

# Junjie Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1042245/publications.pdf>

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10  
papers

6,733  
citations

1163117

8  
h-index

1372567

10  
g-index

11  
all docs

11  
docs citations

11  
times ranked

13024  
citing authors

#	ARTICLE	IF	CITATIONS
1	Selection-adjusted inference: an application to confidence intervals for <i>cis</i> -eQTL effect sizes. <i>Biostatistics</i> , 2021, 22, 181-197.	1.5	6
2	Progenitor identification and SARS-CoV-2 infection in human distal lung organoids. <i>Nature</i> , 2020, 588, 670-675.	27.8	273
3	Exploratory Gene Ontology Analysis with Interactive Visualization. <i>Scientific Reports</i> , 2019, 9, 7793.	3.3	10
4	SIMLR: A Tool for Large-scale Genomic Analyses by Multi-kernel Learning. <i>Proteomics</i> , 2018, 18, 1700232.	2.2	81
5	Inflammatory Cytokine TNF $\alpha$ Promotes the Long-Term Expansion of Primary Hepatocytes in 3D Culture. <i>Cell</i> , 2018, 175, 1607-1619.e15.	28.9	211
6	Organoid Modeling of the Tumor Immune Microenvironment. <i>Cell</i> , 2018, 175, 1972-1988.e16.	28.9	870
7	Network enhancement as a general method to denoise weighted biological networks. <i>Nature Communications</i> , 2018, 9, 3108.	12.8	82
8	Massively parallel digital transcriptional profiling of single cells. <i>Nature Communications</i> , 2017, 8, 14049.	12.8	4,535
9	Visualization and analysis of single-cell RNA-seq data by kernel-based similarity learning. <i>Nature Methods</i> , 2017, 14, 414-416.	19.0	577
10	scRNASeqDB: A Database for RNA-Seq Based Gene Expression Profiles in Human Single Cells. <i>Genes</i> , 2017, 8, 368.	2.4	80