Bryan R Lajoie

List of Publications by Year
in descending order

38 papers	24,541 citations	117625 34 h-index	302126 39 g-index
45 all docs	45 docs citations	45 times ranked	24770 citing authors

#	Article	IF	Citations
1	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	12.6	7,170
2	Spatial partitioning of the regulatory landscape of the X-inactivation centre. Nature, 2012, 485, 381-385.	27.8	2,595
3	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. Nature, 2011, 472, 120-124.	27.8	1,760
4	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. Genome Biology, 2015, 16, 259.	8.8	1,632
5	The long-range interaction landscape of gene promoters. Nature, 2012, 489, 109-113.	27.8	1,323
6	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. Nature Methods, 2012, 9, 999-1003.	19.0	1,187
7	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. Cell, 2013, 153, 1281-1295.	28.9	1,050
8	Organization of the Mitotic Chromosome. Science, 2013, 342, 948-953.	12.6	894
9	Activation of proto-oncogenes by disruption of chromosome neighborhoods. Science, 2016, 351, 1454-1458.	12.6	880
10	Condensin-driven remodelling of X chromosome topology during dosage compensation. Nature, 2015, 523, 240-244.	27.8	787
11	Spatial Organization of the Mouse Genome and Its Role in Recurrent Chromosomal Translocations. Cell, 2012, 148, 908-921.	28.9	489
12	Heterochromatin drives compartmentalization of inverted and conventional nuclei. Nature, 2019, 570, 395-399.	27.8	464
13	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. New England Journal of Medicine, 2016, 374, 1842-1852.	27.0	456
14	Structural organization of the inactive X chromosome in the mouse. Nature, 2016, 535, 575-579.	27.8	369
15	The Hitchhiker's guide to Hi-C analysis: Practical guidelines. Methods, 2015, 72, 65-75.	3.8	327
16	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. Genome Research, 2013, 23, 2066-2077.	5.5	282
17	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. Science, 2012, 336, 1448-1451.	12.6	279
18	Detection of long repeat expansions from PCR-free whole-genome sequence data. Genome Research, 2017, 27, 1895-1903.	5.5	277

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19	The three-dimensional folding of the Î±-globin gene domain reveals formation of chromatin globules. Nature Structural and Molecular Biology, 2011, 18, 107-114.	8.2	274
20	Integrative detection and analysis of structural variation in cancer genomes. Nature Genetics, 2018, 50, 1388-1398.	21.4	268
21	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i>. Genes and Development, 2015, 29, 1661-1675.	5.9	215
22	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. Genome Biology, 2015, 16, 214.	8.8	206
23	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. Bioinformatics, 2019, 35, 4754-4756.	4.1	183
24	HiTC: exploration of high-throughput â€˜Câ€™ experiments. Bioinformatics, 2012, 28, 2843-2844.	4.1	165
25	Invariant TAD Boundaries Constrain Cell-Type-Specific Looping Interactions between Promoters and Distal Elements around the CFTR Locus. American Journal of Human Genetics, 2016, 98, 185-201.	6.2	131
26	Measuring the reproducibility and quality of Hi-C data. Genome Biology, 2019, 20, 57.	8.8	125
27	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. Genome Biology, 2020, 21, 102.	8.8	114
28	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. Genome Research, 2016, 26, 1188-1201.	5.5	90
29	My5C: web tools for chromosome conformation capture studies. Nature Methods, 2009, 6, 690-691.	19.0	86
30	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in Drosophila. Molecular Cell, 2015, 60, 146-162.	9.7	70
31	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 1389-1397.	1.9	60
32	Higher-Order Organization Principles of Pre-translational mRNPs. Molecular Cell, 2018, 72, 715-726.e3.	9.7	59
33	Highly structured homolog pairing reflects functional organization of the Drosophila genome. Nature Communications, 2019, 10, 4485.	12.8	51
34	X-linked hypomyelination with spondylometaphyseal dysplasia (H-SMD) associated with mutations in AIFM1. Neurogenetics, 2017, 18, 185-194.	1.4	38
35	The genome-wide multi-layered architecture of chromosome pairing in early Drosophila embryos. Nature Communications, 2019, 10, 4486.	12.8	38
36	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. Cell Reports, 2015, 13, 1855-1867.	6.4	33

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37	Genome sequencing in persistently unsolved white matter disorders. Annals of Clinical and Translational Neurology, 2020, 7, 144-152.	3.7	26
38	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. American Journal of Respiratory and Critical Care Medicine, 2016, 194, 1465-1474.	5.6	20