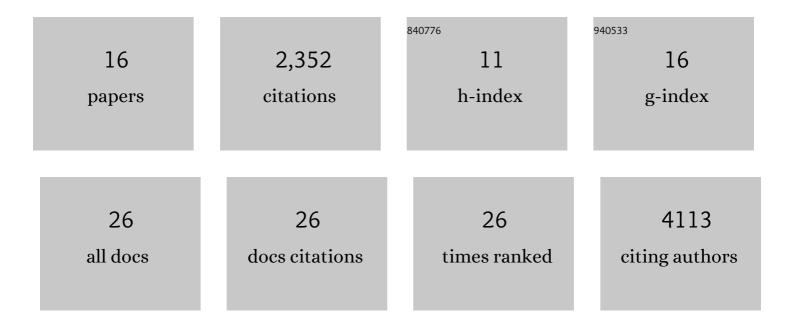
## Catalina A Vallejos

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8922750/publications.pdf Version: 2024-02-01



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