

Bryan R Lajoie

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.

44
papers

17,195
citations

31
h-index

45
g-index

45
ext. papers

21,960
ext. citations

24.1
avg, IF

6.16
L-index

#	Paper	IF	Citations
44	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. <i>Science</i> , 2009 , 326, 289-93	33.3	4993
43	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , 2012 , 485, 381-5	50.4	1894
42	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011 , 472, 120-4	50.4	1502
41	The long-range interaction landscape of gene promoters. <i>Nature</i> , 2012 , 489, 109-13	50.4	1066
40	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <i>Cell</i> , 2013 , 153, 1281-95	56.2	848
39	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012 , 9, 999-1003	21.6	822
38	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <i>Genome Biology</i> , 2015 , 16, 259	18.3	811
37	Organization of the mitotic chromosome. <i>Science</i> , 2013 , 342, 948-53	33.3	654
36	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016 , 351, 1454-1458	35.8	600
35	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015 , 523, 240-4	50.4	501
34	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. <i>Cell</i> , 2012 , 148, 908-21	56.2	411
33	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. <i>New England Journal of Medicine</i> , 2016 , 374, 1842-1852	59.2	312
32	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016 , 535, 575-9	50.4	261
31	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019 , 570, 395-399	50.4	236
30	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013 , 23, 2066-77	9.7	232
29	The three-dimensional folding of the β globin gene domain reveals formation of chromatin globules. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 107-14	17.6	232
28	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , 2012 , 336, 1448-51	33.3	220

27	The Hitchhiker's guide to Hi-C analysis: practical guidelines. <i>Methods</i> , 2015 , 72, 65-75	4.6	209
26	Detection of long repeat expansions from PCR-free whole-genome sequence data. <i>Genome Research</i> , 2017 , 27, 1895-1903	9.7	159
25	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , 2015 , 29, 1661-75	12.6	150
24	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018 , 50, 1388-1398	36.3	147
23	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , 2015 , 16, 214	18.3	123
22	HiTC: exploration of high-throughput Hi-C experiments. <i>Bioinformatics</i> , 2012 , 28, 2843-4	7.2	119
21	Invariant TAD Boundaries Constrain Cell-Type-Specific Looping Interactions between Promoters and Distal Elements around the CFTR Locus. <i>American Journal of Human Genetics</i> , 2016 , 98, 185-201	11	91
20	My5C: web tools for chromosome conformation capture studies. <i>Nature Methods</i> , 2009 , 6, 690-1	21.6	74
19	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , 2016 , 26, 1188-201	9.7	64
18	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. <i>Bioinformatics</i> , 2019 , 35, 4754-4756	7.2	62
17	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019 , 20, 57	18.3	62
16	High-Affinity Sites Form an Interaction Network to Facilitate Spreading of the MSL Complex across the X Chromosome in <i>Drosophila</i> . <i>Molecular Cell</i> , 2015 , 60, 146-62	17.6	58
15	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 1389-1397	6	43
14	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018 , 72, 715-726.e3	17.6	39
13	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. <i>Genome Biology</i> , 2020 , 21, 102	18.3	29
12	X-linked hypomyelination with spondylometaphyseal dysplasia (H-SMD) associated with mutations in AIFM1. <i>Neurogenetics</i> , 2017 , 18, 185-194	3	28
11	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome. <i>Nature Communications</i> , 2019 , 10, 4485	17.4	26
10	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , 2015 , 13, 1855-67	10.6	23

9	Heterochromatin drives organization of conventional and inverted nuclei		19
8	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2016 , 194, 1465-1474	10.2	18
7	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
6	Genome sequencing in persistently unsolved white matter disorders. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 144-152	5.3	13
5	An Integrative Framework for Detecting Structural Variations in Cancer Genomes		11
4	Measuring the reproducibility and quality of Hi-C data		6
3	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome		4
2	The genome-wide, multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos		3
1	Higher-Order Organization Principles of Pre-translational mRNPs		1