

Sijia Huang

List of Publications by Year in descending order

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12
papers

1,270
citations

932766

10
h-index

1199166

12
g-index

12
all docs

12
docs citations

12
times ranked

3117
citing authors

#	ARTICLE	IF	CITATIONS
1	DeepProg: an ensemble of deep-learning and machine-learning models for prognosis prediction using multi-omics data. <i>Genome Medicine</i> , 2021, 13, 112.	3.6	90
2	Multimodal Meta-Analysis of 1,494 Hepatocellular Carcinoma Samples Reveals Significant Impact of Consensus Driver Genes on Phenotypes. <i>Clinical Cancer Research</i> , 2019, 25, 463-472.	3.2	41
3	Lilikoi: an R package for personalized pathway-based classification modeling using metabolomics data. <i>GigaScience</i> , 2018, 7, .	3.3	25
4	More Is Better: Recent Progress in Multi-Omics Data Integration Methods. <i>Frontiers in Genetics</i> , 2017, 8, 84.	1.1	517
5	Using single-cell multiple omics approaches to resolve tumor heterogeneity. <i>Clinical and Translational Medicine</i> , 2017, 6, 46.	1.7	73
6	Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer. <i>Oncotarget</i> , 2016, 7, 55249-55263.	0.8	14
7	A Nomogram Derived by Combination of Demographic and Biomarker Data Improves the Noninvasive Evaluation of Patients at Risk for Bladder Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1361-1366.	1.1	8
8	Time Series miRNA-mRNA integrated analysis reveals critical miRNAs and targets in macrophage polarization. <i>Scientific Reports</i> , 2016, 6, 37446.	1.6	79
9	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. <i>Genome Medicine</i> , 2016, 8, 34.	3.6	122
10	Pan-Cancer Analyses Reveal Long Intergenic Non-Coding RNAs Relevant to Tumor Diagnosis, Subtyping and Prognosis. <i>EBioMedicine</i> , 2016, 7, 62-72.	2.7	33
11	A Novel Model to Combine Clinical and Pathway-Based Transcriptomic Information for the Prognosis Prediction of Breast Cancer. <i>PLoS Computational Biology</i> , 2014, 10, e1003851.	1.5	64
12	Power analysis and sample size estimation for RNA-Seq differential expression. <i>Rna</i> , 2014, 20, 1684-1696.	1.6	204