Leping Li

List of Publications by Year
in descending order

93 papers	8,541 citations	57758 44 h-index	48315 88 g-index
95 all docs	95 docs citations	95 times ranked	13349 citing authors

#	ARTICLE	IF	CITATIONS
1	ART: a next-generation sequencing read simulator. Bioinformatics, 2012, 28, 593-594.	4.1	1,234
2	New tricks for modelers from the crystallography toolkit: the particle mesh Ewald algorithm and its use in nucleic acid simulations. Structure, 1999, 7, R55-R60.	3.3	571
3	Gene selection for sample classification based on gene expression data: study of sensitivity to choice of parameters of the GA/KNN method. Bioinformatics, 2001, 17, 1131-1142.	4.1	560
4	Oct4/Sox2-Regulated miR-302 Targets Cyclin D1 in Human Embryonic Stem Cells. Molecular and Cellular Biology, 2008, 28, 6426-6438.	2.3	462
5	Pausing of RNA Polymerase II Disrupts DNA-Specified Nucleosome Organization to Enable Precise Gene Regulation. Cell, 2010, 143, 540-551.	28.9	369
6	ENmix: a novel background correction method for Illumina HumanMethylation450 BeadChip. Nucleic Acids Research, 2016, 44, e20-e20.	14.5	267
7	NELF-mediated stalling of Pol II can enhance gene expression by blocking promoter-proximal nucleosome assembly. Genes and Development, 2008, 22, 1921-1933.	5.9	256
8	Prediction of Compound Signature Using High Density Gene Expression Profiling. Toxicological Sciences, 2002, 67, 232-240.	3.1	251
9	Gene Expression Profiling of Rat Livers Reveals Indicators of Potential Adverse Effects. Toxicological Sciences, 2004, 80, 193-202.	3.1	199
10	Gene selection and clustering for time-course and dose-response microarray experiments using order-restricted inference. Bioinformatics, 2003, 19, 834-841.	4.1	185
11	Gene Assessment and Sample Classification for Gene Expression Data Using a Genetic Algorithm / k-nearest Neighbor Method. Combinatorial Chemistry and High Throughput Screening, 2001, 4, 727-739.	1.1	169
12	The Ubiquitin-Interacting Motif–Containing Protein RAP80 Interacts with BRCA1 and Functions in DNA Damage Repair Response. Cancer Research, 2007, 67, 6647-6656.	0.9	150
13	PAVIS: a tool for <u>P</u>eak <u>A</u>nnotation and <u>Vis</u>ualization. Bioinformatics, 2013, 29, 3097-3099.	4.1	148
14	A comprehensive genomic pan-cancer classification using The Cancer Genome Atlas gene expression data. BMC Genomics, 2017, 18, 508.	2.8	145
15	Cloning ofCYP2J2Gene and Identification of Functional Polymorphisms. Molecular Pharmacology, 2002, 61, 840-852.	2.3	132
16	DNA methylation prevents CTCF-mediated silencing of the oncogene <i>BCL6</i> in B cell lymphomas. Journal of Experimental Medicine, 2010, 207, 1939-1950.	8.5	124
17	An Atomic Model for the Pleated β-Sheet Structure of Aβ Amyloid Protofilaments. Biophysical Journal, 1999, 76, 2871-2878.	0.5	120
18	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. Journal of Medicinal Chemistry, 1994, 37, 1126-1135.	6.4	119

