Lectin-like oxidized low-density lipoprotein receptor (LOX-1) is a recently identified receptor for oxidized low-density lipoprotein, one of the major atherogenic substances. Although LOX-1 was reported to be expressed abundantly in endothelial cells, including atheromatous lesions, the regulation of LOX-1 gene has not yet been clarified. In the present study, we isolated the rat LOX-1 gene and investigated the regulation of gene expression. The rat LOX-1 gene was encoded by a single copy gene spanning over 19 kilobases and consisted of eight exons. exon boundaries correlated well with the functional domain boundaries of the receptor protein. The promoter region contained putative TATA and CAAT boxes and multiple cis-elements such as NF-κB, AP-1 and AP-2 sites, and a shear stress response element. Northern blot analysis revealed that LOX-1 gene expression was up-regulated 9-fold by shear stress, 21-fold by lipopolysaccharide, and 4-fold by tumor necrosis factor-α, in cultured vascular endothelial cells. LOX-1 was also expressed in macrophages but not in vascular smooth muscle cells. These data provide important information for elucidating the molecular mechanisms of LOX-1 gene regulation and suggest a role for LOX-1 in the pathophysiology of atherosclerotic cardiovascular disease.

Oxidized low-density lipoprotein (OxLDL) is implicated in the pathogenesis of atherosclerotic cardiovascular disease (1, 2). Previous studies indicate that OxLDL is present in atheromatous lesions (3) and that antioxidant drugs slow the progression of atherosclerosis (4, 5). OxLDL possesses many atherogenic properties. First, OxLDL is thought to be taken up into macrophages via scavenger receptors, which promotes the deposition of lipid-laden foam cells in the vascular walls and leads to fatty streaks (1). Second, recent data indicate that OxLDL alters various endothelial functions. OxLDL induces endothelial expression of several proteins, including adhesion molecules (6, 7), monocyte chemotactic protein-1 (8, 9), smooth muscle growth factors (10), and colony-stimulating factors (11), some of which might be involved in endothelial cell-mediated recruitment of monocytes/macrophages into the intima. OxLDL also attenuates the endothelium-dependent vasodilatory response through reduced production of nitric oxide (12, 13).

It has long been thought that there is a specific endothelial receptor for OxLDL. In 1997, Sawamura et al. (14) identified a novel receptor for OxLDL (LOX-1) using expression cloning with bovine cultured endothelial cells. LOX-1 is a membrane protein abundantly expressed in endothelial cells. It binds, internalizes, and degrades OxLDL, but not native LDL or acetylated LDL. Its mRNA was shown to be expressed in human atheromatous lesions. This endothelial receptor might mediate some of the actions of OxLDL in the endothelium. The biologic roles of LOX-1, however, remain to be determined.

In a previous study, we performed rat LOX-1 cDNA cloning and demonstrated that it encodes a single-transmembrane protein with its N terminus in the cytoplasm (15). The extracellular region consists of a spacer, 46-amino acid triple repeats, and C-type lectin-like domains. Quite unexpectedly, LOX-1 expression was markedly (>20-fold) up-regulated in the aorta of hypertensive rats (16), which implies a pathophysiologic role for LOX-1 in hypertension or in hypertensive vascular remodeling. However, the genomic structure of LOX-1 or its regulation of expression in vitro has not yet been reported in any species. Here we report the genomic organization of rat LOX-1 and identified several consensus sequences in the 5′-flanking region. We demonstrated that the LOX-1 gene expression was markedly up-regulated by shear stress (9-fold), bacterial lipopolysaccharide (LPS) (21-fold), and tumor necrosis factor (TNF)-α (4-fold), in cultured vascular endothelial cells. We also examined its expression in cells other than endothelial cells, such as macrophages and vascular smooth muscle cells.

