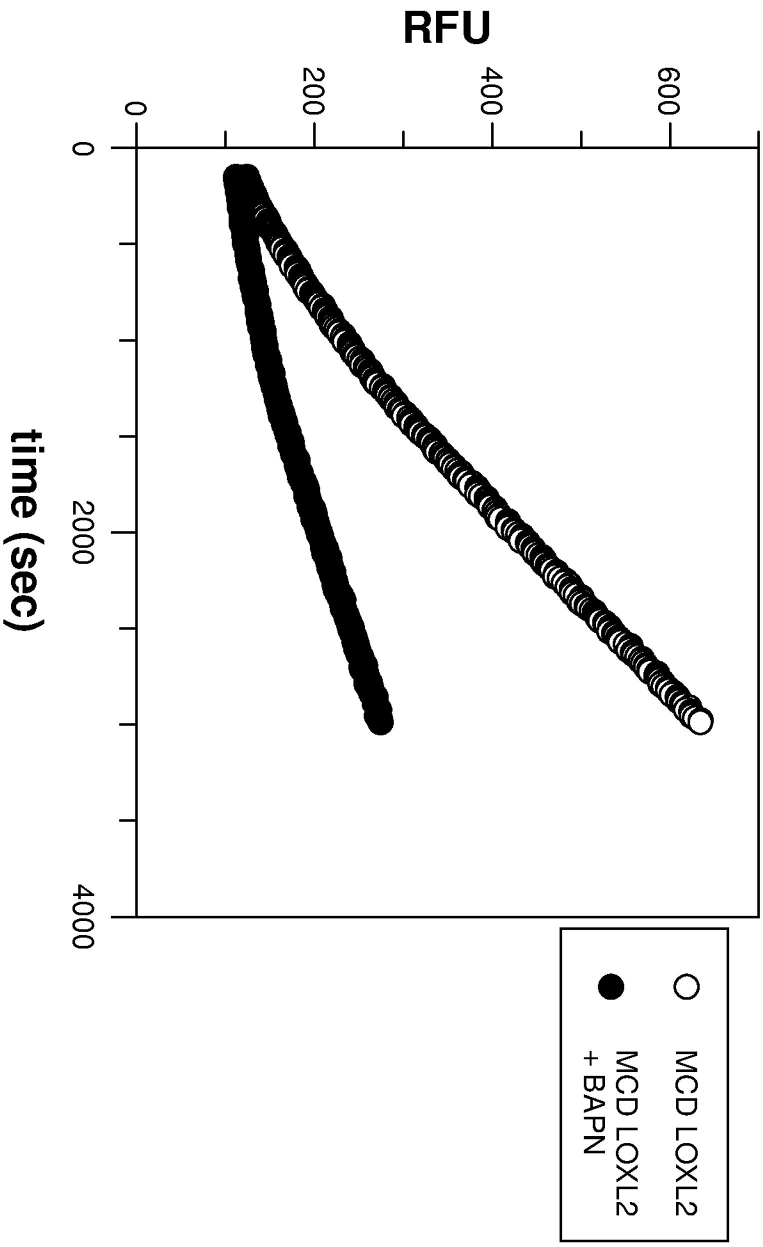
# FIGURE 3


Mouse LOX MCD Stable Cell Line (Hek293)
Minimal Catalytic Domain
myc
6X his
29.3 kD
GLPDLVA...
Minimal Catalytic Domain
myc
6X his
26.7 kD
neat CM
Cell Pellet (1E5 cells per lane)
soluble
insoluble
97
64
51
39
28
19
14
4 9 12 16* 18 19 +
4 9 12 18 19 4 9 12 18 19 +
* Clone #16 did not grow well and therefore there was not enough cells to analyze the pellet

# FIGURE 4


Variable Expression Between mLOX and hLOX MCDs
10X CM (Hek293)
M
H
97
64
51
39
28
19
GLPDLVA...
human LOX MCD
A
T
G
K
7
38
146
160
P
S
A
Q
Amino acid position:
GLPDLVP...
mouse LOX MCD

