

Hung Nguyen

List of Publications by Citations

Source: <https://exaly.com/author-pdf/4672541/hung-nguyen-publications-by-citations.pdf>

Version: 2024-04-26

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

160
citations

7
h-index

12
g-index

20
ext. papers

350
ext. citations

7.3
avg, IF

3.71
L-index

#	Paper	IF	Citations
18	PINSPlus: a tool for tumor subtype discovery in integrated genomic data. <i>Bioinformatics</i> , 2019 , 35, 2843-2846	7.24	32
17	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , 2019 , 10, 155	4.5	25
16	Functional analysis tools for post-translational modification: a post-translational modification database for analysis of proteins and metabolic pathways. <i>Plant Journal</i> , 2019 , 99, 1003-1013	6.9	21
15	A comprehensive survey of regulatory network inference methods using single cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	19
14	Fast and precise single-cell data analysis using a hierarchical autoencoder. <i>Nature Communications</i> , 2021 , 12, 1029	17.4	16
13	A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. <i>Frontiers in Genetics</i> , 2019 , 10, 159	4.5	12
12	Multi-Omics Analysis Detects Novel Prognostic Subgroups of Breast Cancer. <i>Frontiers in Genetics</i> , 2020 , 11, 574661	4.5	11
11	A Novel Method for Cancer Subtyping and Risk Prediction Using Consensus Factor Analysis. <i>Frontiers in Oncology</i> , 2020 , 10, 1052	5.3	6
10	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2021 , 49, W114-W124	20.1	4
9	MGKA: A genetic algorithm-based clustering technique for genomic data 2019 ,		3
8	Fast and precise single-cell data analysis using hierarchical autoencoder		3
7	RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing 2019 ,		3
6	SMRT: Randomized Data Transformation for Cancer Subtyping and Big Data Analysis. <i>Frontiers in Oncology</i> , 2021 , 11, 725133	5.3	2
5	Disease subtyping using community detection from consensus networks 2020 ,		1
4	Thioesterase enzyme families: functions, structures, and mechanisms.. <i>Protein Science</i> , 2021 ,	6.3	1
3	MIA 2018 ,		1
2	Single-Cell RNA Sequencing Data Imputation Using Deep Neural Network. <i>Advances in Intelligent Systems and Computing</i> , 2021 , 403-410	0.4	0

- 1 A novel method for single-cell data imputation using subspace regression.. *Scientific Reports*, **2022**, 12, 2697 4.9 ○