

# Leonard Lipovich

## List of Publications by Year in descending order

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76  
papers

17,435  
citations

81743

39  
h-index

85405

71  
g-index

79  
all docs

79  
docs citations

79  
times ranked

29460  
citing authors

#	ARTICLE	IF	CITATIONS
1	A collective statement in support of saving pangolins. <i>Science of the Total Environment</i> , 2022, 824, 153666.	3.9	6
2	Estrogen distinctly regulates transcription and translation of lncRNAs and pseudogenes in breast cancer cells. <i>Genomics</i> , 2022, 114, 110421.	1.3	5
3	lncRNA-Associated Genetic Etiologies Are Shared between Type 2 Diabetes and Cancers in the UAE Population. <i>Cancers</i> , 2022, 14, 3313.	1.7	1
4	miRCOVID-19: Potential Targets of Human miRNAs in SARS-CoV-2 for RNA-Based Drug Discovery. <i>Non-coding RNA</i> , 2021, 7, 18.	1.3	37
5	Dietary Patterns and Associated Microbiome Changes that Promote Oncogenesis. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 725821.	1.8	8
6	Gestational Age Dependence of the Maternal Circulating Long Non-Coding RNA Transcriptome During Normal Pregnancy Highlights Antisense and Pseudogene Transcripts. <i>Frontiers in Genetics</i> , 2021, 12, 760849.	1.1	7
7	FuncPEP: A Database of Functional Peptides Encoded by Non-Coding RNAs. <i>Non-coding RNA</i> , 2020, 6, 41.	1.3	34
8	YY1 directly interacts with myocardin to repress the triad myocardin/SRF/CArG box-mediated smooth muscle gene transcription during smooth muscle phenotypic modulation. <i>Scientific Reports</i> , 2020, 10, 21781.	1.6	12
9	A Long Non-coding RNA, LOC157273, Is an Effector Transcript at the Chromosome 8p23.1-PPP1R3B Metabolic Traits and Type 2 Diabetes Risk Locus. <i>Frontiers in Genetics</i> , 2020, 11, 615.	1.1	14
10	Association study of the leptin receptor gene allelic variants with delayed puberty in boys in the peri-pubertal period. <i>Live and Bioabiotic Systems</i> , 2020, , .	0.1	0
11	Prevalence of miRNA and lncRNA binding sites around obesity associated genes. <i>Live and Bioabiotic Systems</i> , 2020, , .	0.1	0
12	Genome-wide meta-analysis of SNP-by-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. <i>Pharmacogenomics Journal</i> , 2019, 19, 97-108.	0.9	3
13	The Growth-Arrest-Specific (GAS)-5 Long Non-Coding RNA: A Fascinating lncRNA Widely Expressed in Cancers. <i>Non-coding RNA</i> , 2019, 5, 46.	1.3	54
14	The long non-coding RNA NEAT1 is responsive to neuronal activity and is associated with hyperexcitability states. <i>Scientific Reports</i> , 2017, 7, 40127.	1.6	92
15	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
16	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. <i>Circulation Research</i> , 2017, 120, 341-353.	2.0	166
17	Association of Body Mass Index with DNA Methylation and Gene Expression in Blood Cells and Relations to Cardiometabolic Disease: A Mendelian Randomization Approach. <i>PLoS Medicine</i> , 2017, 14, e1002215.	3.9	246
18	Unintended target effect of anti-BCL-2 DNAs. <i>Cancer Management and Research</i> , 2017, Volume 9, 427-432.	0.9	5

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19	Global Intersection of Long Non-Coding RNAs with Processed and Unprocessed Pseudogenes in the Human Genome. <i>Frontiers in Genetics</i> , 2016, 7, 26.	1.1	29
20	High-throughput RNA sequencing reveals structural differences of orthologous brain-expressed genes between western lowland gorillas and humans. <i>Journal of Comparative Neurology</i> , 2016, 524, 288-308.	0.9	2
21	Primate-specific oestrogen-responsive long non-coding RNAs regulate proliferation and viability of human breast cancer cells. <i>Open Biology</i> , 2016, 6, 150262.	1.5	10
22	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	2.4	95
23	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016, 6, 28199.	1.6	16
24	Trans-ethnic Meta-analysis and Functional Annotation Illuminates the Genetic Architecture of Fasting Glucose and Insulin. <i>American Journal of Human Genetics</i> , 2016, 99, 56-75.	2.6	55
25	Association of the IGF1 gene with fasting insulin levels. <i>European Journal of Human Genetics</i> , 2016, 24, 1337-1343.	1.4	5
26	Abstract 1262: Primate-specific estrogen-induced long noncoding RNAs as targets for breast cancer treatment. , 2016, , .		0
27	Identification of long noncoding <scp>RNA</scp>s dysregulated in the midbrain of human cocaine abusers. <i>Journal of Neurochemistry</i> , 2015, 135, 50-59.	2.1	38
28	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173
29	Abstract P2-08-01: Autoimmunity in breast carcinogenesis. A new paradigm. , 2015, , .		0
30	Developmental Changes in the Transcriptome of Human Cerebral Cortex Tissue: Long Noncoding RNA Transcripts. <i>Cerebral Cortex</i> , 2014, 24, 1451-1459.	1.6	58
31	Transcriptome interrogation of human myometrium identifies differentially expressed sense-antisense pairs of protein-coding and long non-coding RNA genes in spontaneous labor at term. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2014, 27, 1397-1408.	0.7	25
32	Anti-centrosome antibodies in breast cancer are the expression of autoimmunity. <i>Immunologic Research</i> , 2014, 60, 339-347.	1.3	11
33	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
34	Evolutionary conservation of long non-coding RNAs; sequence, structure, function. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2014, 1840, 1063-1071.	1.1	575
35	Reply to Skoyles: Decline in growth rate, not muscle mass, predicts the human childhood peak in brain metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4910.	3.3	1
36	Metabolic costs and evolutionary implications of human brain development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13010-13015.	3.3	409

