FIGURE 1

MERPLCSHLC SCLAMLALLS PLSLAQYDSW PHYPEYFQQP APEYHQPQAP ANVAKIQLRL 60
SIGNAL PEPTIDE

AGQKRKHSEG RVEVYYDGQW GTVCDDDFSI HAAHVVCREL GYVEAKSWTA SSSYGKGEGP 120
SRCR1

IWLDNLHCTG NEATLAACTS NGWGVTDCKH TEDVGVVCSD KRIPGFKFDN SLINQIENLN 180

IQVEDIRIRA ILSTYRKRTP VMEGYVEVKE GKTWKQICDK HWTAKNSRVV CGMFGFPGER 240

TYNTKVYKMF ASRRKQRYWP FSMDCTGTEA HISSCKLGPQ VSLDPMKNVT CENGLPAVVS 300
SRCR2

CVPGQVFSPD GPSRFRKAYK PEQPLVRLRG GAYIGEGRVE VLKNGEWGTV CDDKWDLVSA 360

SVVCRELGFG SAKEAVTGSR LGQGIGPIHL NEIQCTGNEK SIIDCKFNAE SQGCNHEEDA 420
SRCR3

GVRCNTPAMG LQKKLRLNGG RNPYEGRVEV LVERNGSLVW GMVCGQNWGI VEAMVVCRQL 480

GLGFASNAFQ ETWYWHGDVN SNKVVMSGVK CSGTELSLAH CRHDGEDVAC PQGGVQYGAG 540
SRCR4

VACSETAPDL VLNAEMVQQT TYLEDRPMFM LQCAMEENCL SASAAQTDPT TGYRRLLRFS 600
CATALYTIC DOMAIN

SQIHNNGQSD FRPKNGRHAW IWHDCHRHYH SMEVFTHYDL LNLNGTKVAE GHKASFCLED 660

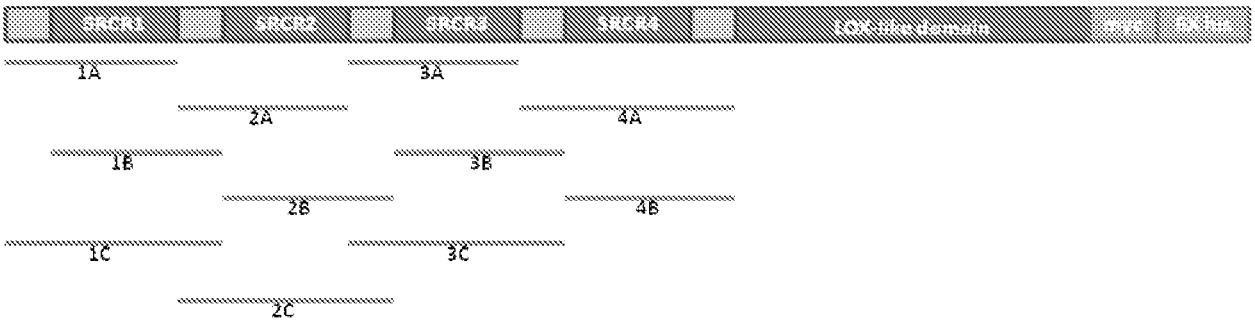
TECEGDIQKN YECANFGDQG ITMGCWDMYR HDIDCQWVDI TDVPPGDYLF QVVINPNFEV 720

AESDYSNNIM KCRSRYDGHR IWMYNCHIGG SFSEETEKKF EHFSGLLNNQ LSPQ 774

SEQ ID NO:1

FIGURE 2

A



B

SRCR1A (aa1-159)

MERPLCSHLCSCLAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPQAPANVAKIQLRLAGQK
RKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGPIWLDNLHC
TGNEATLAACTSNGWGVTDCKHTEDVGVVCS (SEQ ID NO:14)

SRCR1B (aa58-187)
LRLAGQKRKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGPI
WLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLNIQVED
IR (SEQ ID NO:15)

SRCR1C (aa1-187)
MERPLCSHLCSCLAMLALLSPLSLAQYDSWPHYPEYFQQPAPEYHQPQAPANVAKIQLRLAGQK
RKHSEGRVEVYYDGQWGTVCDDDFSIHAAHVVCRELGYVEAKSWTASSSYGKGEGPIWLDNLHC
TGNEATLAACTSNGWGVTDCKHTEDVGVVCSDKRIPGFKFDNSLINQIENLNIQVEDIR
(SEQ ID NO:16)

SRCR2A (aa160-302)
DKRIPGFKFDNSLINQIENLNIQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWT
AKNSRVVCGMFGFPGERTYNTKVYKMFASRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMK
NVTCENGLPAVVSCV (SEQ ID NO:17)

FIGURE 2 (CON'T)

B (CON'T)

SRCR2B (aa188-324)
IRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWTAKNSRVVCGMFGFPGERTYNTKVYKMFA
SRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMKNVTCENGLPAVVSCVPGQVFSPDGPSRF
RKAYKPEQP (SEQ ID NO:18)

