

Xiangjie Li

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.

18
papers

1,003
citations

7
h-index

20
g-index

20
ext. papers

1,482
ext. citations

8.4
avg, IF

5.51
L-index

#	Paper	IF	Citations
18	The ACE2 expression in human heart indicates new potential mechanism of heart injury among patients infected with SARS-CoV-2. <i>Cardiovascular Research</i> , 2020 , 116, 1097-1100	9.9	641
17	The SARS-CoV-2 receptor ACE2 expression of maternal-fetal interface and fetal organs by single-cell transcriptome study. <i>PLoS ONE</i> , 2020 , 15, e0230295	3.7	216
16	Deep learning enables accurate clustering with batch effect removal in single-cell RNA-seq analysis. <i>Nature Communications</i> , 2020 , 11, 2338	17.4	58
15	SpaGCN: Integrating gene expression, spatial location and histology to identify spatial domains and spatially variable genes by graph convolutional network. <i>Nature Methods</i> , 2021 , 18, 1342-1351	21.6	27
14	Iterative transfer learning with neural network for clustering and cell type classification in single-cell RNA-seq analysis. <i>Nature Machine Intelligence</i> , 2020 , 2, 607-618	22.5	23
13	The SARS-CoV-2 receptor ACE2 expression of maternal-fetal interface and fetal organs by single cell transcriptome study		9
12	Integrating gene expression, spatial location and histology to identify spatial domains and spatially variable genes by graph convolutional network		7
11	Plasma testosterone and arrhythmic events in male patients with arrhythmogenic right ventricular cardiomyopathy. <i>ESC Heart Failure</i> , 2020 , 7, 1547-1559	3.7	6
10	A joint deep learning model enables simultaneous batch effect correction, denoising, and clustering in single-cell transcriptomics. <i>Genome Research</i> , 2021 , 31, 1753-1766	9.7	6
9	A Joint Deep Learning Model for Simultaneous Batch Effect Correction, Denoising and Clustering in Single-Cell Transcriptomics		5
8	ScCAEs: deep clustering of single-cell RNA-seq via convolutional autoencoder embedding and soft K-means. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	2
7	Sufficient dimension reduction and prediction through cumulative slicing PFC. <i>Journal of Statistical Computation and Simulation</i> , 2018 , 88, 1172-1190	0.9	1
6	Single-cell transcriptomic identified HIF1A as a target for attenuating acute rejection after heart transplantation. <i>Basic Research in Cardiology</i> , 2021 , 116, 64	11.8	1
5	Identification of reference genes for gene expression studies among different developmental stages of murine hearts. <i>BMC Developmental Biology</i> , 2021 , 21, 13	3.1	0
4	Sufficient dimension folding via tensor inverse regression. <i>Journal of Statistical Computation and Simulation</i> , 2020 , 90, 1413-1429	0.9	
3	A model-free feature screening approach based on kernel density estimation. <i>Journal of Statistical Computation and Simulation</i> , 2017 , 87, 2450-2468	0.9	
2	Detailed Analyses of the Expression Patterns of Potential Severe Acute Respiratory Syndrome Coronavirus 2 Receptors in the Human Heart Using Single-Nucleus RNA Sequencing.. <i>Frontiers in Cardiovascular Medicine</i> , 2021 , 8, 757362	5.4	

- 1 Ultrahigh dimensional feature screening for additive model with multivariate response. *Journal of Statistical Computation and Simulation*, **2020**, 90, 775-799 0.9