**Experimental Procedures**

**Screening of the Genomic Library**—A rat genomic DNA library (Sau3AI partial digest constructed in the λ phage, EMBL3 SP6/T7) (CLONTECH) was screened with a rat LOX-1 cDNA probe (432-bp XhoI/HindIII fragment, probe 1 in Fig. 1A). Approximately 5 × 10^6 phages were plated at a density of 30,000 plaques/15-cm plate, and two replica nitrocellulose filters were prepared from each plate. High-stringency screening was performed with hybridization in 50% formamide and final washes in 0.1 × SSC (1 × SSC is 150 mM NaCl, 15 mM sodium citrate, pH 7.0) containing 0.1% SDS at 60 °C. Plaques that produced...
positive signals on both replicas were selected and purified. The second
and the third rounds of screening were carried out under the same
conditions to isolate positive clones. Positive clones were digested with
XhoI, EcoRI, SacI, HindIII, and ApaI. Each restriction fragment was
subcloned into pBluescript II SK.

Polymerase Chain Reaction (PCR)—The 3’ portion was determined by
PCR. Rat genomic DNA (100 ng) prepared from Wistar rat kidneys
was amplified by PCR with an Expand Long Template PCR System
(Boehringer Mannheim, Mannheim, Germany). Primer sets used were:
5'-AACATGGTCGCACTTGGAGAGGC-3' (forward 1) and
5'-GGCTTGACCGGTTGTTATCCTGCTCT-3' (reverse 1) for
RLG11, 5'-CTGAACTTCTTCAAGAGGCAGAGGCTGAG-3' (forward
2) and 5'-GGGCCCAGGAAGGAGTTTGAACAGTTTTCTTT-3' (reverse 2)
for RLG12, 5'-AAAAGAATTGCTCTTCATCTGCTGTGACC-3' (forward
3) and 5'-CATGTCACCGAGCCATGTGTTCCACACCA-3' (reverse 3) for
RLG13, and 5'-AGAGTGTCAGGAGAAGCTAAAGAACAGAGA-3' (forward 4)
and 5'-CTGCTAGATGTGGCTGCCTCTCCGCTT-3' (reverse 4) for RLG14. The amplification was carried out for 35
cycles of 94 °C for 10 s, 60 °C for 30 s, and 68 °C for 2 min. The products
were subcloned into pBluescript II.

Sequence Analysis—Nucleotide sequences were determined on both
strands using the dideoxynucleotide chain-termination method with a
Sequi Therm Long-Read cycle sequencing kit (Epicentre Technologies,
Madison, WI) and an Automated Laser Fluorescent DNA Sequencer
(model 373A; LI-COR, Lincoln, NE). The sequence and consensus nu-
cleotide motifs were determined using the GENETYX-MAC soft-
ware (Software Development, Tokyo, Japan).

Southern Blot Analysis—Southern blot analysis was carried out ac-
sording to Sambrook et al. (17). Rat genomic DNA (20 μg each) was
digested with restriction enzymes (PstI, EcoRV, EcoRI, and BamHI),
electrophoresed on a 0.7% agarose gel, and transferred onto a nylon
membrane filter. An EcoRI/BamHI genomic DNA fragment (1.8 kb,
probe 2 in Fig. 1A) was used as a probe. Hybridization and wash
were performed as described for the screening.

Primer Extension—Primer extension analysis was performed accord-
ing to the manufacturer’s recommendation (Promega, Madison, WI).
In brief, a synthetic oligonucleotide, 5'-ACATGGTCGCACTTGGAGAGGC-3'
was hybridized to 20 ng of poly(A)+ RNA using T4 polynucleotide kinase. Labeled primer (1 pmol) was annealed
for 15 min at 65 °C. Nonannealed nucleic acids were digested with 1000 units/ml S1
nuclease and the probe was labeled with [γ-32P]ATP using T7 DNA polymerase. The products were digested with XhoI, puri-
ﬁed using alkaline gel electrophoresis, and used as a probe. The probe
was hybridized to 20 μg of rat endothelial polyA+ RNA at 30 °C
overnight. Nonannealed nucleic acids were digested with 1000 units/ml S1
nuclease. The nuclease-resistant products were ethanol-precipitated and
electrophoresed in parallel with the primer extension product on a
7 m urea/6% polyacrylamide sequencing gel followed by autoradiography.

