

Jesse R Dixon

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5398046/publications.pdf>

Version: 2024-02-01

34
papers

19,849
citations

218592

26
h-index

395590

33
g-index

47
all docs

47
docs citations

47
times ranked

29186
citing authors

#	ARTICLE	IF	CITATIONS
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	13.7	5,786
2	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
3	Chromatin architecture reorganization during stem cell differentiation. <i>Nature</i> , 2015, 518, 331-336.	13.7	1,442
4	A map of the cis-regulatory sequences in the mouse genome. <i>Nature</i> , 2012, 488, 116-120.	13.7	1,306
5	A high-resolution map of the three-dimensional chromatin interactome in human cells. <i>Nature</i> , 2013, 503, 290-294.	13.7	1,074
6	Cohesin and CTCF differentially affect chromatin architecture and gene expression in human cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 996-1001.	3.3	700
7	Chromatin Domains: The Unit of Chromosome Organization. <i>Molecular Cell</i> , 2016, 62, 668-680.	4.5	653
8	Allelic reprogramming of 3D chromatin architecture during early mammalian development. <i>Nature</i> , 2017, 547, 232-235.	13.7	406
9	Integrative detection and analysis of structural variation in cancer genomes. <i>Nature Genetics</i> , 2018, 50, 1388-1398.	9.4	268
10	Whole-genome haplotype reconstruction using proximity-ligation and shotgun sequencing. <i>Nature Biotechnology</i> , 2013, 31, 1111-1118.	9.4	257
11	Bcl-6 and NF- κ B cistromes mediate opposing regulation of the innate immune response. <i>Genes and Development</i> , 2010, 24, 2760-2765.	2.7	224
12	Simultaneous profiling of 3D genome structure and DNA methylation in single human cells. <i>Nature Methods</i> , 2019, 16, 999-1006.	9.0	200
13	Bayesian Inference of Spatial Organizations of Chromosomes. <i>PLoS Computational Biology</i> , 2013, 9, e1002893.	1.5	188
14	Disruption of chromatin folding domains by somatic genomic rearrangements in human cancer. <i>Nature Genetics</i> , 2020, 52, 294-305.	9.4	180
15	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 152-161.	3.6	172
16	CRISPR Reveals a Distal Super-Enhancer Required for Sox2 Expression in Mouse Embryonic Stem Cells. <i>PLoS ONE</i> , 2014, 9, e114485.	1.1	168
17	A non-canonical BRD9-containing BAF chromatin remodeling complex regulates naive pluripotency in mouse embryonic stem cells. <i>Nature Communications</i> , 2018, 9, 5139.	5.8	149
18	Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. <i>Nature Genetics</i> , 2019, 51, 1252-1262.	9.4	139

#	ARTICLE	IF	CITATIONS
19	DNA methylation atlas of the mouse brain at single-cell resolution. <i>Nature</i> , 2021, 598, 120-128.	13.7	135
20	A new class of temporarily phenotypic enhancers identified by CRISPR/Cas9-mediated genetic screening. <i>Genome Research</i> , 2016, 26, 397-405.	2.4	111
21	Robust single-cell Hi-C clustering by convolution- and random-walk-based imputation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14011-14018.	3.3	101
22	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020, 52, 1178-1188.	9.4	79
23	Incorporation of a nucleoside analog maps genome repair sites in postmitotic human neurons. <i>Science</i> , 2021, 372, 91-94.	6.0	68
24	Tissue-specific SMARCA4 binding at active and repressed regulatory elements during embryogenesis. <i>Genome Research</i> , 2014, 24, 920-929.	2.4	63
25	Dynamic regulation of histone modifications and long-range chromosomal interactions during postmitotic transcriptional reactivation. <i>Genes and Development</i> , 2020, 34, 913-930.	2.7	63
26	Single nucleus multi-omics identifies human cortical cell regulatory genome diversity. <i>Cell Genomics</i> , 2022, 2, 100107.	3.0	58
27	Comparing 3D Genome Organization in Multiple Species Using Phylo-HMRF. <i>Cell Systems</i> , 2019, 8, 494-505.e14.	2.9	27
28	Coming full circle: On the origin and evolution of the looping model for enhancer-promoter communication. <i>Journal of Biological Chemistry</i> , 2022, 298, 102117.	1.6	21
29	Acute myeloid leukemia driven by the CALM-AF10 fusion gene is dependent on BMI1. <i>Experimental Hematology</i> , 2019, 74, 42-51.e3.	0.2	15
30	A CRISPR Connection between Chromatin Topology and Genetic Disorders. <i>Cell</i> , 2015, 161, 955-957.	13.5	13
31	Complete haplotype phasing of the MHC and KIR loci with targeted HaploSeq. <i>BMC Genomics</i> , 2015, 16, 900.	1.2	10
32	Genome reconstruction and haplotype phasing using chromosome conformation capture methodologies. <i>Briefings in Functional Genomics</i> , 2020, 19, 139-150.	1.3	10
33	Analysis of Hi-C Data for Discovery of Structural Variations in Cancer. <i>Methods in Molecular Biology</i> , 2022, 2301, 143-161.	0.4	5
34	TADs for Life: Chromatin Domain Organization Regulates Lifespan in <i>C.Âlegans</i> . <i>Developmental Cell</i> , 2019, 51, 131-132.	3.1	0