# FIGURE 5



# FIGURE 6

```
hLOX    GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQRVK 60
hLOXL1  GLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVLLRFPQRVK 60
mLOX    GLPDLVPDPYYIQASTYVQKMSMYNLRCAAEENCLASSAYRADVRDYDHRVLLRFPQRVK 60
hLOXL2  TAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTDPT-TGYRRLLRFSSQIH 59
mLOXL2  TAPDLVLNAEIVQQTAYLEDRPMSLLQCAMEENCLSASAVHTDPT-RGHRRLLRFSSQIH 59
hLOXL3  TASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWP-YGHRRLLRFSSQIH 59
hLOXL4  SAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWP-YGYRRLLRFSTQIY 59
          .**: ..  :* ::*::    :  * ** **:**: :*    :     . * ****. ::

hLOX    NQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSC 120
hLOXL1  NQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKASFCLEDSTC 120
mLOX    NQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSC 120
hLOXL2  NNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLN-GTKVAEGHKASFCLEDTEC 118
mLOXL2  NNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTYYDLLSLN-GTKVAEGHKASFCLEDTEC 118
hLOXL3  NLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKASFCLEDTEC 118
hLOXL4  NLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLN-GSKVAEGHKASFCLEDTNC 118
        * * :** *.  * :* **.** ****:: *::**:*       :*************: *

hLOX    DYGYHRRFACTAH-TQGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVNPSYLVPES 179
hLOXL1  DFGNLKRYACTSH-TQGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVNPKYIVLES 179
mLOX    DYGYHRRFACTAH-TQGLSPGCYDTYAADIDCQWIDITDVQPGNYILKVSVNPSYLVPES 179
hLOXL2  EGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVINPNFEVAES 178
mLOXL2  EGDIQKSYECANFGEQGITMGCWDMYRHDIDCQWIDITDVPPGDYLFQVVINPNYEVPES 178
hLOXL3  QEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAES 178
hLOXL4  PTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAES 178
          .  : : *: .  **:: **:* *  ******:***** **:*:::* :** : * **

hLOX    DYTNNVVRCDIRYTGHHAYASGCTISPY----------------------- 207
hLOXL1  DFTNNVVRCNIHYTGRYVSATNCKIVQS----------------------- 207
mLOX    DYTNNVVRCDIRYTGHHAYASGCTISPY----------------------- 207
hLOXL2  DYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ 229
mLOXL2  DFSNNIMKCRSRYDGYRIWMYNCHVGGAFSEETEQKFEHFSGLLNNQLSVQ 229
hLOXL3  DFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII-- 227
hLOXL4  DFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI--- 226
        *::** ::*  :* *      .*

hLOX    (SEQ ID NO:1)
hLOXL1  (SEQ ID NO:17)
mLOX    (SEQ ID NO:5)
hLOXL2  (SEQ ID NO:3)
mLOXL2  (SEQ ID NO:7)
hLOXL3  (SEQ ID NO:18)
hLOXL4  (SEQ ID NO:19)
```

# FIGURE 7

```
hLOX      GLPDLVADPYYIQASTYVQKMSMYNLRCAAEENCLASTAYRADVRDYDHRVLLRFPQRVK 60
hLOXL1    GLPDLVPDPNYVQASTYVQRAHLYSLRCAAEEKCLASTAYAPEATDYDVRVLLRFPQRVK 60
hLOXL2    TAPDLVLNAEMVQQTTYLEDRPMFMLQCAMEENCLSASAAQTDPT-TGYRRLLRFSSQIH 59
hLOXL3    TASDLLLHSALVQETAYIEDRPLHMLYCAAEENCLASSARSANWP-YGHRRLLRFSSQIH 59
hLOXL4    SAPDLVMNAQLVQETAYLEDRPLSQLYCAHEENCLSKSADHMDWP-YGYRRLLRFSTQIY 59
            .**: ..  :* ::*::   :  * ** **:**: :*   :    . * ****. ::

hLOX      NQGTSDFLPSRPRYSWEWHSCHQHYHSMDEFSHYDLLDANTQRRVAEGHKASFCLEDTSC 120
hLOXL1    NQGTADFLPNRPRHTWEWHSCHQHYHSMDEFSHYDLLDAATGKKVAEGHKASFCLEDSTC 120
hLOXL2    NNGQSDFRPKNGRHAWIWHDCHRHYHSMEVFTHYDLLNLN-GTKVAEGHKASFCLEDTEC 118
hLOXL3    NLGRADFRPKAGRHSWVWHECHGHYHSMDIFTHYDILTPN-GTKVAEGHKASFCLEDTEC 118
hLOXL4    NLGRTDFRPKTGRDSWVWHQCHRHYHSIEVFTHYDLLTLN-GSKVAEGHKASFCLEDTNC 118
          * * :** *.  * :* **.** ****:: *:***:*      :*************: *

hLOX      DYGYHRRFACTAH-TQGLSPGCYDTYGADIDCQWIDITDVKPGNYILKVSVNPSYLVPES 179
hLOXL1    DFGNLKRYACTSH-TQGLSPGCYDTYNADIDCQWIDITDVQPGNYILKVHVNPKYIVLES 179
hLOXL2    EGDIQKNYECANFGDQGITMGCWDMYRHDIDCQWVDITDVPPGDYLFQVVINPNFEVAES 178
hLOXL3    QEDVSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVVINPNFEVAES 178
hLOXL4    PTGLQRRYACANFGEQGVTVGCWDTYRHDIDCQWVDITDVGPGNYIFQVIVNPHYEVAES 178
            .  :.: *: .  **:: **:* *  ******:***** **:*:::* :** : * **

hLOX      DYTNNVVRCDIRYTGHHAYASGCTISPY----------------------- 207
hLOXL1    DFTNNVVRCNIHYTGRYVSATNCKIVQS----------------------- 207
hLOXL2    DYSNNIMKCRSRYDGHRIWMYNCHIGGSFSEETEKKFEHFSGLLNNQLSPQ 229
hLOXL3    DFTNNAMKCNCKYDGHRIWVHNCHIGDAFSEEANRRFERYPGQTSNQII-- 227
hLOXL4    DFSNNMLQCRCKYDGHRVWLHNCHTGNSYPANAELSLEQEQRLRNNLI--- 226
          *::** ::*  :* *:     .*
```

```
hLOX      (SEQ ID NO:1)
hLOXL1    (SEQ ID NO:17)
hLOXL2    (SEQ ID NO:3)
hLOXL3    (SEQ ID NO:18)
hLOXL4    (SEQ ID NO:19)
```