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19	Antitumor Agents 155. Synthesis and Biological Evaluation of 3',6,7-Substituted 2-Phenyl-4-quinolones as Antimicrotubule Agents. Journal of Medicinal Chemistry, 1994, 37, 3400-3407.	6.4	118
20	A minor groove binding track in reverse transcriptase. Nature Structural Biology, 1997, 4, 194-197.	9.7	111
21	Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. Genome Research, 2010, 20, 1037-1051.	5.5	109
22	Research Resource: Whole-Genome Estrogen Receptor Î± Binding in Mouse Uterine Tissue Revealed by ChIP-Seq. Molecular Endocrinology, 2012, 26, 887-898.	3.7	109
23	Estrogen-mediated Regulation of Igf1 Transcription and Uterine Growth Involves Direct Binding of Estrogen Receptor Î± to Estrogen-responsive Elements. Journal of Biological Chemistry, 2010, 285, 2676-2685.	3.4	105
24	MAP3K4/CBP-Regulated H2B Acetylation Controls Epithelial-Mesenchymal Transition in Trophoblast Stem Cells. Cell Stem Cell, 2011, 8, 525-537.	11.1	102
25	GADEM: A Genetic Algorithm Guided Formation of Spaced Dyads Coupled with an EM Algorithm for Motif Discovery. Journal of Computational Biology, 2009, 16, 317-329.	1.6	95
26	Transcriptional Repression by the BRG1-SWI/SNF Complex Affects the Pluripotency of Human Embryonic Stem Cells. Stem Cell Reports, 2014, 3, 460-474.	4.8	93
27	Application of the GA/KNN method to SELDI proteomics data. Bioinformatics, 2004, 20, 1638-1640.	4.1	85
28	Identification of Residues 99, 220, and 221 of Human Cytochrome P450 2C19 as Key Determinants of Omeprazole Hydroxylase Activity. Journal of Biological Chemistry, 1996, 271, 12496-12501.	3.4	77
29	The Three-Dimensional Structure of Bovine Calcium Ion-Bound Osteocalcin Using 1H NMR Spectroscopyâ€. Biochemistry, 2003, 42, 7769-7779.	2.5	76
30	Revealing a human p53 universe. Nucleic Acids Research, 2018, 46, 8153-8167.	14.5	75
31	Antitumor Agents, 138. Rotenoids and Isoflavones as Cytotoxic Constituents from Amorpha fruticosa. Journal of Natural Products, 1993, 56, 690-698.	3.0	74
32	HNF4Î± regulates sulfur amino acid metabolism and confers sensitivity to methionine restriction in liver cancer. Nature Communications, 2020, 11, 3978.	12.8	73
33	Characterization of constitutive CTCF/cohesin loci: a possible role in establishing topological domains in mammalian genomes. BMC Genomics, 2013, 14, 553.	2.8	69
34	Regulation of DNA Replication Fork Genes by 17Î²-Estradiol. Molecular Endocrinology, 2002, 16, 1215-1229.	3.7	66
35	Haploinsufficiency of SIRT1 Enhances Glutamine Metabolism and Promotes Cancer Development. Current Biology, 2017, 27, 483-494.	3.9	59
36	Identification of Residues 286 and 289 as Critical for Conferring Substrate Specificity of Human CYP2C9 for Diclofenac and Ibuprofen. Archives of Biochemistry and Biophysics, 1998, 357, 240-248.	3.0	58

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37	Identification and analysis of murine pancreatic islet enhancers. Diabetologia, 2013, 56, 542-552.	6.3	55
38	Role of Î³-Carboxyglutamic Acid in the Calcium-Induced Structural Transition of Conantokin G, a Conotoxin from the Marine SnailConus geographusâ€šâ€¡. Biochemistry, 1997, 36, 15677-15684.	2.5	54
39	p53 integrates host defense and cell fate during bacterial pneumonia. Journal of Experimental Medicine, 2013, 210, 891-904.	8.5	54
40	Refinement of the NMR Solution Structure of the Î³-Carboxyglutamic Acid Domain of Coagulation Factor IX Using Molecular Dynamics Simulation with Initial Ca2+Positions Determined by a Genetic Algorithmâ€. Biochemistry, 1997, 36, 2132-2138.	2.5	53
41	Identification of distinct and common gene expression changes after oxidative stress and gamma and ultraviolet radiation. Molecular Carcinogenesis, 2003, 37, 65-82.	2.7	53
42	ATM-Dependent and -Independent Gene Expression Changes in Response to Oxidative Stress, Gamma Irradiation, and UV Irradiation. Radiation Research, 2003, 160, 273-290.	1.5	52
43	Identification and functional characterization of polymorphisms in human cyclooxygenase-1 (PTGS1). Pharmacogenetics and Genomics, 2007, 17, 145-160.	1.5	52
44	Molecular Dynamics Simulations of the d(CCAACGTTGG)2 Decamer: Influence of the Crystal Environment. Biophysical Journal, 2000, 78, 668-682.	0.5	51
45	A random-periods model for expression of cell-cycle genes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7240-7245.	7.1	45
46	Novel DNA Motif Binding Activity Observed In Vivo With an Estrogen Receptor Î± Mutant Mouse. Molecular Endocrinology, 2014, 28, 899-911.	3.7	42
47	CDSeq: A novel complete deconvolution method for dissecting heterogeneous samples using gene expression data. PLoS Computational Biology, 2019, 15, e1007510.	3.2	42
48	Regulation of DNA Replication Fork Genes by 17Â-Estradiol. Molecular Endocrinology, 2002, 16, 1215-1229.	3.7	42
49	Diethylstilbestrol (DES)-Stimulated Hormonal Toxicity is Mediated by ER Î± Alteration of Target Gene Methylation Patterns and Epigenetic Modifiers (DNMT3A , MBD2 , and HDAC2) in the Mouse Seminal Vesicle. Environmental Health Perspectives, 2014, 122, 262-268.	6.0	40
50	An Integrated Pipeline for the Genome-Wide Analysis of Transcription Factor Binding Sites from ChIP-Seq. PLoS ONE, 2011, 6, e16432.	2.5	39
51	Protection against Methoxyacetic-Acid-Induced Spermatocyte Apoptosis with Calcium Channel Blockers in Cultured Rat Seminiferous Tubules: Possible Mechanisms. Toxicology and Applied Pharmacology, 1997, 144, 105-119.	2.8	37
52	Sleep Apnea and Hypoventilation in Patients with Down Syndrome: Analysis of 144 Polysomnogram Studies. Children, 2017, 4, 55.	1.5	37
53	Conformational Changes in Conantokin-G Induced upon Binding of Calcium and Magnesium as Revealed by NMR Structural Analysis. Journal of Biological Chemistry, 1998, 273, 16248-16258.	3.4	36
54	Accurate anchoring alignment of divergent sequences. Bioinformatics, 2006, 22, 29-34.	4.1	36

