Zhijun Duan

List of Publications by Year in descending order

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394421 552781 2,835 29 19 26 h-index citations g-index papers 36 36 36 4073 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Lamin B1 deletion in myeloid neoplasms causes nuclear anomaly and altered hematopoietic stem cell function. Cell Stem Cell, 2022, 29, 577-592.e8.	11.1	13
2	Single-cell landscape of nuclear configuration and gene expression during stem cell differentiation and X inactivation. Genome Biology, 2021, 22, 279.	8.8	11
3	Targeted DNase Hi-C. Methods in Molecular Biology, 2021, 2157, 65-83.	0.9	3
4	Sci-Hi-C: A single-cell Hi-C method for mapping 3D genome organization in large number of single cells. Methods, 2020, 170, 61-68.	3.8	53
5	Capturing cell type-specific chromatin compartment patterns by applying topic modeling to single-cell Hi-C data. PLoS Computational Biology, 2020, 16, e1008173.	3.2	59
6	Trans- and cis-acting effects of Firre on epigenetic features of the inactive X chromosome. Nature Communications, 2020, 11, 6053.	12.8	33
7	Unsupervised manifold alignment for single-cell multi-omics data. , 2020, 2020, 1-10.		33
8	Understanding the 3D genome: Emerging impacts on human disease. Seminars in Cell and Developmental Biology, 2019, 90, 62-77.	5.0	55
9	Replication Timing Becomes Intertwined with 3D Genome Organization. Cell, 2019, 176, 681-684.	28.9	9
10	Orientation-dependent Dxz4 contacts shape the 3D structure of the inactive X chromosome. Nature Communications, 2018, 9, 1445.	12.8	63
11	Using DNase Hi-C techniques to map global and local three-dimensional genome architecture at high resolution. Methods, 2018, 142, 59-73.	3.8	20
12	Massively multiplex single-cell Hi-C. Nature Methods, 2017, 14, 263-266.	19.0	441
13	Form and function of topologically associating genomic domains in budding yeast. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3061-E3070.	7.1	67
14	Mapping 3D genome architecture through in situ DNase Hi-C. Nature Protocols, 2016, 11, 2104-2121.	12.0	106
15	Understanding Spatial Genome Organization: Methods and Insights. Genomics, Proteomics and Bioinformatics, 2016, 14, 7-20.	6.9	54
16	Bipartite structure of the inactive mouse X chromosome. Genome Biology, 2015, 16, 152.	8.8	211
17	Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of human lincRNA genes. Nature Methods, 2015, 12, 71-78.	19.0	177
18	A genome-wide 3C-method for characterizing the three-dimensional architectures of genomes. Methods, 2012, 58, 277-288.	3.8	31

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19	The genome in space and time: Does form always follow function?. BioEssays, 2012, 34, 800-810.	2.5	20
20	A three-dimensional model of the yeast genome. Nature, 2010, 465, 363-367.	27.8	894
21	Epigenetic Regulation of Protein-Coding and MicroRNA Genes by the Gfi1-Interacting Tumor Suppressor PRDM5. Molecular and Cellular Biology, 2007, 27, 6889-6902.	2.3	79
22	Neutropenia-Associated Mutations in PRDM5, a Novel Epigenetic Regulator of Hematopoiesis Blood, 2006, 108, 503-503.	1.4	1
23	A 17q25.3 Duplication Defines a New Dosage-Sensitive Congenital Neutropenia Locus and Implicates SOCS3 as a Candidate Gene for Cases Unexplained by ELA2 Mutation Blood, 2006, 108, 1277-1277.	1.4	0
24	Gfi1 Coordinates Epigenetic Repression of $\langle i \rangle p21 \langle i \rangle \langle sup \rangle \langle i \rangle Cip/WAF1 \langle i \rangle \langle sup \rangle$ by Recruitment of Histone Lysine Methyltransferase G9a and Histone Deacetylase 1. Molecular and Cellular Biology, 2005, 25, 10338-10351.	2.3	157
25	Gfi-1 takes center stage in hematopoietic stem cells. Trends in Molecular Medicine, 2005, 11, 49-52.	6.7	30
26	A Novel Notch Protein, N2N, Targeted by Neutrophil Elastase and Implicated in Hereditary Neutropenia. Molecular and Cellular Biology, 2004, 24, 58-70.	2.3	57
27	Targets of the transcriptional repressor oncoprotein Gfi-1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5932-5937.	7.1	93
28	Gfi-1 Oncoproteins in Hematopoiesis. Hematology, 2003, 8, 339-344.	1.5	41
29	Massively multiplex single-cell Hi-C by combinatorial indexing. Protocol Exchange, 0, , .	0.3	2