

# Hung Nguyen

## 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.

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	A novel method for single-cell data imputation using subspace regression.. <i>Scientific Reports</i> , <b>2022</b> , 12, 2697	4.9	0
17	Thioesterase enzyme families: functions, structures, and mechanisms.. <i>Protein Science</i> , <b>2021</b> ,	6.3	1
16	SMRT: Randomized Data Transformation for Cancer Subtyping and Big Data Analysis. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 725133	5.3	2
15	CPA: a web-based platform for consensus pathway analysis and interactive visualization. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W114-W124	20.1	4
14	A comprehensive survey of regulatory network inference methods using single cell RNA sequencing data. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	19
13	Single-Cell RNA Sequencing Data Imputation Using Deep Neural Network. <i>Advances in Intelligent Systems and Computing</i> , <b>2021</b> , 403-410	0.4	0
12	Fast and precise single-cell data analysis using a hierarchical autoencoder. <i>Nature Communications</i> , <b>2021</b> , 12, 1029	17.4	16
11	Multi-Omics Analysis Detects Novel Prognostic Subgroups of Breast Cancer. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 574661	4.5	11
10	A Novel Method for Cancer Subtyping and Risk Prediction Using Consensus Factor Analysis. <i>Frontiers in Oncology</i> , <b>2020</b> , 10, 1052	5.3	6
9	Disease subtyping using community detection from consensus networks <b>2020</b> ,		1
8	MGKA: A genetic algorithm-based clustering technique for genomic data <b>2019</b> ,		3
7	Functional analysis tools for post-translational modification: a post-translational modification database for analysis of proteins and metabolic pathways. <i>Plant Journal</i> , <b>2019</b> , 99, 1003-1013	6.9	21
6	A Multi-Cohort and Multi-Omics Meta-Analysis Framework to Identify Network-Based Gene Signatures. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 159	4.5	12
5	A Comprehensive Survey of Tools and Software for Active Subnetwork Identification. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 155	4.5	25
4	RIA: a novel Regression-based Imputation Approach for single-cell RNA sequencing <b>2019</b> ,		3
3	PINSPlus: a tool for tumor subtype discovery in integrated genomic data. <i>Bioinformatics</i> , <b>2019</b> , 35, 2843-2846	7.2	32
2	MIA <b>2018</b> ,		1

1 Fast and precise single-cell data analysis using hierarchical autoencoder

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