Cell Culture—Primary cultures of endothelial cells (ECs) were ob-
tained from the rat aorta or the descending thoracic aorta of a bovine
fetus by brief collagenase digestion of the intimal lining, as described
previously (18). An established cultured vascular smooth muscle cell
line (A10 cells) were purchased from the American Type Culture Col-
lection (Rockville, MD). Cells were grown in Dulbecco’s modiﬁed Eagle’s
medium supplemented with 10% fetal bovine serum, 50 units/ml peni-
cillin, and 50 μg/ml streptomycin in a controlled atmosphere of 5%
CO2/95% air at 37 °C. ECs within the 20th passage were exposed to
5% CO2/95% air at 37 °C. ECs were cultured on the glass plate (10 cm × 70 mm) prior to
flow in the chamber. The inner dimensions of the flow channel were:
85 × 55 × 0.25 mm. The chamber was ﬁlled with culture medium.
A peristaltic pump and silicone tubing (ATTO Co., Tokyo, Japan) were
used to generate a constant flow. The entire system was placed in an
incubator maintained in an atmosphere of 5% CO2/95% air at 37 °C.
The intensity of fluid shear stress (τ, dyne/cm2) was calculated as fol-
lowing: τ = 8μ/ρD2, where μ is the fluid viscosity (0.0094 poise at 37 °C; Q is the velocity of the flow (m/s); ρ (0.02 cm) and (1.4 cm) are
cross-sectional dimensions of the flow path. Fluid shear stress (20
dyne/cm2) was applied to the ECs for 0–24 h. Control experiments
were simultaneously performed in a static condition with cells derived
from the same pool.

Northern Blot Analysis—Total RNA was prepared using the acid
guanidinium thiocyanate/phenol/chloroform method (20). Poly(A)+
RNA was puriﬁed using an mRNA puriﬁcation kit (Amersham Phar-
macia Biotech, Uppsala, Sweden). RNA was fractionated on a formal-
dehyde-denatured 1.2% agarose gel and transferred to a nylon
membrane filter. The probe was synthesized using reverse transcrip-
PCR with total RNA from ECs and the following primers: 5'-CTGCC-
TCTGCGATAGAAAGGA-3' and 5'-CCCTCTTTGATCATGATCTC-3'. The
probe was hybridized to 40 ng of total RNA from ECs for 1 h, 45 °C
for 1 min, and 75 °C for 3 min with Pfu polymerase (Stratagene, La
Jolla, CA). The probe was labeled with [α-32P]dCTP using the random
primer labeling method. After prehybridization, nylon membranes were
hybridized with the [32P]-labeled cDNA probe (1 × 106 cpm/ml) in
a solution containing 50% formamide at 42 °C for 16 h. Blots were then
washed in 0.2 x SSC containing 0.1% SDS at 60 °C. Filters were
exposed to Kodak X-Omat AR ﬁlm with an intensifying screen at
−80 °C. For quantitative analysis, the Northern filters were exposed to
an imaging plate and the radioactivity of the bands was quantiﬁed as photo-
stimulated luminescence with a Bioimage Analyzer (model BAS 2000;
Fuji Film, Tokyo, Japan). The photo-stimulated luminescence value
for LOX-1 was standardized with that of glyceraldehyde-3-phosphate dehy-
drogenase (GAPDH).

Anti-LOX-1 Polyclonal Antibody—Rabbit antiserum was raised
against rat LOX-1. In brief, the extracellular region of LOX-1 (a
molecule residues 60–364) was subcloned into a (His)6-tagged vector. Ex-
cision against rat LOX-1. In brief, the extracellular region of LOX-1 (amino
acids residues 60–364) was subcloned into a (His)6-tagged vector. Ex-
cision was standardized with that of glyceraldehyde-3-phosphate dehy-
drogenase (GAPDH).

