

# Julien Mozziconacci

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/311918/publications.pdf>

Version: 2024-02-01

22  
papers

1,495  
citations

840776

11  
h-index

794594

19  
g-index

27  
all docs

27  
docs citations

27  
times ranked

1707  
citing authors

#	ARTICLE	IF	CITATIONS
1	3D genome reconstruction from chromosomal contacts. <i>Nature Methods</i> , 2014, 11, 1141-1143.	19.0	254
2	Condensin- and Replication-Mediated Bacterial Chromosome Folding and Origin Condensation Revealed by Hi-C and Super-resolution Imaging. <i>Molecular Cell</i> , 2015, 59, 588-602.	9.7	245
3	Normalization of a chromosomal contact map. <i>BMC Genomics</i> , 2012, 13, 436.	2.8	190
4	Structural plasticity of single chromatin fibers revealed by torsional manipulation. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 444-450.	8.2	156
5	Cohesins and condensins orchestrate the 4D dynamics of yeast chromosomes during the cell cycle. <i>EMBO Journal</i> , 2017, 36, 2684-2697.	7.8	137
6	Nucleosome Chiral Transition under Positive Torsional Stress in Single Chromatin Fibers. <i>Molecular Cell</i> , 2007, 27, 135-147.	9.7	122
7	3D organization of synthetic and scrambled chromosomes. <i>Science</i> , 2017, 355, .	12.6	116
8	Spatial reorganization of telomeres in long-lived quiescent cells. <i>Genome Biology</i> , 2015, 16, 206.	8.8	75
9	Characterizing meiotic chromosomes' structure and pairing using a designer sequence optimized for Hi-C. <i>Molecular Systems Biology</i> , 2018, 14, e8293.	7.2	63
10	How the chromatin fiber deals with topological constraints. <i>Physical Review E</i> , 2005, 71, 031910.	2.1	29
11	Network concepts for analyzing 3D genome structure from chromosomal contact maps. <i>EPJ Nonlinear Biomedical Physics</i> , 2016, 4, .	0.8	21
12	Generation and Analysis of Chromosomal Contact Maps of Yeast Species. <i>Methods in Molecular Biology</i> , 2016, 1361, 227-245.	0.9	16
13	Kinetic Signature of Cooperativity in the Irreversible Collapse of a Polymer. <i>Physical Review Letters</i> , 2018, 121, 057801.	7.8	14
14	Contribution of 3D genome topological domains to genetic risk of cancers: a genome-wide computational study. <i>Human Genomics</i> , 2022, 16, 2.	2.9	9
15	The 3D Genome Shapes the Regulatory Code of Developmental Genes. <i>Journal of Molecular Biology</i> , 2020, 432, 712-723.	4.2	8
16	Genome-wide prediction of DNA mutation effect on nucleosome positions for yeast synthetic genomics. <i>Genome Research</i> , 2021, 31, 317-326.	5.5	8
17	Genome annotation across species using deep convolutional neural networks. <i>PeerJ Computer Science</i> , 2020, 6, e278.	4.5	8
18	Filling the gap: Micro-C accesses the nucleosomal fiber at 100-1000 bp resolution. <i>Genome Biology</i> , 2015, 16, 169.	8.8	4

#	ARTICLE	IF	CITATIONS
19	keras_dna: a wrapper for fast implementation of deep learning models in genomics. <i>Bioinformatics</i> , 2021, 37, 1593-1594.	4.1	4
20	MNHN-Tree-Tools: a toolbox for tree inference using multi-scale clustering of a set of sequences. <i>Bioinformatics</i> , 2021, 37, 3947-3949.	4.1	1
21	The 3D Organization of Chromatin Colors in Mammalian Nuclei. <i>Methods in Molecular Biology</i> , 2022, 2301, 317-336.	0.9	1
22	Chromosomes : Ã©tonnants polymÃ©res !. , 2018, , 10-15.	0.1	0