

# Catalina A Vallejos

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8922750/publications.pdf>

Version: 2024-02-01

16  
papers

2,352  
citations

840776

11  
h-index

940533

16  
g-index

26  
all docs

26  
docs citations

26  
times ranked

4113  
citing authors

#	ARTICLE	IF	CITATIONS
1	High-sensitivity cardiac troponin and the diagnosis of myocardial infarction in patients with kidney impairment. <i>Kidney International</i> , 2022, 102, 149-159.	5.2	9
2	SCRaPL: A Bayesian hierarchical framework for detecting technical associates in single cell multiomics data. <i>PLoS Computational Biology</i> , 2022, 18, e1010163.	3.2	2
3	scMET: Bayesian modeling of DNA methylation heterogeneity at single-cell resolution. <i>Genome Biology</i> , 2021, 22, 114.	8.8	14
4	Single-nucleus RNA-seq2 reveals functional crosstalk between liver zonation and ploidy. <i>Nature Communications</i> , 2021, 12, 4264.	12.8	46
5	High-Sensitivity Cardiac Troponin and the Universal Definition of Myocardial Infarction. <i>Circulation</i> , 2020, 141, 161-171.	1.6	124
6	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , 2020, 21, 31.	8.8	742
7	Exploring a world of a thousand dimensions. <i>Nature Biotechnology</i> , 2019, 37, 1423-1424.	17.5	12
8	Correcting the Mean-Variance Dependency for Differential Variability Testing Using Single-Cell RNA Sequencing Data. <i>Cell Systems</i> , 2018, 7, 284-294.e12.	6.2	71
9	High-sensitivity troponin in the evaluation of patients with suspected acute coronary syndrome: a stepped-wedge, cluster-randomised controlled trial. <i>Lancet</i> , The, 2018, 392, 919-928.	13.7	263
10	Normalizing single-cell RNA sequencing data: challenges and opportunities. <i>Nature Methods</i> , 2017, 14, 565-571.	19.0	405
11	Ageing increases cell-to-cell transcriptional variability upon immune stimulation. <i>Science</i> , 2017, 355, 1433-1436.	12.6	265
12	Incorporating unobserved heterogeneity in Weibull survival models: A Bayesian approach. <i>Econometrics and Statistics</i> , 2017, 3, 73-88.	0.8	3
13	Beyond comparisons of means: understanding changes in gene expression at the single-cell level. <i>Genome Biology</i> , 2016, 17, 70.	8.8	90
14	BASiCS: Bayesian Analysis of Single-Cell Sequencing Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004333.	3.2	264
15	Objective Bayesian Survival Analysis Using Shape Mixtures of Log-Normal Distributions. <i>Journal of the American Statistical Association</i> , 2015, 110, 697-710.	3.1	18
16	BASiCS workflow: a step-by-step analysis of expression variability using single cell RNA sequencing data. <i>F1000Research</i> , 0, 11, 59.	1.6	0