

Duc Tran

List of Publications by Year in Descending Order

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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.

14
papers

96
citations

5
h-index

9
g-index

16
ext. papers

218
ext. citations

9.7
avg, IF

3.16
L-index

#	Paper	IF	Citations
14	A novel method for single-cell data imputation using subspace regression.. <i>Scientific Reports</i> , 2022 , 12, 2697	4.9	0
13	SMRT: Randomized Data Transformation for Cancer Subtyping and Big Data Analysis. <i>Frontiers in Oncology</i> , 2021 , 11, 725133	5.3	2
12	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021 , 49, W114-W124	20.1	4
11	A comprehensive survey of regulatory network inference methods using single cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	19
10	Single-Cell RNA Sequencing Data Imputation Using Deep Neural Network. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 403-410	0.4	0
9	Fast and precise single-cell data analysis using a hierarchical autoencoder. <i>Nature Communications</i> , 2021 , 12, 1029	17.4	16
8	A Novel Method for Cancer Subtyping and Risk Prediction Using Consensus Factor Analysis. <i>Frontiers in Oncology</i> , 2020 , 10, 1052	5.3	6
7	Disease subtyping using community detection from consensus networks 2020 ,		1
6	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020 , 3,	5.8	11
5	R Tutorial: Detection of Differentially Interacting Chromatin Regions From Multiple Hi-C Datasets. <i>Current Protocols in Bioinformatics</i> , 2019 , 66, e76	24.2	3
4	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 2019 , 10, 155	4.5	25
3	RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing 2019 ,		3
2	Predicting cellular position in the Drosophila embryo from Single-Cell Transcriptomics data		3
1	Fast and precise single-cell data analysis using hierarchical autoencoder		3