Flow Loading—ECs were exposed to a well deﬁned steady laminar
flow using a parallel plate ﬂow chamber, as described previously (19).
In brief, the ﬂow chamber consisted of upper acrylic and lower glass plates,
which were separated by a rectangular silicon rubber gasket (250 μm
thick). ECs were cultured on the glass plate (10 cm × 70 mm) prior to
flow in the chamber. The inner dimensions of the chamber were:
85 × 55 × 0.25 mm. The chamber was ﬁlled with culture medium.
A peristaltic pump and silicone tubing (ATTO Co., Tokyo, Japan) were
used to generate a constant flow. The entire system was placed in an
incubator maintained in an atmosphere of 5% CO2/95% air at 37 °C.
The intensity of fluid shear stress (τ, dyne/cm2) was calculated as fol-
lowing: τ = 8μ/ρD2, where μ is the fluid viscosity (0.0094 poise at 37 °C; Q is the velocity of the flow (m/s); ρ (0.02 cm) and (1.4 cm) are
cross-sectional dimensions of the flow path. Fluid shear stress (20
dyne/cm2) was applied to the ECs for 0–24 h. Control experiments
were simultaneously performed in a static condition with cells derived
from the same pool.

Isolation of Genomic Clones of Rat LOX-1—We isolated
genomic clones encoding rat LOX-1 using a combination of screening
and PCR. Fig. 1A summarizes the cloning strategy, genomic
structure, and partial restriction map. A rat genomic
library was polymerized with a rat LOX-1 cDNA probe (probe 1 in
Fig. 1A). Four genomic clones (ARLG1–4) were subcloned from
6 × 105 plaques. The four clones did not cover the 3’ end of
the LOX-1 gene, therefore, the missing portion was determined
using PCR (RLG11–14). The nucleotide sequence was determined
using the restriction fragments of the six overlapping
clones (ARLG2, ARLG3, RLG11–14). Comparison of the genotype
and cDNA sequences revealed that the coding region
consisted of 8 exons distributed over 19 kilobases. Exons 1–8
corresponded to nucleotides 1 through 73, 74 through 175, 176

Downloaded from http://www.jbc.org/ by guest on July 23, 2018
Genomic Structure and Regulation of the LOX-1 Gene

Fig. 1. Genomic organization of rat LOX-1. A, cloning strategy and schematic representation of cDNA and genomic DNA for rat LOX-1. The top panel shows the cDNA structure. Vertical lines indicate the positions of exon boundaries. The size of each exon is indicated above. The middle panel shows the genomic structure. Open and filled boxes represent non-translated and coding regions in the exons, respectively. Horizontal lines indicate the flanking and intron regions. The length of each intron is indicated above. Restriction sites are shown below. The abbreviations are: B, BamHI; H, HindIII; E, EcoRI; X, XhoI; A, ApaI; P, PsI; and S, SacI. The bottom panel shows the cloning strategy. The isolated clones (RLG2 and RLG3) and the PCR products (RLG11–14) are indicated by bars. The probes used for screening (probe 1) and Southern blot analysis (probe 2) are indicated by hatched boxes. B, exon-intron boundaries. The uppercase letters represent the coding nucleotides. The lower-case letters represent the flanking and intron sequences. The consensus 5’ splice-donor and 3’ splice-acceptor regions are indicated by white letters on a black background. C, schematic representation of the cDNA and protein. Exons in the cDNA and functional domains in the protein are indicated by boxes. The solid box represents the transmembrane (TM) domain. Hatched boxes represent the 46-amino acid repeat unit (repeats 1–3). The dotted box represents the C-type lectin-like domain.