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55	Purification of Soluble Cytochrome b 5 as a Component of the Reductive Activation of Porcine Methionine Synthase. Journal of Biological Chemistry, 1998, 273, 26248-26255.	3.4	35
56	Vertical-scanning Mutagenesis of a Critical Tryptophan in the Minor Groove Binding Track of HIV-1 Reverse Transcriptase. Journal of Biological Chemistry, 1998, 273, 30435-30442.	3.4	35
57	GAPWM: a genetic algorithm method for optimizing a position weight matrix. Bioinformatics, 2007, 23, 1188-1194.	4.1	34
58	PIK3CÎ´ expression by fibroblasts promotes triple-negative breast cancer progression. Journal of Clinical Investigation, 2020, 130, 3188-3204.	8.2	33
59	The novel p53 target TNFAIP8 variant 2 is increased in cancer and offsets p53-dependent tumor suppression. Cell Death and Differentiation, 2017, 24, 181-191.	11.2	32
60	Identification of potential target genes for RFX4_v3, a transcription factor critical for brain development. Journal of Neurochemistry, 2006, 98, 860-875.	3.9	30
61	Novel consensus DNA-binding sequence for BRCA1 protein complexes. Molecular Carcinogenesis, 2003, 38, 85-96.	2.7	29
62	Efficiently identifying genome-wide changes with next-generation sequencing data. Nucleic Acids Research, 2011, 39, e130-e130.	14.5	29
63	The Roles of Individual Î³-Carboxyglutamate Residues in the Solution Structure and Cation-dependent Properties of Conantokin-T. Journal of Biological Chemistry, 1998, 273, 7512-7522.	3.4	27
64	Toward predicting metastatic progression of melanoma based on gene expression data. Pigment Cell and Melanoma Research, 2015, 28, 453-463.	3.3	25
65	Predicting tumor response to drugs based on gene-expression biomarkers of sensitivity learned from cancer cell lines. BMC Genomics, 2021, 22, 272.	2.8	25
66	Posttranscriptional Regulation of Cell-Cell Interaction Protein-Encoding Transcripts by Zfs1p in <i>Schizosaccharomyces pombe</i>. Molecular and Cellular Biology, 2012, 32, 4206-4214.	2.3	23
67	Mediator complex component MED13 regulates zygotic genome activation and is required for postimplantation development in the mouseâ€‚â€¡. Biology of Reproduction, 2018, 98, 449-464.	2.7	23
68	IUTA: a tool for effectively detecting differential isoform usage from RNA-Seq data. BMC Genomics, 2014, 15, 862.	2.8	21
69	Prediction of solution structures of the Ca2+-bound gamma-carboxyglutamic acid domains of protein S and homolog growth arrest specific protein 6: use of the particle mesh Ewald method. Biophysical Journal, 1997, 73, 1847-1856.	0.5	19
70	Phase analysis of circadian-related genes in two tissues. BMC Bioinformatics, 2006, 7, 87.	2.6	19
71	Postâ€‚transcriptional regulation of transcript abundance by a conserved member of the tristetraprolin family in <scp><i>C</i></scp><i>andida albicans</i>. Molecular Microbiology, 2015, 95, 1036-1053.	2.5	19
72	Homology modeling and molecular dynamics simulation of human prothrombin fragment 1. Protein Science, 1995, 4, 2341-2348.	7.6	18

