

Jie Liao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10041273/publications.pdf>

Version: 2024-02-01

16
papers

960
citations

687363

13
h-index

996975

15
g-index

21
all docs

21
docs citations

21
times ranked

1075
citing authors

#	ARTICLE	IF	CITATIONS
1	scCATCH: Automatic Annotation on Cell Types of Clusters from Single-Cell RNA Sequencing Data. <i>IScience</i> , 2020, 23, 100882.	4.1	178
2	Copy number variation is highly correlated with differential gene expression: a pan-cancer study. <i>BMC Medical Genetics</i> , 2019, 20, 175.	2.1	174
3	CellTalkDB: a manually curated database of ligand-receptor interactions in humans and mice. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	146
4	Uncovering an Organ's Molecular Architecture at Single-Cell Resolution by Spatially Resolved Transcriptomics. <i>Trends in Biotechnology</i> , 2021, 39, 43-58.	9.3	145
5	New avenues for systematically inferring cell-cell communication: through single-cell transcriptomics data. <i>Protein and Cell</i> , 2020, 11, 866-880.	11.0	82
6	scDeepSort: a pre-trained cell-type annotation method for single-cell transcriptomics using deep learning with a weighted graph neural network. <i>Nucleic Acids Research</i> , 2021, 49, e122-e122.	14.5	61
7	Multiplexing Methods for Simultaneous Large-scale Transcriptomic Profiling of Samples at Single-Cell Resolution. <i>Advanced Science</i> , 2021, 8, e2101229.	11.2	29
8	Network pharmacology study reveals energy metabolism and apoptosis pathways-mediated cardioprotective effects of Shenqi Fuzheng. <i>Journal of Ethnopharmacology</i> , 2018, 227, 155-165.	4.1	28
9	An ultra-robust fingerprinting method for quality assessment of traditional Chinese medicine using multiple reaction monitoring mass spectrometry. <i>Journal of Pharmaceutical Analysis</i> , 2021, 11, 88-95.	5.3	26
10	Transcriptomics: a sword to cut the Gordian knot of traditional Chinese medicine. <i>Biomarkers in Medicine</i> , 2015, 9, 1201-1213.	1.4	23
11	Deciphering chemical interactions between Glycyrrhizae Radix and Coptidis Rhizoma by liquid chromatography with transformed multiple reaction monitoring mass spectrometry. <i>Journal of Separation Science</i> , 2017, 40, 1254-1265.	2.5	22
12	Revealing topics and their evolution in biomedical literature using Bio-DTM: a case study of ginseng. <i>Chinese Medicine</i> , 2017, 12, 27.	4.0	16
13	Prediction of Adverse Drug Reactions by Combining Biomedical Tripartite Network and Graph Representation Model. <i>Chemical Research in Toxicology</i> , 2020, 33, 202-210.	3.3	16
14	Identify differential genes and cell subclusters from time-series scRNA-seq data using scTITANS. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4132-4141.	4.1	6
15	Tracing the cell-type-specific modules of immune responses during COVID-19 progression using scDisProcema. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 3545-3555.	4.1	1
16	A Clinical Genomics-Guided Prioritizing Strategy Enables Selecting Proper Cancer Cell Lines for Biomedical Research. <i>IScience</i> , 2020, 23, 101748.	4.1	0