Fig. 2. Genomic Southern blot analysis of rat LOX-1. Rat genomic DNA (20 μg each) was digested with the indicated restriction enzymes. Southern blot analysis was performed at high stringency with a 32P-labeled rat LOX-1 genomic DNA probe (probe 2 as illustrated in Fig. 1A).
Regulation of LOX-1 Gene Expression by Mechanical Stress, Endotoxin, and TNF-α—

We examined the effects of shear stress, bacterial LPS, and TNF-α on LOX-1 gene expression. In the first experiment, confluent monolayers of ECs were exposed to steady laminar shear flow (20 dyne/cm²). Cells were harvested at 0, 1, 3, 6, 12, 24 h and assayed for LOX-1 mRNA with Northern blotting. As a control, cells were incubated without flow stimulus for 24 h. As shown in Fig. 5 (left), we detected a 2.4-kb band for LOX-1 mRNA in ECs. Incubation of ECs in a static condition for 24 h did not produce any significant changes in LOX-1 gene expression. In contrast, fluid shear stress induced a marked time-dependent increase in LOX-1 message levels. The amount of LOX-1 mRNA began to increase within 3 h of shear stress and reached a maximum (9-fold increase over basal levels) at 6 h. The mRNA level declined to a 3-fold increase over basal levels at 24 h.

Next, ECs were exposed to LPS (100 ng/ml) and TNF-α (10 ng/ml). LPS induced a dramatic increase in LOX-1 gene expression. The level increased up to 21-fold at 6 h and declined to 16-fold over basal levels at 24 h (Fig. 5, middle). TNF-α, on the other hand, increased LOX-1 expression to a much lesser extent (4-fold). The level remained high, however, over 24 h (Fig. 5, right).

The LPS-induced LOX-1 regulation was also examined at the
protein level (Fig. 6). Western blot analysis with the rabbit antiserum against rat LOX-1 detected a band of 45 kDa in the extract from control ECs (lane 3). The intensity of the band increased after 12 h of LPS exposure (lane 4). Control preimmune serum detected no band (lanes 1 and 2). We also confirmed the specificity of the band by preadsorption of antibody with antigen (data not shown).

**LOX-1 Gene Expression in Macrophages and Smooth Muscle Cells**—To examine cell type specificity of LOX-1 gene expression, we performed Northern blot analysis with RNA from peritoneal and alveolar macrophages and cultured vascular smooth muscle cells as well as cultured ECs (Fig. 7). As expected, LOX-1 was expressed in ECs (lane 3), but not in cultured vascular smooth muscle cells (lane 4). Interestingly, LOX-1 expression was abundantly expressed in peritoneal (lane 1) and alveolar (lane 2) macrophages in vivo.

**DISCUSSION**

In the present study, we isolated and characterized the rat LOX-1 gene. The 5’-flanking region contained putative TATA and CAAT boxes and multiple cis-elements, such as NF-kB, AP-1 and AP-2 sites, and a SSRE. LOX-1 gene expression was markedly up-regulated in response to hemodynamic mechanical force, bacterial endotoxin, and cytokine, suggesting a role for LOX-1 in the pathogenesis of atherosclerosis.

LOX-1 is a recently identified OxLDL receptor abundantly expressed in endothelial cells (14). It is a type II single-transmembrane protein with a cytoplasmic N terminus. It was first isolated in bovine and human, and subsequently our group identified the rat counterpart (16). Previous data revealed that the LOX-1 protein binds, internalizes, and degrades OxLDL specifically. The protein does not appear to couple to G protein, and does not possess definite kinase or cyclase domains or serine, threonine, or tyrosine phosphorylation sites. The functions of this receptor, including the signaling pathways, are yet to be elucidated. In the present study, we determined the genomic structure of the rat LOX-1 gene. The LOX-1 gene consists of 8 exons, and each exon roughly corresponds to the functional domain of the protein: exon 2 to the transmembrane domain and exons 6 through 8 to the lectin-like domain. We reported previously that a 46-amino acid motif in the extracellular domain of the bovine and human LOX-1 was triplicated in the rat LOX-1 (16). Repeats 2 and 3 correspond to all of exons 4 and 5, respectively. The exon organization supports the structural basis of this motif as a functional unit. The repeat struc-
tured to constitute a complex network, which interactively leads to the development of atherosclerotic plaque. It was demonstrated that OxLDL and its receptors on ECs and macrophages interacted, which was partially displaced by OxLDL. Thus, it can be speculated that OxLDL and its receptors on ECs and macrophages constitute a complex network, which interactively leads to the atherosclerotic vascular lesion development.