SRCR2C (aa160-324)
DKRIPGFKFDNSLINQIENLNIQVEDIRIRAILSTYRKRTPVMEGYVEVKEGKTWKQICDKHWT
AKNSRVVCGMFGFPGERTYNTKVYKMFASRRKQRYWPFSMDCTGTEAHISSCKLGPQVSLDPMK
NVTCENGLPAVVSCVPGQVFSPDGPSRFRKAYKPEQP (SEQ ID NO:19)

SRCR3A (aa303-425)
PGQVFSPDGPSRFRKAYKPEQPLVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRE
LGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNAESQGCNHEEDAGVRCN
(SEQ ID NO:20)

SRCR3B (aa325-434)
LVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRELGFGSAKEAVTGSRLGQGIGPI
HLNEIQCTGNEKSIIDCKFNAESQGCNHEEDAGVRCNTPAMGLQKK (SEQ ID NO:21)

SRCR3C (303-434)
PGQVFSPDGPSRFRKAYKPEQPLVRLRGGAYIGEGRVEVLKNGEWGTVCDDKWDLVSASVVCRE
LGFGSAKEAVTGSRLGQGIGPIHLNEIQCTGNEKSIIDCKFNAESQGCNHEEDAGVRCNTPAMG
LQKK (SEQ ID NO:22)

SRCR4A (aa426-547)
TPAMGLQKKLRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAF
QETWYWHGDVNSNKVVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQYGAGVACSETA (SEQ
ID NO:23)

SRCR4B (435-547)
LRLNGGRNPYEGRVEVLVERNGSLVWGMVCGQNWGIVEAMVVCRQLGLGFASNAFQETWYWHGD
VNSNKVVMSGVKCSGTELSLAHCRHDGEDVACPQGGVQYGAGVACSETA (SEQ ID NO:24)

FIGURE 3

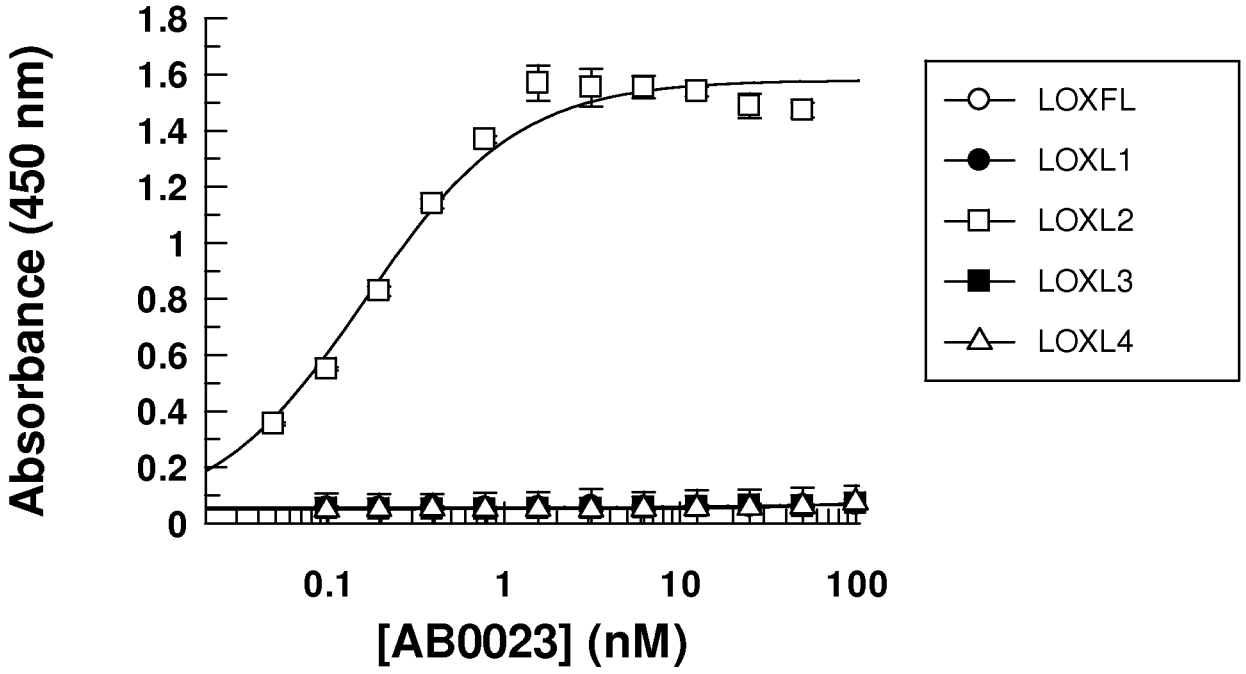

Absorbance (450 nm)
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0.1
1
10
100
[AB0023] (nM)
LOXFL
LOXL1
LOXL2
LOXL3
LOXL4

