

# Lixin Cheng

## List of Publications by Year in descending order

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Version: 2024-02-01

42  
papers

1,149  
citations

361296

20  
h-index

434063

31  
g-index

50  
all docs

50  
docs citations

50  
times ranked

1175  
citing authors

#	ARTICLE	IF	CITATIONS
1	Magnetic Resonance/Infrared Dual-Modal Imaging-Guided Synergistic Photothermal/Photodynamic Therapy Nanoplatfrom Based on Cu <sub>1.96</sub> S-Gd@FA for Precision Cancer Theranostics. <i>Journal of Colloid and Interface Science</i> , 2022, 615, 95-109.	5.0	11
2	Improving bulk RNA-seq classification by transferring gene signature from single cells in acute myeloid leukemia. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	18
3	meGPS: a multi-omics signature for hepatocellular carcinoma detection integrating methylome and transcriptome data. <i>Bioinformatics</i> , 2022, 38, 3513-3522.	1.8	20
4	Systematic prediction of autophagy-related proteins using <i>Arabidopsis thaliana</i> interactome data. <i>Plant Journal</i> , 2021, 105, 708-720.	2.8	9
5	GNL-Scorer: a generalized model for predicting CRISPR on-target activity by machine learning and featurization. <i>Journal of Molecular Cell Biology</i> , 2021, 12, 909-911.	1.5	22
6	HCMB: A stable and efficient algorithm for processing the normalization of highly sparse Hi-C contact data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 2637-2645.	1.9	5
7	A robust and generalizable immune-related signature for sepsis diagnostics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	1.9	15
8	Long non-coding RNA pairs to assist in diagnosing sepsis. <i>BMC Genomics</i> , 2021, 22, 275.	1.2	21
9	Evaluating the Consistency of Gene Methylation in Liver Cancer Using Bisulfite Sequencing Data. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 671302.	1.8	11
10	A microfluidic array device for single cell capture and intracellular Ca <sup>2+</sup> response analysis induced by dynamic biochemical stimulus. <i>Bioscience Reports</i> , 2021, 41, .	1.1	3
11	Blood Circulating miRNA Pairs as a Robust Signature for Early Detection of Esophageal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 723779.	1.3	7
12	A network-based algorithm for the identification of moonlighting noncoding RNAs and its application in sepsis. <i>Briefings in Bioinformatics</i> , 2021, 22, 581-588.	3.2	28
13	A distinct giant coat protein complex II vesicle population in <i>Arabidopsis thaliana</i> . <i>Nature Plants</i> , 2021, 7, 1335-1346.	4.7	15
14	An overview and metanalysis of machine and deep learning-based CRISPR gRNA design tools. <i>RNA Biology</i> , 2020, 17, 13-22.	1.5	57
15	Preservation of microvascular barrier function requires CD31 receptor-induced metabolic reprogramming. <i>Nature Communications</i> , 2020, 11, 3595.	5.8	22
16	Up-regulation of autophagy by low concentration of salicylic acid delays methyl jasmonate-induced leaf senescence. <i>Scientific Reports</i> , 2020, 10, 11472.	1.6	18
17	Knockdown of lncRNA MALAT1 Alleviates LPS-Induced Acute Lung Injury via Inhibiting Apoptosis Through the miR-194-5p/FOXP2 Axis. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 586869.	1.8	39
18	Metagenomic analysis of the gut microbiome in atherosclerosis patients identify cross-cohort microbial signatures and potential therapeutic target. <i>FASEB Journal</i> , 2020, 34, 14166-14181.	0.2	44

#	ARTICLE	IF	CITATIONS
19	Whole blood transcriptomic investigation identifies long non-coding RNAs as regulators in sepsis. <i>Journal of Translational Medicine</i> , 2020, 18, 217.	1.8	40
20	Polypoid Endometriosis of the Rectum and Vagina in an Adolescent. <i>Journal of Pediatric and Adolescent Gynecology</i> , 2020, 33, 581-585.	0.3	7
21	Host-Guest Protein Assembly for Affinity Purification of Methyllysine Proteomes. <i>Analytical Chemistry</i> , 2020, 92, 9322-9329.	3.2	24
22	SIRT7 Is a Prognostic Biomarker Associated With Immune Infiltration in Luminal Breast Cancer. <i>Frontiers in Oncology</i> , 2020, 10, 621.	1.3	32
23	A long non-coding RNA signature for diagnostic prediction of sepsis upon ICU admission. <i>Clinical and Translational Medicine</i> , 2020, 10, e123.	1.7	21
24	Phase-Separated Multienzyme Biosynthesis. <i>Biomacromolecules</i> , 2020, 21, 2391-2399.	2.6	24
25	Exploiting locational and topological overlap model to identify modules in protein interaction networks. <i>BMC Bioinformatics</i> , 2019, 20, 23.	1.2	30
26	RST1 Is a FREE1 Suppressor That Negatively Regulates Vacuolar Trafficking in Arabidopsis. <i>Plant Cell</i> , 2019, 31, 2152-2168.	3.1	20
27	Predicting associations among drugs, targets and diseases by tensor decomposition for drug repositioning. <i>BMC Bioinformatics</i> , 2019, 20, 628.	1.2	20
28	Normalization Methods for the Analysis of Unbalanced Transcriptome Data: A Review. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 358.	2.0	72
29	Quantification of non-coding RNA target localization diversity and its application in cancers. <i>Journal of Molecular Cell Biology</i> , 2018, 10, 130-138.	1.5	36
30	Identification and characterization of moonlighting long non-coding RNAs based on RNA and protein interactome. <i>Bioinformatics</i> , 2018, 34, 3519-3528.	1.8	26
31	SMILE: a novel procedure for subcellular module identification with localisation expansion. <i>IET Systems Biology</i> , 2018, 12, 55-61.	0.8	21
32	Full Characterization of Localization Diversity in the Human Protein Interactome. <i>Journal of Proteome Research</i> , 2017, 16, 3019-3029.	1.8	22
33	SMILE. , 2017, , .		7
34	CrossNorm: a novel normalization strategy for microarray data in cancers. <i>Scientific Reports</i> , 2016, 6, 18898.	1.6	46
35	ICN: a normalization method for gene expression data considering the over-expression of informative genes. <i>Molecular BioSystems</i> , 2016, 12, 3057-3066.	2.9	28
36	VirBase: a resource for virus-host ncRNA-associated interactions. <i>Nucleic Acids Research</i> , 2015, 43, D578-D582.	6.5	81

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37	Mammalian ncRNA-disease repository: a global view of ncRNA-mediated disease network. <i>Cell Death and Disease</i> , 2013, 4, e765-e765.	2.7	96
38	Extensive up-regulation of gene expression in cancer: the normalised use of microarray data. <i>Molecular BioSystems</i> , 2012, 8, 818.	2.9	27
39	Comparison of different normalization assumptions for analyses of DNA methylation data from the cancer genome. <i>Gene</i> , 2012, 506, 36-42.	1.0	14
40	Extensive increase of microarray signals in cancers calls for novel normalization assumptions. <i>Computational Biology and Chemistry</i> , 2011, 35, 126-130.	1.1	25
41	Evaluating the Consistency of Differential Expression of MicroRNA Detected in Human Cancers. <i>Molecular Cancer Therapeutics</i> , 2011, 10, 752-760.	1.9	9
42	Extracting consistent knowledge from highly inconsistent cancer gene data sources. <i>BMC Bioinformatics</i> , 2010, 11, 76.	1.2	46