We reported previously that LOX-1 gene expression is markedly enhanced in the aorta of hypertensive rats, stroke-prone spontaneously hypertensive rats, and salt-loaded Dahl salt-sensitive rats, as compared with the low level in control rats (15). This finding implicates a role for LOX-1 in the pathophysiology of hypertension. On the other hand, LOX-1 expression is not enhanced in prehypertensive young stroke-prone spontaneously hypertensive rats and salt-unloaded Dahl salt-sensitive rats (16). Thus, the up-regulation might be induced by hemodynamic, humoral, or other factors related to the hypertensive state. The present study demonstrated that, in vitro, LOX-1 expression was markedly increased by mechanical factor. Hence, it is possible that the mechanical factor has a strong influence on LOX-1 expression in hypertensive rats. Alternatively, enhanced LOX-1 expression might reflect the hypertensive vascular remodeling.

In conclusion, we determined the genomic structure of the rat LOX-1 gene. The up-regulation of LOX-1 gene expression by biomechanical stress and cytokines, as well as the presence of NF-κB, AP-1 and AP-2 sites, and SSRE suggest a role for LOX-1 in the pathophysiology of atherosclerosis.

Acknowledgments—We are grateful to Yoko Saruta and Setsuko Sato for their technical and secretarial assistance.

REFERENCES

1. Steinberg, D., Parthasarathy, S., Carew, T. E., Kario, J. C., and Witztum, J. L. (1989) N. Engl. J. Med. 320, 915–924
2. Witztum, J. L., and Steinberg, D. (1991) J. Clin. Invest. 88, 1758–1792
3. Yla-Herttuala, S., Palinski, W., Rosenfeld, M. E., Parhami, F., Gerrity, R. G., Schwartz, C. J., and Fogelman, A. M. (1990) Proc. Natl. Acad. Sci. U. S. A. 87, 7264–7268
4. Cushman, S. D., Berliner, J. A., Valente, A. J., Territo, M. C., Navab, M., Parhami, F., Gerrity, R. G., Schwartz, C. J., and Fogelman, A. M. (1990) Proc. Natl. Acad. Sci. U. S. A. 87, 5134–5138
5. Kitamura, T., Nagano, Y., Yokode, M., Ishii, K., Kume, N., Ooshima, A., Yoshida, H., and Inagami, T. (1987) Proc. Natl. Acad. Sci. U. S. A. 84, 5924–5931
6. Khan, B. V., Parthasarathy, S. S., Alexander, R. W., and Medford, R. M. (1995) J. Clin. Invest. 95, 1262–1270
7. Kume, N., Cybulsky, M. I., and Gimbrone, J. M. A. (1992) J. Clin. Invest. 90, 1138–1144
8. Cushing, S. D., Berliner, J. A., Valente, A. J., Territo, M. C., Navah, M., Parhami, F., Gerrity, R. G., Schwartz, C. J., and Fogelman, A. M. (1990) Proc. Natl. Acad. Sci. U. S. A. 87, 7374–7378
9. Liao, F., Berliner, J. A., Mehriban, M., Navah, M., Demer, L. L., Lusis, A. J., and Fogelman, A. M. (1991) J. Clin. Invest. 87, 2253–2257
10. Ross, R. (1993) Nature 362, 801–809
11. Rajavashisth, T. B., Andalibi, A., Territo, M. C., Berliner, J. A., Navah, M., Parhami, F., Gerrity, R. G., Schwartz, C. J., and Fogelman, A. M. (1990) Proc. Natl. Acad. Sci. U. S. A. 87, 160–162
12. Kugiyama, K., Kerns, S. A., Marrsitt, J. D., Roberts, R., and Henry, P. D. (1990) Nature 344, 160–162
