

# Leping Li

## List of Publications by Year in descending order

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93  
papers

8,541  
citations

57758

44  
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48315

88  
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95  
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95  
docs citations

95  
times ranked

13349  
citing authors

#	ARTICLE	IF	CITATIONS
1	Predicting tumor response to drugs based on gene-expression biomarkers of sensitivity learned from cancer cell lines. <i>BMC Genomics</i> , 2021, 22, 272.	2.8	25
2	CDSegR: fast complete deconvolution for gene expression data from bulk tissues. <i>BMC Bioinformatics</i> , 2021, 22, 262.	2.6	11
3	Intestinal epithelial glucocorticoid receptor promotes chronic inflammation-associated colorectal cancer. <i>JCI Insight</i> , 2021, 6, .	5.0	9
4	GADGETS: a genetic algorithm for detecting epistasis using nuclear families. <i>Bioinformatics</i> , 2021, , .	4.1	1
5	HNF4 $\beta$ regulates sulfur amino acid metabolism and confers sensitivity to methionine restriction in liver cancer. <i>Nature Communications</i> , 2020, 11, 3978.	12.8	73
6	Non-targeted urinary metabolomics in pregnancy and associations with fetal growth restriction. <i>Scientific Reports</i> , 2020, 10, 5307.	3.3	17
7	PIK3C $\gamma$ expression by fibroblasts promotes triple-negative breast cancer progression. <i>Journal of Clinical Investigation</i> , 2020, 130, 3188-3204.	8.2	33
8	Glypican 6 is a putative biomarker for metastatic progression of cutaneous melanoma. <i>PLoS ONE</i> , 2019, 14, e0218067.	2.5	14
9	CDSeg: A novel complete deconvolution method for dissecting heterogeneous samples using gene expression data. <i>PLoS Computational Biology</i> , 2019, 15, e1007510.	3.2	42
10	Mediator complex component MED13 regulates zygotic genome activation and is required for postimplantation development in the mouse. <i>Biology of Reproduction</i> , 2018, 98, 449-464.	2.7	23
11	Loss of Glis3 causes dysregulation of retrotransposon silencing and germ cell demise in fetal mouse testis. <i>Scientific Reports</i> , 2018, 8, 9662.	3.3	3
12	Id Proteins Suppress E2A-Driven Invariant Natural Killer T Cell Development prior to TCR Selection. <i>Frontiers in Immunology</i> , 2018, 9, 42.	4.8	13
13	Revealing a human p53 universe. <i>Nucleic Acids Research</i> , 2018, 46, 8153-8167.	14.5	75
14	Haploinsufficiency of SIRT1 Enhances Glutamine Metabolism and Promotes Cancer Development. <i>Current Biology</i> , 2017, 27, 483-494.	3.9	59
15	Putative genomic characteristics of BRAF V600K versus V600E cutaneous melanoma. <i>Melanoma Research</i> , 2017, 27, 527-535.	1.2	18
16	The novel p53 target TNFAIP8 variant 2 is increased in cancer and offsets p53-dependent tumor suppression. <i>Cell Death and Differentiation</i> , 2017, 24, 181-191.	11.2	32
17	Genome-Wide Association Analysis of the Sense of Smell in U.S. Older Adults: Identification of Novel Risk Loci in African-Americans and European-Americans. <i>Molecular Neurobiology</i> , 2017, 54, 8021-8032.	4.0	17
18	A comprehensive genomic pan-cancer classification using The Cancer Genome Atlas gene expression data. <i>BMC Genomics</i> , 2017, 18, 508.	2.8	145

