

# Cankun Wang

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17  
papers

234  
citations

10  
h-index

15  
g-index

25  
ext. papers

433  
ext. citations

8.2  
avg, IF

3.44  
L-index

#	Paper	IF	Citations
17	LncFinder: an integrated platform for long non-coding RNA identification utilizing sequence intrinsic composition, structural information and physicochemical property. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 2009-2027	13.4	47
16	scGNN is a novel graph neural network framework for single-cell RNA-Seq analyses. <i>Nature Communications</i> , <b>2021</b> , 12, 1882	17.4	23
15	QUBIC2: a novel and robust biclustering algorithm for analyses and interpretation of large-scale RNA-Seq data. <i>Bioinformatics</i> , <b>2020</b> , 36, 1143-1149	7.2	23
14	IRIS-EDA: An integrated RNA-Seq interpretation system for gene expression data analysis. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006792	5	20
13	scREAD: A Single-Cell RNA-Seq Database for Alzheimer's Disease. <i>IScience</i> , <b>2020</b> , 23, 101769	6.1	19
12	CirRNAPL: A web server for the identification of circRNA based on extreme learning machine. <i>Computational and Structural Biotechnology Journal</i> , <b>2020</b> , 18, 834-842	6.8	19
11	IRIS3: integrated cell-type-specific regulon inference server from single-cell RNA-Seq. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W275-W286	20.1	18
10	Using Machine Learning to Measure Relatedness Between Genes: A Multi-Features Model. <i>Scientific Reports</i> , <b>2019</b> , 9, 4192	4.9	16
9	Prediction of regulatory motifs from human Chip-sequencing data using a deep learning framework. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 7809-7824	20.1	13
8	A New Machine Learning-Based Framework for Mapping Uncertainty Analysis in RNA-Seq Read Alignment and Gene Expression Estimation. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 313	4.5	11
7	Water Deficit Transcriptomic Responses Differ in the Invasive and Established in the Southern and Northern United States. <i>Plants</i> , <b>2020</b> , 9,	4.5	4
6	scGNN: a novel graph neural network framework for single-cell RNA-Seq analyses		4
5	Spatially resolved transcriptomics reveals unique gene signatures associated with human temporal cortical architecture and Alzheimer's pathology		4
4	GeneQC: A quality control tool for gene expression estimation based on RNA-sequencing reads mapping		3
3	Improved Draft Genome Sequence of <i>Pseudomonas poae</i> A2-S9, a Strain with Plant Growth-Promoting Activity. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	2
2	Use of scREAD to explore and analyze single-cell and single-nucleus RNA-seq data for Alzheimer's disease. <i>STAR Protocols</i> , <b>2021</b> , 2, 100513	1.4	1
1	Prediction of Moonlighting Proteins Using Multimodal Deep Ensemble Learning. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 630379	4.5	1