FIGURE 4

Alignment of SRCR4 Domain of Human LOXL2, LOXL3, and LOXL4

```
LOXL2    LRLNGGRNPY EGRVEVLVER NGSLVWGMVC GQNWGIVEAM VVCRQLGLGF ASNAFQETWY
LOXL3    IRLSGGRSQH EGRVEVQIGG PGPLRWGLIC GDDWGTLEAM VACRQLGLGY ANHGLQETWY
LOXL4    VRLAGGRIPE EGLLEVQVEV NGVPRWGSVC SENWGLTEAM VACRQLGLGF AIHAYKETWF

LOXL2    WHGDVNSNKV VMSGVKCSGT ELSLAHCRHD GEDVACPQGG VQYGAGVACS (SEQ ID NO:35)
LOXL3    WDSG-NITEV VMSGVRCTGT ELSLDQCAHH GTHITCKRTG TRFTAGVICS (SEQ ID NO:36)
LOXL4    WSGTPRAQEV VMSGVRCSGT ELALQQCQRH GP-VHCSHGG GRFLAGVSCM (SEQ ID NO:37)
```

FIGURE 5

```
                                                                  *
H:  PDLVLNAEMV QQTTYLEDRP MFMLQCAMEE NCLSASAAQT DPTTGYRRLL RFSSQIHNNG
M:  PDLVLNAEIV QQTAYLEDRP MSLLQCAMEE NCLSASAVHT DPTRGHRRLL RFSSQIHNNG
R:  PDLVLNAEIV QQTAYLEDRP MALLQCAMEE NCLSASAVHT DPTRGHRRLL RFSSQIHNNG
C:  PDLVLNAEMV QQTTYLEDRP MFMLQCAMEE NCLSASAAQT NPTTGYRRLL RFSSQIHNNG

H:  QSDFRPKNGR HAWIWHDCHR HYHSMEVFTH YDLLNLNGTK VAEGHKASFC LEDTECEGDI
M:  QSDFRPKNGR HAWIWHDCHR HYHSMEVFTY YDLLSLNGTK VAEGHKASFC LEDTECEGDI
R:  QSDFRPKNGR HAWIWHDCHR HYHSMEVFTY YDLLSLNGTK VAEGHKASFC LEDTECEGDI
C:  QSDFRPKNGR HAWIWHDCHR HYHSMEVFTH YDLLNLNGTK VAEGHKASFC LEDTECEGDI

H:  QKNYECANFG DQGITMGCWD MYRHDIDCQW VDITDVPPGD YLFQVVINPN FEVAESDYSN
M:  QKSYECANFG EQGITMGCWD MYRHDIDCQW IDITDVPPGD YLFQVVINPN YEVPESDFSN
R:  QKSYECANFG EQGITMGCWD MYRHDIDCQW IDITDVPPGD YLFQVVINPN YEVPESDFSN
C:  QKNYECANFG DQGITMGCWD MYRHDIDCQW IDITDVPPGD YLFQVVINPN FEVAESDYSN

                 *
H:  NIMKCRSRYD GHRIWMYNCH IGGSFSEETE KKFEHFSGLL NNQLSPQ (SEQ ID NO:38)
M:  NIMKCRSRYD GYRIWMYNCH VGGAFSEETE QKFEHFSGLL NNQLSVQ (SEQ ID NO:39)
R:  NIMKCRSRYD GYRIWMYNCH VGGAFSEETE QKFEHFSGLL NNQLSVQ (SEQ ID NO:40)
C:  NIMKCRSRYD GHRIWMYNCH IGGSFSEETE KKFEHFSGLL NNQLSPQ (SEQ ID NO:41)
```

FIGURE 6

AB0023 V_H sequence:

MEWSRVFIFLLSVTAGVHSQVQLQQSGAELVRPGTSVKVSCKASGYAFTYYLIEWVKQ
RPGQGLEWIGVINPGSGGTNYNEKFKGKATLTADKSSSTAYMQLSSLTSDDSAVYFCAR
NWMNFDYWGQGTTLTVSS (SEQ ID NO:42)

AB0023 V_L sequence:

MRCLAEFLGLLVLWIPGAIGDIVMTQAAPSVSVTPGESVSISCRSSKSLLHSNGNTYLYW
FLQRPGQSPQFLIYRMSNLASGVPDRFSGSGSGTAFTLRISRVEAEDVGVYYCMQHLEYP
YTFGGGTKLEIK (SEQ ID NO:43)

AB0024 V_H sequence:

MGWSLILLFLVAVATRVHSQVQLVQSGAEVKKPGASVKVSCKASGYAFTYYLIEWVRQ
APGQGLEWIGVINPGSGGTNYNEKFKGRATITADKSTSTAYMELSSLRSEDTAVYFCAR
NWMNFDYWGQGTTVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVS
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTKTYTCNVDHKPSNTKVDKRVE
SKYGPPCPPCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPEVQFNWYV
DGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEKTISK
AKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV
LDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK (SEQ ID
NO:44)

AB0024 V_L sequence:

MRVPAQLLGLLLLWLPGARCDIVMTQTPLSLSVTPGQPASISCRSSKSLLHSNGNTYLY
WFLQKPGQSPQFLIYRMSNLASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQHLE
YPYTFGGGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDN
ALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNR
GEC (SEQ ID NO:45)