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73	Deficiency of the placenta- and yolk sac-specific tristetraprolin family member ZFP36L3 identifies likely mRNA targets and an unexpected link to placental iron metabolism. Development (Cambridge), 2016, 143, 1424-33.	2.5	18
74	Putative genomic characteristics of BRAF V600K versus V600E cutaneous melanoma. Melanoma Research, 2017, 27, 527-535.	1.2	18
75	Heparan sulphate N-sulphotransferase activity: reaction mechanism and substrate recognition. Biochemical Society Transactions, 2003, 31, 331-334.	3.4	17
76	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. Molecular Neurobiology, 2017, 54, 8021-8032.	4.0	17
77	Non-targeted urinary metabolomics in pregnancy and associations with fetal growth restriction. Scientific Reports, 2020, 10, 5307.	3.3	17
78	Deuterium and its role in the machinery of evolution. Journal of Theoretical Biology, 2006, 238, 914-918.	1.7	16
79	Optimized mixed Markov models for motif identification. BMC Bioinformatics, 2006, 7, 279.	2.6	16
80	The Drosophila Tis11 Protein and Its Effects on mRNA Expression in Flies. Journal of Biological Chemistry, 2014, 289, 35042-35060.	3.4	16
81	Glypican 6 is a putative biomarker for metastatic progression of cutaneous melanoma. PLoS ONE, 2019, 14, e0218067.	2.5	14
82	Id Proteins Suppress E2A-Driven Invariant Natural Killer T Cell Development prior to TCR Selection. Frontiers in Immunology, 2018, 9, 42.	4.8	13
83	CDSeqR: fast complete deconvolution for gene expression data from bulk tissues. BMC Bioinformatics, 2021, 22, 262.	2.6	11
84	Gene set enrichment analysis for non-monotone association and multiple experimental categories. BMC Bioinformatics, 2008, 9, 481.	2.6	10
85	Characterization of γ-Carboxyglutamic Acid Residue 21 of Human Factor IXâ€. Biochemistry, 1996, 35, 10321-10327.	2.5	9
86	Intestinal epithelial glucocorticoid receptor promotes chronic inflammationâ€"associated colorectal cancer. JCI Insight, 2021, 6, .	5.0	9
87	fdrMotif: identifying *cis*-elements by an EM algorithm coupled with false discovery rate control. Bioinformatics, 2008, 24, 629-636.	4.1	8
88	coMOTIF: a mixture framework for identifying transcription factor and a coregulator motif in ChIP-seq Data. Bioinformatics, 2011, 27, 2625-2632.	4.1	6
89	The 1H NMR structure of bovine Pb2+-osteocalcin and implications for lead toxicity. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2008, 1784, 1534-1545.	2.3	5
90	T-KDE: a method for genome-wide identification of constitutive protein binding sites from multiple ChIP-seq data sets. BMC Genomics, 2014, 15, 27.	2.8	3

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91	Loss of Glis3 causes dysregulation of retrotransposon silencing and germ cell demise in fetal mouse testis. Scientific Reports, 2018, 8, 9662.	3.3	3
92	Computational Studies of Human Prothrombin Fragment 1 the Gla Domain of Factor IX and Several Biological Interesting Mutants. Pathophysiology of Haemostasis and Thrombosis: International Journal on Haemostasis and Thrombosis Research, 1996, 26, 54-59.	0.3	2
93	GADGETS: a genetic algorithm for detecting epistasis using nuclear families. Bioinformatics, 2021, , .	4.1	1