

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	The GENCODE v7 catalog of human long noncoding RNAs: Analysis of their gene structure, evolution, and expression. <i>Genome Research</i> , 2012, 22, 1775-1789.	2.4	4,428
2	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
3	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	13.7	1,838
4	Computational and Experimental Analysis of Microsatellites in Rice (<i>Oryza sativa</i> L.): Frequency, Length Variation, Transposon Associations, and Genetic Marker Potential. <i>Genome Research</i> , 2001, 11, 1441-1452.	2.4	1,285
5	An atlas of human long non-coding RNAs with accurate 5' ends. <i>Nature</i> , 2017, 543, 199-204.	13.7	898
6	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
7	Prolonged myelination in human neocortical evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16480-16485.	3.3	492
8	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
9	Whole-Genome Cartography of Estrogen Receptor β Binding Sites. <i>PLoS Genetics</i> , 2007, 3, e87.	1.5	400
10	Genome-wide computational identification and manual annotation of human long noncoding RNA genes. <i>Rna</i> , 2010, 16, 1478-1487.	1.6	354
11	Long noncoding RNAs are rarely translated in two human cell lines. <i>Genome Research</i> , 2012, 22, 1646-1657.	2.4	346
12	Conserved long noncoding RNAs transcriptionally regulated by Oct4 and Nanog modulate pluripotency in mouse embryonic stem cells. <i>Rna</i> , 2010, 16, 324-337.	1.6	306
13	Complex Loci in Human and Mouse Genomes. <i>PLoS Genetics</i> , 2006, 2, e47.	1.5	290
14	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
15	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005, 2, 105-111.	9.0	244
16	Sall4 Regulates Distinct Transcription Circuitries in Different Blastocyst-Derived Stem Cell Lineages. <i>Cell Stem Cell</i> , 2008, 3, 543-554.	5.2	209
17	MacroRNA underdogs in a microRNA world: Evolutionary, regulatory, and biomedical significance of mammalian long non-protein-coding RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2010, 1799, 597-615.	0.9	200
18	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF- κ B upon TLR4 Activation. <i>Molecular Cell</i> , 2007, 27, 622-635.	4.5	180

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19	Activity-Dependent Human Brain Coding/Noncoding Gene Regulatory Networks. <i>Genetics</i> , 2012, 192, 1133-1148.	1.2	175
20	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
21	REST Regulates Distinct Transcriptional Networks in Embryonic and Neural Stem Cells. <i>PLoS Biology</i> , 2008, 6, e256.	2.6	172
22	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
23	Mining Affymetrix microarray data for long non-coding RNAs: altered expression in the nucleus accumbens of heroin abusers. <i>Journal of Neurochemistry</i> , 2011, 116, 459-466.	2.1	152
24	Characterization of the myometrial transcriptome and biological pathways of spontaneous human labor at term. <i>Journal of Perinatal Medicine</i> , 2010, 38, 617-43.	0.6	150
25	Synaptogenesis and development of pyramidal neuron dendritic morphology in the chimpanzee neocortex resembles humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 10395-10401.	3.3	112
26	Pseudogene-derived lncRNAs: emerging regulators of gene expression. <i>Frontiers in Genetics</i> , 2014, 5, 476.	1.1	110
27	5' Long serial analysis of gene expression (LongSAGE) and 3' LongSAGE for transcriptome characterization and genome annotation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 11701-11706.	3.3	103
28	Mice and Men: Their Promoter Properties. <i>PLoS Genetics</i> , 2006, 2, e54.	1.5	95
29	Pangolin genomes and the evolution of mammalian scales and immunity. <i>Genome Research</i> , 2016, 26, 1312-1322.	2.4	95
30	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
31	Regulation of neural macroRNAs by the transcriptional repressor REST. <i>Rna</i> , 2009, 15, 85-96.	1.6	90
32	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
33	Promoter Analysis Reveals Globally Differential Regulation of Human Long Non-Coding RNA and Protein-Coding Genes. <i>PLoS ONE</i> , 2014, 9, e109443.	1.1	72
34	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
35	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
36	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