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19	Sleep Apnea and Hypoventilation in Patients with Down Syndrome: Analysis of 144 Polysomnogram Studies. <i>Children</i> , 2017, 4, 55.	1.5	37
20	Deficiency of the placenta- and yolk sac-specific tristetraprolin family member ZFP36L3 identifies likely mRNA targets and an unexpected link to placental iron metabolism. <i>Development (Cambridge)</i> , 2016, 143, 1424-33.	2.5	18
21	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. <i>Nucleic Acids Research</i> , 2016, 44, e20-e20.	14.5	267
22	Posttranscriptional regulation of transcript abundance by a conserved member of the tristetraprolin family in <i>Candida albicans</i> . <i>Molecular Microbiology</i> , 2015, 95, 1036-1053.	2.5	19
23	Toward predicting metastatic progression of melanoma based on gene expression data. <i>Pigment Cell and Melanoma Research</i> , 2015, 28, 453-463.	3.3	25
24	The Drosophila Tis11 Protein and Its Effects on mRNA Expression in Flies. <i>Journal of Biological Chemistry</i> , 2014, 289, 35042-35060.	3.4	16
25	Diethylstilbestrol (DES)-Stimulated Hormonal Toxicity is Mediated by ER $\alpha$ Alteration of Target Gene Methylation Patterns and Epigenetic Modifiers ( DNMT3A , MBD2 , and HDAC2 ) in the Mouse Seminal Vesicle. <i>Environmental Health Perspectives</i> , 2014, 122, 262-268.	6.0	40
26	Novel DNA Motif Binding Activity Observed In Vivo With an Estrogen Receptor $\alpha$ Mutant Mouse. <i>Molecular Endocrinology</i> , 2014, 28, 899-911.	3.7	42
27	ILUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. <i>BMC Genomics</i> , 2014, 15, 862.	2.8	21
28	Transcriptional Repression by the BRG1-SWI/SNF Complex Affects the Pluripotency of Human Embryonic Stem Cells. <i>Stem Cell Reports</i> , 2014, 3, 460-474.	4.8	93
29	T-KDE: a method for genome-wide identification of constitutive protein binding sites from multiple ChIP-seq data sets. <i>BMC Genomics</i> , 2014, 15, 27.	2.8	3
30	Identification and analysis of murine pancreatic islet enhancers. <i>Diabetologia</i> , 2013, 56, 542-552.	6.3	55
31	Characterization of constitutive CTCF/cohesin loci: a possible role in establishing topological domains in mammalian genomes. <i>BMC Genomics</i> , 2013, 14, 553.	2.8	69
32	PAVIS: a tool for peak annotation and visualization. <i>Bioinformatics</i> , 2013, 29, 3097-3099.	4.1	148
33	p53 integrates host defense and cell fate during bacterial pneumonia. <i>Journal of Experimental Medicine</i> , 2013, 210, 891-904.	8.5	54
34	Posttranscriptional Regulation of Cell-Cell Interaction Protein-Encoding Transcripts by Zfs1p in <i>Schizosaccharomyces pombe</i> . <i>Molecular and Cellular Biology</i> , 2012, 32, 4206-4214.	2.3	23
35	Research Resource: Whole-Genome Estrogen Receptor $\alpha$ Binding in Mouse Uterine Tissue Revealed by ChIP-Seq. <i>Molecular Endocrinology</i> , 2012, 26, 887-898.	3.7	109
36	ART: a next-generation sequencing read simulator. <i>Bioinformatics</i> , 2012, 28, 593-594.	4.1	1,234

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37	MAP3K4/CBP-Regulated H2B Acetylation Controls Epithelial-Mesenchymal Transition in Trophoblast Stem Cells. <i>Cell Stem Cell</i> , 2011, 8, 525-537.	11.1	102
38	coMOTIF: a mixture framework for identifying transcription factor and a coregulator motif in ChIP-seq Data. <i>Bioinformatics</i> , 2011, 27, 2625-2632.	4.1	6
39	Efficiently identifying genome-wide changes with next-generation sequencing data. <i>Nucleic Acids Research</i> , 2011, 39, e130-e130.	14.5	29
40	An Integrated Pipeline for the Genome-Wide Analysis of Transcription Factor Binding Sites from ChIP-Seq. <i>PLoS ONE</i> , 2011, 6, e16432.	2.5	39
41	DNA methylation prevents CTCF-mediated silencing of the oncogene <i>BCL6</i> in B cell lymphomas. <i>Journal of Experimental Medicine</i> , 2010, 207, 1939-1950.	8.5	124
42	Estrogen-mediated Regulation of Igf1 Transcription and Uterine Growth Involves Direct Binding of Estrogen Receptor $\beta$ to Estrogen-responsive Elements. <i>Journal of Biological Chemistry</i> , 2010, 285, 2676-2685.	3.4	105
43	Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. <i>Genome Research</i> , 2010, 20, 1037-1051.	5.5	109
44	Pausing of RNA Polymerase II Disrupts DNA-Specified Nucleosome Organization to Enable Precise Gene Regulation. <i>Cell</i> , 2010, 143, 540-551.	28.9	369
45	GADEM: A Genetic Algorithm Guided Formation of Spaced Dyads Coupled with an EM Algorithm for Motif Discovery. <i>Journal of Computational Biology</i> , 2009, 16, 317-329.	1.6	95
46	The $^1\text{H}$ NMR structure of bovine $\text{Pb}^{2+}$ -osteocalcin and implications for lead toxicity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 1534-1545.	2.3	5
47	Gene set enrichment analysis for non-monotone association and multiple experimental categories. <i>BMC Bioinformatics</i> , 2008, 9, 481.	2.6	10
48	NELF-mediated stalling of Pol II can enhance gene expression by blocking promoter-proximal nucleosome assembly. <i>Genes and Development</i> , 2008, 22, 1921-1933.	5.9	256
49	fdrMotif: identifying cis-elements by an EM algorithm coupled with false discovery rate control. <i>Bioinformatics</i> , 2008, 24, 629-636.	4.1	8
50	Oct4/Sox2-Regulated miR-302 Targets Cyclin D1 in Human Embryonic Stem Cells. <i>Molecular and Cellular Biology</i> , 2008, 28, 6426-6438.	2.3	462
51	GAPWM: a genetic algorithm method for optimizing a position weight matrix. <i>Bioinformatics</i> , 2007, 23, 1188-1194.	4.1	34
52	The Ubiquitin-Interacting Motif-containing Protein RAP80 Interacts with BRCA1 and Functions in DNA Damage Repair Response. <i>Cancer Research</i> , 2007, 67, 6647-6656.	0.9	150
53	Identification and functional characterization of polymorphisms in human cyclooxygenase-1 (PTGS1). <i>Pharmacogenetics and Genomics</i> , 2007, 17, 145-160.	1.5	52
54	Identification of potential target genes for RFX4_v3, a transcription factor critical for brain development. <i>Journal of Neurochemistry</i> , 2006, 98, 860-875.	3.9	30

