

Maxim Imakaev

List of Publications by Citations

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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.

43
papers

10,862
citations

21
h-index

48
g-index

48
ext. papers

14,424
ext. citations

19.6
avg. IF

6.11
L-index

#	Paper	IF	Citations
43	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. <i>Science</i> , 2009 , 326, 289-93	33.3	4993
42	Formation of Chromosomal Domains by Loop Extrusion. <i>Cell Reports</i> , 2016 , 15, 2038-49	10.6	973
41	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012 , 9, 999-1003	21.6	822
40	Organization of the mitotic chromosome. <i>Science</i> , 2013 , 342, 948-53	33.3	654
39	Super-resolution imaging reveals distinct chromatin folding for different epigenetic states. <i>Nature</i> , 2016 , 529, 418-22	50.4	544
38	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. <i>Nature</i> , 2017 , 544, 110-114	50.4	418
37	High-resolution mapping of the spatial organization of a bacterial chromosome. <i>Science</i> , 2013 , 342, 731-43	33.3	389
36	Chromatin organization by an interplay of loop extrusion and compartmental segregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E6697-E6706	11.5	299
35	Genome-wide maps of nuclear lamina interactions in single human cells. <i>Cell</i> , 2015 , 163, 134-47	56.2	291
34	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019 , 570, 395-399	50.4	236
33	Hi-C: a method to study the three-dimensional architecture of genomes. <i>Journal of Visualized Experiments</i> , 2010 ,	1.6	212
32	A mechanism of cohesin-dependent loop extrusion organizes zygotic genome architecture. <i>EMBO Journal</i> , 2017 , 36, 3600-3618	13	190
31	Emerging Evidence of Chromosome Folding by Loop Extrusion. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2017 , 82, 45-55	3.9	142
30	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019 , 51, 138-150	36.3	99
29	Two major mechanisms of chromosome organization. <i>Current Opinion in Cell Biology</i> , 2019 , 58, 142-152	9	87
28	Chromatin loops as allosteric modulators of enhancer-promoter interactions. <i>PLoS Computational Biology</i> , 2014 , 10, e1003867	5	82
27	FISH-ing for captured contacts: towards reconciling FISH and 3C. <i>Nature Methods</i> , 2017 , 14, 673-678	21.6	79

26	Chromosomal architecture changes upon cell differentiation. <i>Epigenetics and Chromatin</i> , 2013 , 6,	5.8	78
25	Effects of topological constraints on globular polymers. <i>Soft Matter</i> , 2015 , 11, 665-71	3.6	41
24	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018 , 72, 715-726.e3	17.6	39
23	Genome-wide transcription start site mapping of <i>Bradyrhizobium japonicum</i> grown free-living or in symbiosis - a rich resource to identify new transcripts, proteins and to study gene regulation. <i>BMC Genomics</i> , 2016 , 17, 302	4.5	38
22	Diminished Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. <i>Circulation: Cardiovascular Genetics</i> , 2017 , 10,		20
21	Heterochromatin drives organization of conventional and inverted nuclei		19
20	Quantitative SARS-CoV-2 Alpha Variant B.1.1.7 Tracking in Wastewater by Allele-Specific RT-qPCR. <i>Environmental Science and Technology Letters</i> , 2021 , 8, 675-682	11	17
19	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. <i>American Journal of Human Genetics</i> , 2020 , 107, 46-59	11	16
18	The genome-wide multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos. <i>Nature Communications</i> , 2019 , 10, 4486	17.4	16
17	Making waves: Defining the lead time of wastewater-based epidemiology for COVID-19. <i>Water Research</i> , 2021 , 202, 117433	12.5	11
16	Emerging Evidence of Chromosome Folding by Loop Extrusion		8
15	FISH-ing for captured contacts: towards reconciling FISH and 3C		5
14	Quantitative detection of SARS-CoV-2 B.1.1.7 variant in wastewater by allele-specific RT-qPCR		5
13	Chromatin organization by an interplay of loop extrusion and compartmental segregation		4
12	Limited evidence of tumour mutational burden as a biomarker of response to immunotherapy		4
11	Metrics to relate COVID-19 wastewater data to clinical testing dynamics.. <i>Water Research</i> , 2022 , 212, 118070	12.5	3
10	The 4D Nucleome Data Portal: a resource for searching and visualizing curated nucleomics data		3
9	The genome-wide, multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos		3

8	Metrics to relate COVID-19 wastewater data to clinical testing dynamics 2021 ,		3
7	Variant abundance estimation for SARS-CoV-2 in wastewater using RNA-Seq quantification 2021 ,		3
6	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data.. <i>Nature Communications</i> , 2022 , 13, 2365	17.4	3
5	A Mechanism of Cohesin-Dependent Loop Extrusion Organizes Zygotic Genome Architecture		2
4	Heterochromatin diversity modulates genome compartmentalization and loop extrusion barriers		2
3	Nationwide trends in COVID-19 cases and SARS-CoV-2 wastewater concentrations in the United States		2
2	Higher-Order Organization Principles of Pre-translational mRNPs		1
1	Abstract 18865: Identification of a Functional SNP Regulating PRRX1 at the 1q24 Locus for Atrial Fibrillation. <i>Circulation</i> , 2014 , 130,	16.7	1