

A Compendium of Chromatin Contact Maps Reveals Spatial Organization of the Human Genome

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Citation Report

#	ARTICLE	IF	CITATIONS
1	The Ties That Bind: Mapping the Dynamic Enhancer-Promoter Interactome. <i>Cell</i> , 2016, 167, 1163-1166.	13.5	27
2	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	13.5	404
3	Predicting chromatin architecture from models of polymer physics. <i>Chromosome Research</i> , 2017, 25, 25-34.	1.0	42
4	Discovery of novel heart rate-associated loci using the Exome Chip. <i>Human Molecular Genetics</i> , 2017, 26, 2346-2363.	1.4	29
5	HUGIn: Hi-C Unifying Genomic Interrogator. <i>Bioinformatics</i> , 2017, 33, 3793-3795.	1.8	69
6	Regulatory landscape fusion in rhabdomyosarcoma through interactions between the PAX3 promoter and FOXO1 regulatory elements. <i>Genome Biology</i> , 2017, 18, 106.	3.8	24
7	Deciphering non-coding variation with 3D epigenomics. <i>Nature Reviews Genetics</i> , 2017, 18, 4-4.	7.7	5
8	Mammalian Transcription Factor Networks: Recent Advances in Interrogating Biological Complexity. <i>Cell Systems</i> , 2017, 5, 319-331.	2.9	54
9	How to build a cohesive genome in 3D. <i>Nature</i> , 2017, 551, 38-40.	13.7	4
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11	Chromatin interaction networks revealed unique connectivity patterns of broad H3K4me3 domains and super enhancers in 3D chromatin. <i>Scientific Reports</i> , 2017, 7, 14466.	1.6	40
12	Two independent modes of chromatin organization revealed by cohesin removal. <i>Nature</i> , 2017, 551, 51-56.	13.7	935
13	Online resources for studies of genome biology and epigenetics. <i>Current Opinion in Toxicology</i> , 2017, 6, 34-41.	2.6	0
14	Esco1 and Esco2 regulate distinct cohesin functions during cell cycle progression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9906-9911.	3.3	79
15	HiCRep: assessing the reproducibility of Hi-C data using a stratum-adjusted correlation coefficient. <i>Genome Research</i> , 2017, 27, 1939-1949.	2.4	376
16	Static and Dynamic DNA Loops form AP-1-Bound Activation Hubs during Macrophage Development. <i>Molecular Cell</i> , 2017, 67, 1037-1048.e6.	4.5	242
17	Prenatal identification of two discontinuous maternally inherited chromosome 7q36.3 microduplications totaling 507 kb including the sonic hedgehog gene in a fetus with multiple congenital anomalies. <i>Clinical Case Reports (discontinued)</i> , 2017, 5, 993-999.	0.2	3
18	The Three-Dimensional Organization of Mammalian Genomes. <i>Annual Review of Cell and Developmental Biology</i> , 2017, 33, 265-289.	4.0	320

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20	High-Resolution Mapping of Chromatin Conformation in Cardiac Myocytes Reveals Structural Remodeling of the Epigenome in Heart Failure. Circulation, 2017, 136, 1613-1625.	1.6	135
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22	Computational tools for Hi-C data analysis. Quantitative Biology, 2017, 5, 215-225.	0.3	7
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58	Function of BRD4 in the pathogenesis of high glucose-induced cardiac hypertrophy. <i>Molecular Medicine Reports</i> , 2019, 19, 499-507.	1.1	10
59	Genome-wide mega-analysis identifies 16 loci and highlights diverse biological mechanisms in the common epilepsies. <i>Nature Communications</i> , 2018, 9, 5269.	5.8	331
60	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. <i>Genome Biology</i> , 2018, 19, 151.	3.8	393
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94	Understanding direct neuronal reprogramming “from pioneer factors to 3D chromatin. <i>Current Opinion in Genetics and Development</i> , 2018, 52, 65-69.	1.5	8
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132	The role of 3D genome organization in development and cell differentiation. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 535-550.	16.1	451
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