

Maxim Imakaev

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

16,252
citations

236612

25
h-index

433756

31
g-index

48
all docs

48
docs citations

48
times ranked

15425
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	6.0	7,170
2	Formation of Chromosomal Domains by Loop Extrusion. Cell Reports, 2016, 15, 2038-2049.	2.9	1,570
3	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Nature Methods, 2012, 9, 999-1003.	9.0	1,187
4	Organization of the Mitotic Chromosome. Science, 2013, 342, 948-953.	6.0	894
5	Super-resolution imaging reveals distinct chromatin folding for different epigenetic states. Nature, 2016, 529, 418-422.	13.7	750
6	Single-nucleus Hi-C reveals unique chromatin reorganization at oocyte-to-zygote transition. Nature, 2017, 544, 110-114.	13.7	604
7	High-Resolution Mapping of the Spatial Organization of a Bacterial Chromosome. Science, 2013, 342, 731-734.	6.0	531
8	Chromatin organization by an interplay of loop extrusion and compartmental segregation. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6697-E6706.	3.3	510
9	Heterochromatin drives compartmentalization of inverted and conventional nuclei. Nature, 2019, 570, 395-399.	13.7	464
10	Genome-wide Maps of Nuclear Lamina Interactions in Single Human Cells. Cell, 2015, 163, 134-147.	13.5	399
11	Hi-C: A Method to Study the Three-dimensional Architecture of Genomes.. Journal of Visualized Experiments, 2010, , .	0.2	318
12	A mechanism of cohesin-dependent loop extrusion organizes zygotic genome architecture. EMBO Journal, 2017, 36, 3600-3618.	3.5	291
13	Emerging Evidence of Chromosome Folding by Loop Extrusion. Cold Spring Harbor Symposia on Quantitative Biology, 2017, 82, 45-55.	2.0	227
14	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. Nature Genetics, 2019, 51, 138-150.	9.4	177
15	Two major mechanisms of chromosome organization. Current Opinion in Cell Biology, 2019, 58, 142-152.	2.6	167
16	FISH-ing for captured contacts: towards reconciling FISH and 3C. Nature Methods, 2017, 14, 673-678.	9.0	116
17	Chromatin Loops as Allosteric Modulators of Enhancer-Promoter Interactions. PLoS Computational Biology, 2014, 10, e1003867.	1.5	102
18	Making waves: Defining the lead time of wastewater-based epidemiology for COVID-19. Water Research, 2021, 202, 117433.	5.3	85

#	ARTICLE	IF	CITATIONS
19	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.	1.2	70
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.	3.9	68
21	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022, 212, 118070.	5.3	68
22	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018, 72, 715-726.e3.	4.5	59
23	Effects of topological constraints on globular polymers. <i>Soft Matter</i> , 2015, 11, 665-671.	1.2	56
24	The 4D Nucleome Data Portal as a resource for searching and visualizing curated nucleomics data. <i>Nature Communications</i> , 2022, 13, 2365.	5.8	49
25	Nationwide Trends in COVID-19 Cases and SARS-CoV-2 RNA Wastewater Concentrations in the United States. <i>ACS ES&T Water</i> , 2022, 2, 1899-1909.	2.3	46
26	The genome-wide multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos. <i>Nature Communications</i> , 2019, 10, 4486.	5.8	38
27	Diminished <i>PRRX1</i> Expression Is Associated With Increased Risk of Atrial Fibrillation and Shortening of the Cardiac Action Potential. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	33
28	Non-parametric Polygenic Risk Prediction via Partitioned GWAS Summary Statistics. <i>American Journal of Human Genetics</i> , 2020, 107, 46-59.	2.6	30
29	Abstract 18865: Identification of a Functional SNP Regulating <i>PRRX1</i> at the 1q24 Locus for Atrial Fibrillation. <i>Circulation</i> , 2014, 130, .	1.6	1
30	Chromosomal architecture changes upon cell differentiation. <i>Epigenetics and Chromatin</i> , 2013, 6, .	1.8	0