13. Yokoyama, M., Hirata, K., Miyake, R., Akita, H., Ishikawa, Y., and Fukuzaki, H. (1990) Biochem. Biophys. Res. Commun. 168, 301–308
14. Sawamura, T., Kume, N., Matsukura, M., Hoshikawa, H., Hiba, Y., Tanaka, T., Miwa, S., Katsura, Y., Kita, T., and Masaki, T. (1997) Nature 386, 73–77
15. Nagase, M., Hirsse, S., Sawamura, T., Masaki, T., and Fujita, T. (1997) Biochem. Biophys. Res. Commun. 237, 496–498
16. Nagase, M., Hirsse, S., and Fujita, T. (1998) Biochem. J. 330, 1417–1422
17. Sambrook, J., Fritsch, E. F., and Maniatis, T. (1989) Molecular Cloning: A Laboratory Manual, 2nd Ed., pp. 9.16–9.19, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY
18. Korenaga, R., Ando, J., Tsuboi, H., Yang, W., Sakuma, I., Toyo-oka, T., and Kamiya, A. (1994) Biochem. Biophys. Res. Commun. 198, 213–219
19. Wang, Y., Shin, W. S., Kawaguchi, H., Inakui, M., Kato, M., Sakamoto, A., Uemura, Y., Miyamoto, M., Shimamoto, N., Kogenaga, R., Ando, J., and Toyo-o, T. (1996) J. Biol. Chem. 271, 5647–5655
20. Czaczykowski, P., and Saschi, N. (1987) Anal. Biochem. 162, 156–159
21. Russell, D. W., Schneider, W. J., Yamamoto, T., Luskay, K. L., Brown, M. S., and Goldstein, J. L. (1984) Cell 37, 577–585
22. McDonald, P. P., Bald, A., and Cassatella, M. A. (1997) Blood 89, 3421–3433
23. Resnick, L., Collins, T., Atkinson, W., Bonthron, D. T., Dewey, C., Jr., and Fogelman, A. M. (1990) Proc. Natl. Acad. Sci. U. S. A. 87, 8069–8073
24. Khachigian, L. M., Anderson, K. R., Halnon, N. J., Gimbrone, M., Jr., Resnick, N., Collins, T., and Parhami, F. (1997) Arterioscler. Thromb. Vasc. Biol. 17, 2282–2286
25. van Lenten, B. J., and Fogelman, A. M. (1992) J. Clin. Invest. 90, 1689–1695
26. Lin, M. C., Almus-Jacobs, F., Chen, H. H., Parry, G. C., Mackman, N., Shyy, J. Y., and Collins, T. (1995) J. Biol. Chem. 270, 1138–1144
27. Khachigian, L. M., Anderson, K. R., Halnon, N. J., Gimbrone, M., Jr., Resnick, N., Collins, T., and Parhami, F. (1997) Arterioscler. Thromb. Vasc. Biol. 17, 2282–2286
28. van Lenten, B. J., and Fogelman, A. M. (1992) J. Clin. Invest. 90, 1689–1695
29. McDonald, P. P., and Cassatella, M. A. (1997) Blood 89, 5647–5655
30. Khachigian, L. M., Anderson, K. R., Halnon, N. J., Gimbrone, M., Jr., Resnick, N., Collins, T., and Parhami, F. (1997) Arterioscler. Thromb. Vasc. Biol. 17, 2282–2286
31. Adachi, H., Tsujimoto, M., Arai, H., and Inoue, K. (1997) J. Biol. Chem. 272, 31217–31220
Genomic Organization and Regulation of Expression of the Lectin-like Oxidized Low-density Lipoprotein Receptor (LOX-1) Gene
Miki Nagase, Junpei Abe, Katsutoshi Takahashi, Joji Ando, Shigehisa Hirose and Toshiro Fujita

J. Biol. Chem. 1998, 273:33702-33707.
doi: 10.1074/jbc.273.50.33702

Access the most updated version of this article at http://www.jbc.org/content/273/50/33702

Alerts:
• When this article is cited
• When a correction for this article is posted

Click here to choose from all of JBC's e-mail alerts

This article cites 30 references, 11 of which can be accessed free at http://www.jbc.org/content/273/50/33702.full.html#ref-list-1