

# Maria ColomÃ© TatchÃ©

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

3,125  
citations

361413

20  
h-index

414414

32  
g-index

45  
all docs

45  
docs citations

45  
times ranked

4826  
citing authors

#	ARTICLE	IF	CITATIONS
1	Benchmarking atlas-level data integration in single-cell genomics. <i>Nature Methods</i> , 2022, 19, 41-50.	19.0	403
2	Region-level epimutation rates in <i>Arabidopsis thaliana</i> . <i>Heredity</i> , 2021, 127, 190-202.	2.6	21
3	Single-nucleus RNA-seq2 reveals functional crosstalk between liver zonation and ploidy. <i>Nature Communications</i> , 2021, 12, 4264.	12.8	46
4	Brief homogeneous TCR signals instruct common iNKT progenitors whose effector diversification is characterized by subsequent cytokine signaling. <i>Immunity</i> , 2021, 54, 2497-2513.e9.	14.3	19
5	EpiScanpy: integrated single-cell epigenomic analysis. <i>Nature Communications</i> , 2021, 12, 5228.	12.8	59
6	Computational Tool for Assessing Differential Cell-Cell Communication between Two Cohorts of Patients Using Scrna-Seq or Fasc-Sorted Bulk RNA-Seq Data. <i>Blood</i> , 2021, 138, 3285-3285.	1.4	0
7	breakpointR: an R/Bioconductor package to localize strand state changes in Strand-seq data. <i>Bioinformatics</i> , 2020, 36, 1260-1261.	4.1	32
8	Gene networks in cancer are biased by aneuploidies and sample impurities. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194444.	1.9	3
9	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
10	AlphaBeta: computational inference of epimutation rates and spectra from high-throughput DNA methylation data in plants. <i>Genome Biology</i> , 2020, 21, 260.	8.8	24
11	Altering microtubule dynamics is synergistically toxic with spindle assembly checkpoint inhibition. <i>Life Science Alliance</i> , 2020, 3, e201900499.	2.8	18
12	Endogenous retroviral insertions drive non-canonical imprinting in extra-embryonic tissues. <i>Genome Biology</i> , 2019, 20, 225.	8.8	67
13	Widespread long-range cis-regulatory elements in the maize genome. <i>Nature Plants</i> , 2019, 5, 1237-1249.	9.3	250
14	Quantification of Aneuploidy in Mammalian Systems. <i>Methods in Molecular Biology</i> , 2019, 1896, 159-190.	0.9	33
15	Statistical single cell multi-omics integration. <i>Current Opinion in Systems Biology</i> , 2018, 7, 54-59.	2.6	61
16	MLL2 conveys transcription-independent H3K4 trimethylation in oocytes. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 73-82.	8.2	127
17	METHimpute: imputation-guided construction of complete methylomes from WGBS data. <i>BMC Genomics</i> , 2018, 19, 444.	2.8	28
18	Copy number alterations assessed at the single-cell level revealed mono- and polyclonal seeding patterns of distant metastasis in a small-cell lung cancer patient. <i>Annals of Oncology</i> , 2017, 28, 1668-1670.	1.2	19

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19	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	6.4	279
20	Histone propionylation is a mark of active chromatin. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1048-1056.	8.2	148
21	Genetic sources of population epigenomic variation. <i>Nature Reviews Genetics</i> , 2016, 17, 319-332.	16.3	136
22	Single-cell sequencing reveals karyotype heterogeneity in murine and human malignancies. <i>Genome Biology</i> , 2016, 17, 115.	8.8	178
23	Signatures of Dobzhansky's Muller Incompatibilities in the Genomes of Recombinant Inbred Lines. <i>Genetics</i> , 2016, 202, 825-841.	2.9	12
24	histoneHMM: Differential analysis of histone modifications with broad genomic footprints. <i>BMC Bioinformatics</i> , 2015, 16, 60.	2.6	28
25	Rate, spectrum, and evolutionary dynamics of spontaneous epimutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6676-6681.	7.1	251
26	Mapping the Epigenetic Basis of Complex Traits. <i>Science</i> , 2014, 343, 1145-1148.	12.6	403
27	Natural variation of histone modification and its impact on gene expression in the rat genome. <i>Genome Research</i> , 2014, 24, 942-953.	5.5	53
28	Features of the <i>Arabidopsis</i> recombination landscape resulting from the combined loss of sequence variation and DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16240-16245.	7.1	145
29	Adiabatic spin cooling using high-spin Fermi gases. <i>New Journal of Physics</i> , 2011, 13, 113021.	2.9	6
30	Parametric Excitation of a 1D Gas in Integrable and Nonintegrable Cases. <i>Physical Review Letters</i> , 2011, 106, 125302.	7.8	6
31	Mott-Insulator Phases of Spin-3/2 Fermions in the Presence of Quadratic Zeeman Coupling. <i>Physical Review Letters</i> , 2010, 105, 050402.	7.8	20
32	Finite-size effects for the gap in the excitation spectrum of the one-dimensional Hubbard model. <i>Physical Review A</i> , 2010, 81, .	2.5	0
33	Two-component repulsive Fermi gases with population imbalance in elongated harmonic traps. <i>Physical Review A</i> , 2008, 78, .	2.5	10