

Rachel Patton McCord

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

34
papers

3,611
citations

16
h-index

52
g-index

52
ext. papers

4,620
ext. citations

14.8
avg, IF

5.08
L-index

#	Paper	IF	Citations
34	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling.. <i>Scientific Reports</i> , 2022 , 12, 4721	4.9	1
33	Chromosome compartmentalization alterations in prostate cancer cell lines model disease progression. <i>Journal of Cell Biology</i> , 2022 , 221,	7.3	1
32	SMILE: Mutual Information Learning for Integration of Single-cell Omics Data. <i>Bioinformatics</i> , 2021 ,	7.2	3
31	CoSTA: unsupervised convolutional neural network learning for spatial transcriptomics analysis. <i>BMC Bioinformatics</i> , 2021 , 22, 397	3.6	2
30	Using contact statistics to characterize structure transformation of biopolymer ensembles. <i>Physical Review E</i> , 2020 , 101, 012419	2.4	2
29	Chromosome Conformation Capture and Beyond: Toward an Integrative View of Chromosome Structure and Function. <i>Molecular Cell</i> , 2020 , 77, 688-708	17.6	60
28	Lateralized Expression of Cortical Perineuronal Nets during Maternal Experience is Dependent on MECP2. <i>ENeuro</i> , 2020 , 7,	3.9	8
27	Radiation-induced DNA damage and repair effects on 3D genome organization. <i>Nature Communications</i> , 2020 , 11, 6178	17.4	24
26	Inferring chromosome radial organization from Hi-C data. <i>BMC Bioinformatics</i> , 2020 , 21, 511	3.6	3
25	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	8	16
24	Iteratively improving Hi-C experiments one step at a time. <i>Methods</i> , 2018 , 142, 47-58	4.6	21
23	Investigation of Spatial Organization of Chromosome Territories in Chromosome Exchange Aberrations After Ionizing Radiation Exposure. <i>Health Physics</i> , 2018 , 115, 77-89	2.3	10
22	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	20.1	10
21	3D Genome Organization Influences the Chromosome Translocation Pattern. <i>Advances in Experimental Medicine and Biology</i> , 2018 , 1044, 113-133	3.6	10
20	Genome organization during the cell cycle: unity in division. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2017 , 9, e1389	6.6	9
19	Chromosome biology: How to build a cohesive genome in 3D. <i>Nature</i> , 2017 , 551, 38-40	50.4	1
18	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	6	43

17	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015 , 523, 240-4	50.4	501
16	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013 , 23, 2066-77	9.7	232
15	Correlated alterations in genome organization, histone methylation, and DNA-lamin A/C interactions in Hutchinson-Gilford progeria syndrome. <i>Genome Research</i> , 2013 , 23, 260-9	9.7	234
14	Hi-C: a comprehensive technique to capture the conformation of genomes. <i>Methods</i> , 2012 , 58, 268-76	4.6	472
13	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. <i>Cell</i> , 2012 , 148, 908-21	56.2	411
12	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012 , 9, 999-1003	21.6	822
11	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , 2012 , 336, 1448-51	33.3	220
10	Translocation mapping exposes the risky lifestyle of B cells. <i>Cell</i> , 2011 , 147, 20-2	56.2	2
9	Distant cis-regulatory elements in human skeletal muscle differentiation. <i>Genomics</i> , 2011 , 98, 401-11	4.3	10
8	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. <i>Nature Methods</i> , 2011 , 8, 1050-2	21.6	41
7	Inferring condition-specific transcription factor function from DNA binding and gene expression data. <i>Molecular Systems Biology</i> , 2010 , 6, 362	12.2	78
6	High-resolution DNA-binding specificity analysis of yeast transcription factors. <i>Genome Research</i> , 2009 , 19, 556-66	9.7	306
5	Analysis of force generation during flagellar assembly through optical trapping of free-swimming <i>Chlamydomonas reinhardtii</i> . <i>Cytoskeleton</i> , 2005 , 61, 137-44		25
4	Radiation-Induced DNA Damage and Repair Effects on 3D Genome Organization		2
3	Constricted migration is associated with stable 3D genome structure differences in melanoma cells		4
2	CoSTA: Unsupervised Convolutional Neural Network Learning for Spatial Transcriptomics Analysis		1
1	Loops, TADs, Compartments, and Territories are Elastic and Robust to Dramatic Nuclear Volume Swelling		1