Lixin Cheng

List of Publications by Year
in descending order

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	Mammalian ncRNA-disease repository: a global view of ncRNA-mediated disease network. Cell Death and Disease, 2013, 4, e765-e765.	2.7	96
2	ViRBase: a resource for virus–host ncRNA-associated interactions. Nucleic Acids Research, 2015, 43, D578-D582.	6.5	81
3	Normalization Methods for the Analysis of Unbalanced Transcriptome Data: A Review. Frontiers in Bioengineering and Biotechnology, 2019, 7, 358.	2.0	72
4	An overview and metanalysis of machine and deep learning-based CRISPR gRNA design tools. RNA Biology, 2020, 17, 13-22.	1.5	57
5	Extracting consistent knowledge from highly inconsistent cancer gene data sources. BMC Bioinformatics, 2010, 11, 76.	1.2	46
6	CrossNorm: a novel normalization strategy for microarray data in cancers. Scientific Reports, 2016, 6, 18898.	1.6	46
7	Metagenomic analysis of the gut microbiome in atherosclerosis patients identify cross‐cohort microbial signatures and potential therapeutic target. FASEB Journal, 2020, 34, 14166-14181.	0.2	44
8	Whole blood transcriptomic investigation identifies long non-coding RNAs as regulators in sepsis. Journal of Translational Medicine, 2020, 18, 217.	1.8	40
9	Knockdown of lncRNA MALAT1 Alleviates LPS-Induced Acute Lung Injury via Inhibiting Apoptosis Through the miR-194-5p/FOXP2 Axis. Frontiers in Cell and Developmental Biology, 2020, 8, 586869.	1.8	39
10	Quantification of non-coding RNA target localization diversity and its application in cancers. Journal of Molecular Cell Biology, 2018, 10, 130-138.	1.5	36
11	SIRT7 Is a Prognostic Biomarker Associated With Immune Infiltration in Luminal Breast Cancer. Frontiers in Oncology, 2020, 10, 621.	1.3	32
12	Exploiting locational and topological overlap model to identify modules in protein interaction networks. BMC Bioinformatics, 2019, 20, 23.	1.2	30
13	ICN: a normalization method for gene expression data considering the over-expression of informative genes. Molecular BioSystems, 2016, 12, 3057-3066.	2.9	28
14	A network-based algorithm for the identification of moonlighting noncoding RNAs and its application in sepsis. Briefings in Bioinformatics, 2021, 22, 581-588.	3.2	28
15	Extensive up-regulation of gene expression in cancer: the normalised use of microarray data. Molecular BioSystems, 2012, 8, 818.	2.9	27
16	Identification and characterization of moonlighting long non-coding RNAs based on RNA and protein interactome. Bioinformatics, 2018, 34, 3519-3528.	1.8	26
17	Extensive increase of microarray signals in cancers calls for novel normalization assumptions. Computational Biology and Chemistry, 2011, 35, 126-130.	1.1	25
18	Host–Guest Protein Assembly for Affinity Purification of Methyllysine Proteomes. Analytical Chemistry, 2020, 92, 9322-9329.	3.2	24

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19	Phase-Separated Multienzyme Biosynthesis. Biomacromolecules, 2020, 21, 2391-2399.	2.6	24
20	Full Characterization of Localization Diversity in the Human Protein Interactome. Journal of Proteome Research, 2017, 16, 3019-3029.	1.8	22
21	Preservation of microvascular barrier function requires CD31 receptor-induced metabolic reprogramming. Nature Communications, 2020, 11, 3595.	5.8	22
22	GNL-Scorer: a generalized model for predicting CRISPR on-target activity by machine learning and featurization. Journal of Molecular Cell Biology, 2021, 12, 909-911.	1.5	22
23	SMILE: a novel procedure for subcellular module identification with localisation expansion. IET Systems Biology, 2018, 12, 55-61.	0.8	21
24	A long nonâ€coding RNA signature for diagnostic prediction of sepsis upon ICU admission. Clinical and Translational Medicine, 2020, 10, e123.	1.7	21
25	Long non-coding RNA pairs to assist in diagnosing sepsis. BMC Genomics, 2021, 22, 275.	1.2	21
26	RST1 Is a FREE1 Suppressor That Negatively Regulates Vacuolar Trafficking in Arabidopsis. Plant Cell, 2019, 31, 2152-2168.	3.1	20
27	Predicting associations among drugs, targets and diseases by tensor decomposition for drug repositioning. BMC Bioinformatics, 2019, 20, 628.	1.2	20
28	meGPS: a multi-omics signature for hepatocellular carcinoma detection integrating methylome and transcriptome data. Bioinformatics, 2022, 38, 3513-3522.	1.8	20
29	Up-regulation of autophagy by low concentration of salicylic acid delays methyl jasmonate-induced leaf senescence. Scientific Reports, 2020, 10, 11472.	1.6	18
30	Improving bulk RNA-seq classification by transferring gene signature from single cells in acute myeloid leukemia. Briefings in Bioinformatics, 2022, 23, .	3.2	18
31	A robust and generalizable immune-related signature for sepsis diagnostics. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	15
32	A distinct giant coat protein complex II vesicle population in Arabidopsis thaliana. Nature Plants, 2021, 7, 1335-1346.	4.7	15
33	Comparison of different normalization assumptions for analyses of DNA methylation data from the cancer genome. Gene, 2012, 506, 36-42.	1.0	14
34	Evaluating the Consistency of Gene Methylation in Liver Cancer Using Bisulfite Sequencing Data. Frontiers in Cell and Developmental Biology, 2021, 9, 671302.	1.8	11
35	Magnetic Resonance/Infrared Dual-Modal Imaging-Guided Synergistic Photothermal/Photodynamic Therapy Nanoplatform Based on Cu1.96S-Gd@FA for Precision Cancer Theranostics. Journal of Colloid and Interface Science, 2022, 615, 95-109.	5.0	11
36	Evaluating the Consistency of Differential Expression of MicroRNA Detected in Human Cancers. Molecular Cancer Therapeutics, 2011, 10, 752-760.	1.9	9

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37	Systematic prediction of autophagy‑related proteins using <i>Arabidopsis thaliana</i> interactome data. Plant Journal, 2021, 105, 708-720.	2.8	9
38	SMILE. , 2017, , .		7
39	Polypoid Endometriosis of the Rectum and Vagina in an Adolescent. Journal of Pediatric and Adolescent Gynecology, 2020, 33, 581-585.	0.3	7
40	Blood Circulating miRNA Pairs as a Robust Signature for Early Detection of Esophageal Cancer. Frontiers in Oncology, 2021, 11, 723779.	1.3	7
41	HCMB: A stable and efficient algorithm for processing the normalization of highly sparse Hi-C contact data. Computational and Structural Biotechnology Journal, 2021, 19, 2637-2645.	1.9	5
42	A microfluidic array device for single cell capture and intracellular Ca2+ response analysis induced by dynamic biochemical stimulus. Bioscience Reports, 2021, 41, .	1.1	3