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37	Promoter Analysis Reveals Globally Differential Regulation of Human Long Non-Coding RNA and Protein-Coding Genes. PLoS ONE, 2014, 9, e109443.	1.1	72
38	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	1.2	10
39	Pseudogene-derived lncRNAs: emerging regulators of gene expression. Frontiers in Genetics, 2014, 5, 476.	1.1	110
40	Making sense of Dlx1 antisense RNA. Developmental Biology, 2013, 376, 224-235.	0.9	41
41	Characterization of human cortical gene expression in relation to glucose utilization. American Journal of Human Biology, 2013, 25, 418-430.	0.8	6
42	Synaptogenesis and development of pyramidal neuron dendritic morphology in the chimpanzee neocortex resembles humans. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 10395-10401.	3.3	112
43	Challenging paradigms: long non-coding RNAs in breast ductal carcinoma in situ (DCIS). Frontiers in Genetics, 2013, 4, 50.	1.1	3
44	Sense-antisense gene pairs: sequence, transcription, and structure are not conserved between human and mouse. Frontiers in Genetics, 2013, 4, 183.	1.1	46
45	Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. Biology of Reproduction, 2012, 87, 108.	1.2	9
46	Long noncoding RNAs are rarely translated in two human cell lines. Genome Research, 2012, 22, 1646-1657.	2.4	346
47	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. Genome Research, 2012, 22, 1775-1789.	2.4	4,428
48	Prolonged myelination in human neocortical evolution. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16480-16485.	3.3	492
49	Activity-Dependent Human Brain Coding/Noncoding Gene Regulatory Networks. Genetics, 2012, 192, 1133-1148.	1.2	175
50	Dynamic Gene Expression in the Human Cerebral Cortex Distinguishes Children from Adults. PLoS ONE, 2012, 7, e37714.	1.1	32
51	Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. Journal of Neurochemistry, 2011, 116, 459-466.	2.1	152
52	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. Journal of Perinatal Medicine, 2010, 38, 617-43.	0.6	150
53	Conserved long noncoding RNAs transcriptionally regulated by Oct4 and Nanog modulate pluripotency in mouse embryonic stem cells. Rna, 2010, 16, 324-337.	1.6	306
54	MacroRNA underdogs in a microRNA world: Evolutionary, regulatory, and biomedical significance of mammalian long non-protein-coding RNA. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2010, 1799, 597-615.	0.9	200

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55	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010, 16, 1478-1487.	1.6	354
56	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	1.6	90
57	Phylogenomic analyses reveal convergent patterns of adaptive evolution in elephant and human ancestries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 20824-20829.	3.3	75
58	Global discovery of primate-specific genes in the human genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12019-12024.	3.3	66
59	On-the-Fly Integration and Ad Hoc Querying of Life Sciences Databases Using LifeDB. <i>Lecture Notes in Computer Science</i> , 2009, , 561-575.	1.0	11
60	Detailed characterization of the mouse embryonic stem cell transcriptome reveals novel genes and intergenic splicing associated with pluripotency. <i>BMC Genomics</i> , 2008, 9, 155.	1.2	13
61	Structural differences of orthologous genes: Insights from humanâ€“primate comparisons. <i>Genomics</i> , 2008, 92, 134-143.	1.3	1
62	Sall4 Regulates Distinct Transcription Circuitries in Different Blastocyst-Derived Stem Cell Lineages. <i>Cell Stem Cell</i> , 2008, 3, 543-554.	5.2	209
63	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
64	Whole-Genome Cartography of Estrogen Receptor $\beta$ Binding Sites. <i>PLoS Genetics</i> , 2007, 3, e87.	1.5	400
65	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF- $\kappa$ B upon TLR4 Activation. <i>Molecular Cell</i> , 2007, 27, 622-635.	4.5	180
66	Quality assessment of the Affymetrix U133A&B probesets by target sequence mapping and expression data analysis. <i>In Silico Biology</i> , 2007, 7, 241-60.	0.4	18
67	The Oct4 and Nanog transcription network regulates pluripotency in mouse embryonic stem cells. <i>Nature Genetics</i> , 2006, 38, 431-440.	9.4	2,162
68	Primate-Specific Endogenous Cis-Antisense Transcription in the Human 5q31 Protocadherin Gene Cluster. <i>Journal of Molecular Evolution</i> , 2006, 62, 73-88.	0.8	16
69	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	1.5	95
70	Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47.	1.5	290
71	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005, 2, 105-111.	9.0	244
72	Abundant novel transcriptional units and unconventional gene pairs on human chromosome 22. <i>Genome Research</i> , 2005, 16, 45-54.	2.4	9

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73	5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 11701-11706.	3.3	103
74	Pharmaceutical companies need to broaden research. Drug Discovery Today, 2003, 8, 18.	3.2	0
75	Genomic structure and evolutionary context of the human feline leukemia virus subgroup C receptor (hFLVCR) gene: evidence for block duplications and de novo gene formation within duplicons of the hFLVCR locus. Gene, 2002, 286, 203-213.	1.0	18
76	Computational and Experimental Analysis of Microsatellites in Rice ( <i>Oryza sativa</i> L.): Frequency, Length Variation, Transposon Associations, and Genetic Marker Potential. Genome Research, 2001, 11, 1441-1452.	2.4	1,285