Rachel Patton McCord

List of Publications by Year
in descending order

34	5,132	430874	434195
papers	citations	18	31
		h-index	g-index

52	52	52	7639
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Nature Methods, 2012, 9, 999-1003.	19.0	1,187
2	Hi–C: A comprehensive technique to capture the conformation of genomes. Methods, 2012, 58, 268-276.	3.8	792
3	Condensin-driven remodelling of X chromosome topology during dosage compensation. Nature, 2015, 523, 240-244.	27.8	787
4	Spatial Organization of the Mouse Genome and Its Role in Recurrent Chromosomal Translocations. Cell, 2012, 148, 908-921.	28.9	489
5	High-resolution DNA-binding specificity analysis of yeast transcription factors. Genome Research, 2009, 19, 556-566.	5.5	365
6	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. Genome Research, 2013, 23, 2066-2077.	5.5	282
7	Correlated alterations in genome organization, histone methylation, and DNA–lamin A/C interactions in Hutchinson-Gilford progeria syndrome. Genome Research, 2013, 23, 260-269.	5.5	282
8	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. Science, 2012, 336, 1448-1451.	12.6	279
9	Chromosome Conformation Capture and Beyond: Toward an Integrative View of Chromosome Structure and Function. Molecular Cell, 2020, 77, 688-708.	9.7	151
10	Radiation-induced DNA damage and repair effects on 3D genome organization. Nature Communications, 2020, 11, 6178.	12.8	70
11	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1389-1397.	1.9	60
12	Yeast one-hybrid assays for gene-centered human gene regulatory network mapping. Nature Methods, 2011, 8, 1050-1052.	19.0	48
13	Analysis of force generation during flagellar assembly through optical trapping of free-swimmingChlamydomonas reinhardtii. Cytoskeleton, 2005, 61, 137-144.	4.4	32
14	Iteratively improving Hi-C experiments one step at a time. Methods, 2018, 142, 47-58.	3.8	32
15	SMILE: mutual information learning for integration of single-cell omics data. Bioinformatics, 2022, 38, 476-486.	4.1	29
16	Rapid Irreversible Transcriptional Reprogramming in Human Stem Cells Accompanied by Discordance between Replication Timing and Chromatin Compartment. Stem Cell Reports, 2019, 13, 193-206.	4.8	24
17	Distant cis-regulatory elements in human skeletal muscle differentiation. Genomics, 2011, 98, 401-411.	2.9	21
18	Characterizing the 3D structure and dynamics of chromosomes and proteins in a common contact matrix framework. Nucleic Acids Research, 2018, 46, 8143-8152.	14.5	18

#	Article	IF	Citations
19	CoSTA: unsupervised convolutional neural network learning for spatial transcriptomics analysis. BMC Bioinformatics, 2021, 22, 397.	2.6	18
20	Chromosome compartmentalization alterations in prostate cancer cell lines model disease progression. Journal of Cell Biology, 2022, 221, .	5.2	18
21	3D Genome Organization Influences the Chromosome Translocation Pattern. Advances in Experimental Medicine and Biology, 2018, 1044, 113-133.	1.6	15
22	Investigation of Spatial Organization of Chromosome Territories in Chromosome Exchange Aberrations After Ionizing Radiation Exposure. Health Physics, 2018, 115, 77-89.	0.5	15
23	Loops, topologically associating domains, compartments, and territories are elastic and robust to dramatic nuclear volume swelling. Scientific Reports, 2022, 12, 4721.	3.3	14
24	Genome organization during the cell cycle: unity in division. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2017, 9, e1389.	6.6	12
25	Lateralized Expression of Cortical Perineuronal Nets during Maternal Experience is Dependent on MECP2. ENeuro, 2020, 7, ENEURO.0500-19.2020.	1.9	11
26	Inferring chromosome radial organization from Hi-C data. BMC Bioinformatics, 2020, 21, 511.	2.6	9
27	Diagonal integration of multimodal single-cell data: potential pitfalls and paths forward. Nature Communications, 2022, 13, .	12.8	9
28	Using contact statistics to characterize structure transformation of biopolymer ensembles. Physical Review E, 2020, 101, 012419.	2.1	6
29	How to build a cohesive genome in 3D. Nature, 2017, 551, 38-40.	27.8	4
30	Translocation Mapping Exposes the Risky Lifestyle of B Cells. Cell, 2011, 147, 20-22.	28.9	3
31	Abstract 5373: 3D genome architecture changes during cancer cell migration and metastasis. , 2017, , .		1
32	FUNCTIONAL TRENDS IN STRUCTURAL CLASSES OF THE DNA BINDING DOMAINS OF REGULATORY TRANSCRIPTION FACTORS. , 2007, , .		1
33	Linking Yeast Transcription Factor Structural Class and Detailed Binding Preferences with inÂvivo Regulatory Functions. Biophysical Journal, 2009, 96, 62a.	0.5	0
34	Inferring conditionâ€specific transcription factor function from DNA binding and gene expression data. Molecular Systems Biology, 2010, 6, 362.	7.2	0