

# Bryan R Lajoie

## List of Publications by Year in Descending Order

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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	ExpansionHunter Denovo: a computational method for locating known and novel repeat expansions in short-read sequencing data. <i>Genome Biology</i> , <b>2020</b> , 21, 102	18.3	29
43	Genome sequencing in persistently unsolved white matter disorders. <i>Annals of Clinical and Translational Neurology</i> , <b>2020</b> , 7, 144-152	5.3	13
42	Highly structured homolog pairing reflects functional organization of the Drosophila genome. <i>Nature Communications</i> , <b>2019</b> , 10, 4485	17.4	26
41	ExpansionHunter: a sequence-graph-based tool to analyze variation in short tandem repeat regions. <i>Bioinformatics</i> , <b>2019</b> , 35, 4754-4756	7.2	62
40	Heterochromatin drives compartmentalization of inverted and conventional nuclei. <i>Nature</i> , <b>2019</b> , 570, 395-399	50.4	236
39	Measuring the reproducibility and quality of Hi-C data. <i>Genome Biology</i> , <b>2019</b> , 20, 57	18.3	62
38	The genome-wide multi-layered architecture of chromosome pairing in early Drosophila embryos. <i>Nature Communications</i> , <b>2019</b> , 10, 4486	17.4	16
37	Higher-Order Organization Principles of Pre-translational mRNPs. <i>Molecular Cell</i> , <b>2018</b> , 72, 715-726.e3	17.6	39
36	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , <b>2018</b> , 50, 1388-1398	36.3	147
35	X-linked hypomyelination with spondylometaphyseal dysplasia (H-SMD) associated with mutations in AIFM1. <i>Neurogenetics</i> , <b>2017</b> , 18, 185-194	3	28
34	Detection of long repeat expansions from PCR-free whole-genome sequence data. <i>Genome Research</i> , <b>2017</b> , 27, 1895-1903	9.7	159
33	RUNX1 contributes to higher-order chromatin organization and gene regulation in breast cancer cells. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , <b>2016</b> , 1859, 1389-1397	6	43
32	Structural organization of the inactive X chromosome in the mouse. <i>Nature</i> , <b>2016</b> , 535, 575-9	50.4	261
31	SMARCA4 regulates gene expression and higher-order chromatin structure in proliferating mammary epithelial cells. <i>Genome Research</i> , <b>2016</b> , 26, 1188-201	9.7	64
30	Activation of proto-oncogenes by disruption of chromosome neighborhoods. <i>Science</i> , <b>2016</b> , 351, 1454-1458	35.8	600
29	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> , <b>2016</b> , 98, 185-201	11	91
28	Genetics and Genomics of Longitudinal Lung Function Patterns in Individuals with Asthma. <i>American Journal of Respiratory and Critical Care Medicine</i> , <b>2016</b> , 194, 1465-1474	10.2	18

27	Patterns of Growth and Decline in Lung Function in Persistent Childhood Asthma. <i>New England Journal of Medicine</i> , <b>2016</b> , 374, 1842-1852	59.2	312
26	Condensin promotes the juxtaposition of DNA flanking its loading site in <i>Bacillus subtilis</i> . <i>Genes and Development</i> , <b>2015</b> , 29, 1661-75	12.6	150
25	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> , <b>2015</b> , 60, 146-62	17.6	58
24	The Hitchhiker's guide to Hi-C analysis: practical guidelines. <i>Methods</i> , <b>2015</b> , 72, 65-75	4.6	209
23	The Conformation of Yeast Chromosome III Is Mating Type Dependent and Controlled by the Recombination Enhancer. <i>Cell Reports</i> , <b>2015</b> , 13, 1855-67	10.6	23
22	Chromatin interaction analysis reveals changes in small chromosome and telomere clustering between epithelial and breast cancer cells. <i>Genome Biology</i> , <b>2015</b> , 16, 214	18.3	123
21	Condensin-driven remodelling of X chromosome topology during dosage compensation. <i>Nature</i> , <b>2015</b> , 523, 240-4	50.4	501
20	HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. <i>Genome Biology</i> , <b>2015</b> , 16, 259	18.3	811
19	Organization of the mitotic chromosome. <i>Science</i> , <b>2013</b> , 342, 948-53	33.3	654
18	Cohesin-based chromatin interactions enable regulated gene expression within preexisting architectural compartments. <i>Genome Research</i> , <b>2013</b> , 23, 2066-77	9.7	232
17	Architectural protein subclasses shape 3D organization of genomes during lineage commitment. <i>Cell</i> , <b>2013</b> , 153, 1281-95	56.2	848
16	The long-range interaction landscape of gene promoters. <i>Nature</i> , <b>2012</b> , 489, 109-13	50.4	1066
15	Spatial organization of the mouse genome and its role in recurrent chromosomal translocations. <i>Cell</i> , <b>2012</b> , 148, 908-21	56.2	411
14	Iterative correction of Hi-C data reveals hallmarks of chromosome organization. <i>Nature Methods</i> , <b>2012</b> , 9, 999-1003	21.6	822
13	Spatial partitioning of the regulatory landscape of the X-inactivation centre. <i>Nature</i> , <b>2012</b> , 485, 381-5	50.4	1894
12	MORC family ATPases required for heterochromatin condensation and gene silencing. <i>Science</i> , <b>2012</b> , 336, 1448-51	33.3	220
11	HiTC: exploration of high-throughput ChIP experiments. <i>Bioinformatics</i> , <b>2012</b> , 28, 2843-4	7.2	119
10	The three-dimensional folding of the $\beta$ globin gene domain reveals formation of chromatin globules. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 107-14	17.6	232

9	A long noncoding RNA maintains active chromatin to coordinate homeotic gene expression. <i>Nature</i> , <b>2011</b> , 472, 120-4	50.4	1502
8	My5C: web tools for chromosome conformation capture studies. <i>Nature Methods</i> , <b>2009</b> , 6, 690-1	21.6	74
7	Comprehensive mapping of long-range interactions reveals folding principles of the human genome. <i>Science</i> , <b>2009</b> , 326, 289-93	33.3	4993
6	An Integrative Framework for Detecting Structural Variations in Cancer Genomes		11
5	Measuring the reproducibility and quality of Hi-C data		6
4	Heterochromatin drives organization of conventional and inverted nuclei		19
3	Higher-Order Organization Principles of Pre-translational mRNPs		1
2	The genome-wide, multi-layered architecture of chromosome pairing in early <i>Drosophila</i> embryos		3
1	Highly structured homolog pairing reflects functional organization of the <i>Drosophila</i> genome		4