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55	Deuterium and its role in the machinery of evolution. <i>Journal of Theoretical Biology</i> , 2006, 238, 914-918.	1.7	16
56	Optimized mixed Markov models for motif identification. <i>BMC Bioinformatics</i> , 2006, 7, 279.	2.6	16
57	Phase analysis of circadian-related genes in two tissues. <i>BMC Bioinformatics</i> , 2006, 7, 87.	2.6	19
58	Accurate anchoring alignment of divergent sequences. <i>Bioinformatics</i> , 2006, 22, 29-34.	4.1	36
59	A random-periods model for expression of cell-cycle genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7240-7245.	7.1	45
60	Application of the GA/KNN method to SELDI proteomics data. <i>Bioinformatics</i> , 2004, 20, 1638-1640.	4.1	85
61	Gene Expression Profiling of Rat Livers Reveals Indicators of Potential Adverse Effects. <i>Toxicological Sciences</i> , 2004, 80, 193-202.	3.1	199
62	Identification of distinct and common gene expression changes after oxidative stress and gamma and ultraviolet radiation. <i>Molecular Carcinogenesis</i> , 2003, 37, 65-82.	2.7	53
63	Novel consensus DNA-binding sequence for BRCA1 protein complexes. <i>Molecular Carcinogenesis</i> , 2003, 38, 85-96.	2.7	29
64	The Three-Dimensional Structure of Bovine Calcium Ion-Bound Osteocalcin Using <sup>1</sup> H NMR Spectroscopy. <i>Biochemistry</i> , 2003, 42, 7769-7779.	2.5	76
65	ATM-Dependent and -Independent Gene Expression Changes in Response to Oxidative Stress, Gamma Irradiation, and UV Irradiation. <i>Radiation Research</i> , 2003, 160, 273-290.	1.5	52
66	Gene selection and clustering for time-course and dose-response microarray experiments using order-restricted inference. <i>Bioinformatics</i> , 2003, 19, 834-841.	4.1	185
67	Heparan sulphate N-sulphotransferase activity: reaction mechanism and substrate recognition. <i>Biochemical Society Transactions</i> , 2003, 31, 331-334.	3.4	17
68	Cloning of CYP2J2 Gene and Identification of Functional Polymorphisms. <i>Molecular Pharmacology</i> , 2002, 61, 840-852.	2.3	132
69	Prediction of Compound Signature Using High Density Gene Expression Profiling. <i>Toxicological Sciences</i> , 2002, 67, 232-240.	3.1	251
70	Regulation of DNA Replication Fork Genes by 17 $\beta$ -Estradiol. <i>Molecular Endocrinology</i> , 2002, 16, 1215-1229.	3.7	66
71	Regulation of DNA Replication Fork Genes by 17 $\alpha$ -Estradiol. <i>Molecular Endocrinology</i> , 2002, 16, 1215-1229.	3.7	42
72	Gene selection for sample classification based on gene expression data: study of sensitivity to choice of parameters of the GA/KNN method. <i>Bioinformatics</i> , 2001, 17, 1131-1142.	4.1	560