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37	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
38	Sense-antisense gene pairs: sequence, transcription, and structure are not conserved between human and mouse. <i>Frontiers in Genetics</i> , 2013, 4, 183.	1.1	46
39	Making sense of Dlx1 antisense RNA. <i>Developmental Biology</i> , 2013, 376, 224-235.	0.9	41
40	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
41	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
42	FuncPEP: A Database of Functional Peptides Encoded by Non-Coding RNAs. <i>Non-coding RNA</i> , 2020, 6, 41.	1.3	34
43	Dynamic Gene Expression in the Human Cerebral Cortex Distinguishes Children from Adults. <i>PLoS ONE</i> , 2012, 7, e37714.	1.1	32
44	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
45	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
46	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. <i>Gene</i> , 2002, 286, 203-213.	1.0	18
47	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
48	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
49	De novo sequencing, assembly and analysis of eight different transcriptomes from the Malayan pangolin. <i>Scientific Reports</i> , 2016, 6, 28199.	1.6	16
50	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
51	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
52	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
53	Anti-centrosome antibodies in breast cancer are the expression of autoimmunity. <i>Immunologic Research</i> , 2014, 60, 339-347.	1.3	11
54	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

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55	CAGE-defined promoter regions of the genes implicated in Rett Syndrome. BMC Genomics, 2014, 15, 1177.	1.2	10
56	Primate-specific oestrogen-responsive long non-coding RNAs regulate proliferation and viability of human breast cancer cells. Open Biology, 2016, 6, 150262.	1.5	10
57	Abundant novel transcriptional units and unconventional gene pairs on human chromosome 22. Genome Research, 2005, 16, 45-54.	2.4	9
58	Tissue-Restricted Transcription from a Conserved Intragenic CpG Island in the Klf1 Gene in Mice1. Biology of Reproduction, 2012, 87, 108.	1.2	9
59	Dietary Patterns and Associated Microbiome Changes that Promote Oncogenesis. Frontiers in Cell and Developmental Biology, 2021, 9, 725821.	1.8	8
60	Gestational Age Dependence of the Maternal Circulating Long Non-Coding RNA Transcriptome During Normal Pregnancy Highlights Antisense and Pseudogene Transcripts. Frontiers in Genetics, 2021, 12, 760849.	1.1	7
61	Characterization of human cortical gene expression in relation to glucose utilization. American Journal of Human Biology, 2013, 25, 418-430.	0.8	6
62	A collective statement in support of saving pangolins. Science of the Total Environment, 2022, 824, 153666.	3.9	6
63	Association of the IGF1 gene with fasting insulin levels. European Journal of Human Genetics, 2016, 24, 1337-1343.	1.4	5
64	Unintended target effect of anti-BCL-2 DNAi. Cancer Management and Research, 2017, Volume 9, 427-432.	0.9	5
65	Estrogen distinctly regulates transcription and translation of lncRNAs and pseudogenes in breast cancer cells. Genomics, 2022, 114, 110421.	1.3	5
66	Challenging paradigms: long non-coding RNAs in breast ductal carcinoma in situ (DCIS). Frontiers in Genetics, 2013, 4, 50.	1.1	3
67	Genome-wide meta-analysis of SNP-by-9-ACEI/ARB and SNP-by-thiazide diuretic and effect on serum potassium in cohorts of European and African ancestry. Pharmacogenomics Journal, 2019, 19, 97-108.	0.9	3
68	High-throughput RNA sequencing reveals structural differences of orthologous brain-expressed genes between western lowland gorillas and humans. Journal of Comparative Neurology, 2016, 524, 288-308.	0.9	2
69	Structural differences of orthologous genes: Insights from human-primate comparisons. Genomics, 2008, 92, 134-143.	1.3	1
70	Reply to Skoyles: Decline in growth rate, not muscle mass, predicts the human childhood peak in brain metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4910.	3.3	1
71	LncRNA-Associated Genetic Etiologies Are Shared between Type 2 Diabetes and Cancers in the UAE Population. Cancers, 2022, 14, 3313.	1.7	1
72	Pharmaceutical companies need to broaden research. Drug Discovery Today, 2003, 8, 18.	3.2	0

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73	Abstract P2-08-01: Autoimmunity in breast carcinogenesis. A new paradigm. , 2015, , .		0
74	Abstract 1262: Primate-specific estrogen-induced long noncoding RNAs as targets for breast cancer treatment. , 2016, , .		0
75	Association study of the leptin receptor gene allelic variants with delayed puberty in boys in the peri-pubertal period. Live and Bioabiotic Systems, 2020, , .	0.1	0
76	Prevalence of miRNA and lncRNA binding sites around obesity associated genes. Live and Bioabiotic Systems, 2020, , .	0.1	0