

Beate Vieth

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6422308/publications.pdf>

Version: 2024-02-01

11
papers

2,372
citations

840585

11
h-index

1281743

11
g-index

24
all docs

24
docs citations

24
times ranked

4833
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analysis of Single-Cell RNA Sequencing Methods. <i>Molecular Cell</i> , 2017, 65, 631-643.e4.	4.5	1,131
2	zUMIs - A fast and flexible pipeline to process RNA sequencing data with UMIs. <i>GigaScience</i> , 2018, 7, .	3.3	265
3	The impact of amplification on differential expression analyses by RNA-seq. <i>Scientific Reports</i> , 2016, 6, 25533.	1.6	200
4	A systematic evaluation of single cell RNA-seq analysis pipelines. <i>Nature Communications</i> , 2019, 10, 4667.	5.8	190
5	Sensitive and powerful single-cell RNA sequencing using mcSCRB-seq. <i>Nature Communications</i> , 2018, 9, 2937.	5.8	183
6	powsimR: power analysis for bulk and single cell RNA-seq experiments. <i>Bioinformatics</i> , 2017, 33, 3486-3488.	1.8	141
7	Primate iPS cells as tools for evolutionary analyses. <i>Stem Cell Research</i> , 2014, 12, 622-629.	0.3	61
8	Quantitative single-cell transcriptomics. <i>Briefings in Functional Genomics</i> , 2018, 17, 220-232.	1.3	50
9	Niche WNT5A regulates the actin cytoskeleton during regeneration of hematopoietic stem cells. <i>Journal of Experimental Medicine</i> , 2017, 214, 165-181.	4.2	41
10	Altered social behavior in mice carrying a cortical <i>Foxp2</i> deletion. <i>Human Molecular Genetics</i> , 2019, 28, 701-717.	1.4	31
11	Prime-seq, efficient and powerful bulk RNA sequencing. <i>Genome Biology</i> , 2022, 23, 88.	3.8	31