

Rachel Patton McCord

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

5,132
citations

430874

18
h-index

434195

31
g-index

52
all docs

52
docs citations

52
times ranked

7639
citing authors

#	ARTICLE	IF	CITATIONS
1	SMILE: mutual information learning for integration of single-cell omics data. <i>Bioinformatics</i> , 2022, 38, 476-486.	4.1	29
2	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling. <i>Scientific Reports</i> , 2022, 12, 4721.	3.3	14
3	Chromosome compartmentalization alterations in prostate cancer cell lines model disease progression. <i>Journal of Cell Biology</i> , 2022, 221, .	5.2	18
4	Diagonal integration of multimodal single-cell data: potential pitfalls and paths forward. <i>Nature Communications</i> , 2022, 13, .	12.8	9
5	CoSTA: unsupervised convolutional neural network learning for spatial transcriptomics analysis. <i>BMC Bioinformatics</i> , 2021, 22, 397.	2.6	18
6	Radiation-induced DNA damage and repair effects on 3D genome organization. <i>Nature Communications</i> , 2020, 11, 6178.	12.8	70
7	Inferring chromosome radial organization from Hi-C data. <i>BMC Bioinformatics</i> , 2020, 21, 511.	2.6	9
8	Using contact statistics to characterize structure transformation of biopolymer ensembles. <i>Physical Review E</i> , 2020, 101, 012419.	2.1	6
9	Chromosome Conformation Capture and Beyond: Toward an Integrative View of Chromosome Structure and Function. <i>Molecular Cell</i> , 2020, 77, 688-708.	9.7	151
10	Lateralized Expression of Cortical Perineuronal Nets during Maternal Experience is Dependent on MECP2. <i>ENeuro</i> , 2020, 7, ENEURO.0500-19.2020.	1.9	11
11	Rapid Irreversible Transcriptional Reprogramming in Human Stem Cells Accompanied by Discordance between Replication Timing and Chromatin Compartment. <i>Stem Cell Reports</i> , 2019, 13, 193-206.	4.8	24
12	Iteratively improving Hi-C experiments one step at a time. <i>Methods</i> , 2018, 142, 47-58.	3.8	32
13	Characterizing the 3D structure and dynamics of chromosomes and proteins in a common contact matrix framework. <i>Nucleic Acids Research</i> , 2018, 46, 8143-8152.	14.5	18
14	3D Genome Organization Influences the Chromosome Translocation Pattern. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1044, 113-133.	1.6	15
15	Investigation of Spatial Organization of Chromosome Territories in Chromosome Exchange Aberrations After Ionizing Radiation Exposure. <i>Health Physics</i> , 2018, 115, 77-89.	0.5	15
16	Genome organization during the cell cycle: unity in division. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2017, 9, e1389.	6.6	12
17	How to build a cohesive genome in 3D. <i>Nature</i> , 2017, 551, 38-40.	27.8	4
18	Abstract 5373: 3D genome architecture changes during cancer cell migration and metastasis. , 2017, , .		1

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19	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016, 1859, 1389-1397.	1.9	60
20	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015, 523, 240-244.	27.8	787
21	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013, 23, 2066-2077.	5.5	282
22	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. <i>Genome Research</i> , 2013, 23, 260-269.	5.5	282
23	Hi-C: A comprehensive technique to capture the conformation of genomes. <i>Methods</i> , 2012, 58, 268-276.	3.8	792
24	Spatial Organization of the Mouse Genome and Its Role in Recurrent Chromosomal Translocations. <i>Cell</i> , 2012, 148, 908-921.	28.9	489
25	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012, 9, 999-1003.	19.0	1,187
26	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. <i>Science</i> , 2012, 336, 1448-1451.	12.6	279
27	Translocation Mapping Exposes the Risky Lifestyle of B Cells. <i>Cell</i> , 2011, 147, 20-22.	28.9	3
28	Distant cis-regulatory elements in human skeletal muscle differentiation. <i>Genomics</i> , 2011, 98, 401-411.	2.9	21
29	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011, 8, 1050-1052.	19.0	48
30	Inferring condition-specific transcription factor function from DNA binding and gene expression data. <i>Molecular Systems Biology</i> , 2010, 6, 362.	7.2	0
31	High-resolution DNA-binding specificity analysis of yeast transcription factors. <i>Genome Research</i> , 2009, 19, 556-566.	5.5	365
32	Linking Yeast Transcription Factor Structural Class and Detailed Binding Preferences with <i>in Vivo</i> Regulatory Functions. <i>Biophysical Journal</i> , 2009, 96, 62a.	0.5	0
33	FUNCTIONAL TRENDS IN STRUCTURAL CLASSES OF THE DNA BINDING DOMAINS OF REGULATORY TRANSCRIPTION FACTORS. , 2007, , .		1
34	Analysis of force generation during flagellar assembly through optical trapping of free-swimming <i>Chlamydomonas reinhardtii</i> . <i>Cytoskeleton</i> , 2005, 61, 137-144.	4.4	32