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73	Gene Assessment and Sample Classification for Gene Expression Data Using a Genetic Algorithm / k-nearest Neighbor Method. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2001, 4, 727-739.	1.1	169
74	Molecular Dynamics Simulations of the d(CCAACGTTGG) <sub>2</sub> Decamer: Influence of the Crystal Environment. <i>Biophysical Journal</i> , 2000, 78, 668-682.	0.5	51
75	New tricks for modelers from the crystallography toolkit: the particle mesh Ewald algorithm and its use in nucleic acid simulations. <i>Structure</i> , 1999, 7, R55-R60.	3.3	571
76	An Atomic Model for the Pleated $\beta$ -Sheet Structure of A $\beta$ Amyloid Protofilaments. <i>Biophysical Journal</i> , 1999, 76, 2871-2878.	0.5	120
77	Identification of Residues 286 and 289 as Critical for Conferring Substrate Specificity of Human CYP2C9 for Diclofenac and Ibuprofen. <i>Archives of Biochemistry and Biophysics</i> , 1998, 357, 240-248.	3.0	58
78	Purification of Soluble Cytochrome b 5 as a Component of the Reductive Activation of Porcine Methionine Synthase. <i>Journal of Biological Chemistry</i> , 1998, 273, 26248-26255.	3.4	35
79	The Roles of Individual $\beta$ -Carboxyglutamate Residues in the Solution Structure and Cation-dependent Properties of Conantokin-T. <i>Journal of Biological Chemistry</i> , 1998, 273, 7512-7522.	3.4	27
80	Conformational Changes in Conantokin-G Induced upon Binding of Calcium and Magnesium as Revealed by NMR Structural Analysis. <i>Journal of Biological Chemistry</i> , 1998, 273, 16248-16258.	3.4	36
81	Vertical-scanning Mutagenesis of a Critical Tryptophan in the Minor Groove Binding Track of HIV-1 Reverse Transcriptase. <i>Journal of Biological Chemistry</i> , 1998, 273, 30435-30442.	3.4	35
82	Role of $\beta$ -Carboxyglutamic Acid in the Calcium-Induced Structural Transition of Conantokin G, a Conotoxin from the Marine Snail <i>Conus geographus</i> . <i>Biochemistry</i> , 1997, 36, 15677-15684.	2.5	54
83	Refinement of the NMR Solution Structure of the $\beta$ -Carboxyglutamic Acid Domain of Coagulation Factor IX Using Molecular Dynamics Simulation with Initial Ca <sup>2+</sup> Positions Determined by a Genetic Algorithm. <i>Biochemistry</i> , 1997, 36, 2132-2138.	2.5	53
84	Prediction of solution structures of the Ca <sup>2+</sup> -bound gamma-carboxyglutamic acid domains of protein S and homolog growth arrest specific protein 6: use of the particle mesh Ewald method. <i>Biophysical Journal</i> , 1997, 73, 1847-1856.	0.5	19
85	A minor groove binding track in reverse transcriptase. <i>Nature Structural Biology</i> , 1997, 4, 194-197.	9.7	111
86	Protection against Methoxyacetic-Acid-Induced Spermatocyte Apoptosis with Calcium Channel Blockers in Cultured Rat Seminiferous Tubules: Possible Mechanisms. <i>Toxicology and Applied Pharmacology</i> , 1997, 144, 105-119.	2.8	37
87	Characterization of $\beta$ -Carboxyglutamic Acid Residue 21 of Human Factor IX. <i>Biochemistry</i> , 1996, 35, 10321-10327.	2.5	9
88	Identification of Residues 99, 220, and 221 of Human Cytochrome P450 2C19 as Key Determinants of Omeprazole Hydroxylase Activity. <i>Journal of Biological Chemistry</i> , 1996, 271, 12496-12501.	3.4	77
89	Computational Studies of Human Prothrombin Fragment 1 the Gla Domain of Factor IX and Several Biologically Interesting Mutants. <i>Pathophysiology of Haemostasis and Thrombosis: International Journal on Haemostasis and Thrombosis Research</i> , 1996, 26, 54-59.	0.3	2
90	Homology modeling and molecular dynamics simulation of human prothrombin fragment 1. <i>Protein Science</i> , 1995, 4, 2341-2348.	7.6	18

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91	Antitumor Agents 155. Synthesis and Biological Evaluation of 3',6,7-Substituted 2-Phenyl-4-quinolones as Antimicrotubule Agents. <i>Journal of Medicinal Chemistry</i> , 1994, 37, 3400-3407.	6.4	118
92	Antitumor Agents. 150. 2',3',4',5',5,6,7-Substituted 2-Phenyl-4-quinolones and Related Compounds: Their Synthesis, Cytotoxicity, and Inhibition of Tubulin Polymerization. <i>Journal of Medicinal Chemistry</i> , 1994, 37, 1126-1135.	6.4	119
93	Antitumor Agents, 138. Rotenoids and Isoflavones as Cytotoxic Constituents from <i>Amorpha fruticosa</i> . <i>Journal of Natural Products</i> , 1993, 56, 690-698.	3.0	74