

Michele Di Pierro

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,661
citations

759233

12
h-index

996975

15
g-index

18
all docs

18
docs citations

18
times ranked

1941
citing authors

#	ARTICLE	IF	CITATIONS
1	Shaping the genome via lengthwise compaction, phase separation, and lamina adhesion. <i>Nucleic Acids Research</i> , 2022, 50, 4258-4271.	14.5	25
2	3D genomics across the tree of life reveals condensin II as a determinant of architecture type. <i>Science</i> , 2021, 372, 984-989.	12.6	132
3	The Nucleome Data Bank: web-based resources to simulate and analyze the three-dimensional genome. <i>Nucleic Acids Research</i> , 2021, 49, D172-D182.	14.5	25
4	The interplay of chromatin phase separation and lamina interactions in nuclear organization. <i>Biophysical Journal</i> , 2021, 120, 5005-5017.	0.5	25
5	A Liquid State Perspective on Dynamics of Chromatin Compartments. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 781981.	3.5	11
6	Mesoscale Liquid Model of Chromatin Recapitulates Nuclear Order of Eukaryotes. <i>Biophysical Journal</i> , 2020, 118, 2130-2140.	0.5	29
7	Exploring chromosomal structural heterogeneity across multiple cell lines. <i>ELife</i> , 2020, 9, .	6.0	43
8	Inner workings of gene folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4774-4775.	7.1	11
9	The Energetics and Physiological Impact of Cohesin Extrusion. <i>Cell</i> , 2018, 173, 1165-1178.e20.	28.9	399
10	Walking along chromosomes with super-resolution imaging, contact maps, and integrative modeling. <i>PLoS Genetics</i> , 2018, 14, e1007872.	3.5	209
11	Deciphering the structure of the condensin protein complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11911-11916.	7.1	15
12	Anomalous diffusion, spatial coherence, and viscoelasticity from the energy landscape of human chromosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7753-7758.	7.1	133
13	De novo prediction of human chromosome structures: Epigenetic marking patterns encode genome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 12126-12131.	7.1	193
14	Transferable model for chromosome architecture. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12168-12173.	7.1	291
15	A Stochastic Algorithm for the Isothermal Ensemble with Ewald Summations for All Long Range Forces. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5624-5637.	5.3	114