

Bryan R Lajoie

List of Publications by Year in descending order

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Version: 2024-02-01

38
papers

24,541
citations

117625

34
h-index

302126

39
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45
all docs

45
docs citations

45
times ranked

24770
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing in persistently unsolved white matter disorders. <i>Annals of Clinical and Translational Neurology</i> , 2020, 7, 144-152.	3.7	26
2	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. <i>Genome Biology</i> , 2020, 21, 102.	8.8	114
3	The genome-wide multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos. <i>Nature Communications</i> , 2019, 10, 4486.	12.8	38
4	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome. <i>Nature Communications</i> , 2019, 10, 4485.	12.8	51
5	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. <i>Bioinformatics</i> , 2019, 35, 4754-4756.	4.1	183
6	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , 2019, 570, 395-399.	27.8	464
7	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , 2019, 20, 57.	8.8	125
8	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , 2018, 72, 715-726.e3.	9.7	59
9	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018, 50, 1388-1398.	21.4	268
10	X-linked hypomyelination with spondylometaphyseal dysplasia (H-SMD) associated with mutations in AIFM1. <i>Neurogenetics</i> , 2017, 18, 185-194.	1.4	38
11	Detection of long repeat expansions from PCR-free whole-genome sequence data. <i>Genome Research</i> , 2017, 27, 1895-1903.	5.5	277
12	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.	5.6	20
13	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. <i>New England Journal of Medicine</i> , 2016, 374, 1842-1852.	27.0	456
14	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.	1.9	60
15	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , 2016, 535, 575-579.	27.8	369
16	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , 2016, 26, 1188-1201.	5.5	90
17	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , 2016, 351, 1454-1458.	12.6	880
18	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.	6.2	131

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19	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , 2015, 13, 1855-1867.	6.4	33
20	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , 2015, 16, 214.	8.8	206
21	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , 2015, 523, 240-244.	27.8	787
22	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <i>Genome Biology</i> , 2015, 16, 259.	8.8	1,632
23	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , 2015, 29, 1661-1675.	5.9	215
24	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, 146-162.	9.7	70
25	The Hitchhiker's guide to Hi-C analysis: Practical guidelines. <i>Methods</i> , 2015, 72, 65-75.	3.8	327
26	Organization of the Mitotic Chromosome. <i>Science</i> , 2013, 342, 948-953.	12.6	894
27	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , 2013, 23, 2066-2077.	5.5	282
28	Architectural Protein Subclasses Shape 3D Organization of Genomes during Lineage Commitment. <i>Cell</i> , 2013, 153, 1281-1295.	28.9	1,050
29	HiTC: exploration of high-throughput Hi-C experiments. <i>Bioinformatics</i> , 2012, 28, 2843-2844.	4.1	165
30	The long-range interaction landscape of gene promoters. <i>Nature</i> , 2012, 489, 109-113.	27.8	1,323
31	Spatial Organization of the Mouse Genome and Its Role in Recurrent Chromosomal Translocations. <i>Cell</i> , 2012, 148, 908-921.	28.9	489
32	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , 2012, 9, 999-1003.	19.0	1,187
33	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , 2012, 485, 381-385.	27.8	2,595
34	MORC Family ATPases Required for Heterochromatin Condensation and Gene Silencing. <i>Science</i> , 2012, 336, 1448-1451.	12.6	279
35	The three-dimensional folding of the β -globin gene domain reveals formation of chromatin globules. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 107-114.	8.2	274
36	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , 2011, 472, 120-124.	27.8	1,760

#	ARTICLE	IF	CITATIONS
37	My5C: web tools for chromosome conformation capture studies. Nature Methods, 2009, 6, 690-691.	19.0	86
38	Comprehensive Mapping of Long-Range Interactions Reveals Folding Principles of the Human Genome. Science, 2009, 326, 289-293.	12.6	7,170