

Ye Zheng

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6609593/publications.pdf>

Version: 2024-02-01

13
papers

371
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1305906

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1336881

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docs citations

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637
citing authors

#	ARTICLE	IF	CITATIONS
1	scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data. <i>Bioinformatics</i> , 2022, 38, 3642-3644.	1.8	3
2	FreeHi-C spike-in simulations for benchmarking differential chromatin interaction detection. <i>Methods</i> , 2021, 189, 3-11.	1.9	1
3	Optimal therapeutic targeting by HDAC inhibition in biopsy-derived treatment-naïve diffuse midline glioma models. <i>Neuro-Oncology</i> , 2021, 23, 376-386.	0.6	43
4	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. <i>PLoS Genetics</i> , 2021, 17, e1009309.	1.5	14
5	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. <i>Nature Biotechnology</i> , 2021, 39, 819-824.	9.4	121
6	Long-Term Follow-up and Single-Cell Multiomics Characteristics of Infusion Products in Patients with Chronic Lymphocytic Leukemia Treated with CD19 CAR-T Cells. <i>Blood</i> , 2021, 138, 1749-1749.	0.6	1
7	FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. <i>Nature Methods</i> , 2020, 17, 37-40.	9.0	15
8	Discovering How Heme Controls Genome Function Through Heme-omics. <i>Cell Reports</i> , 2020, 31, 107832.	2.9	21
9	Single-nucleotide human disease mutation inactivates a blood-regenerative GATA2 enhancer. <i>Journal of Clinical Investigation</i> , 2019, 129, 1180-1192.	3.9	47
10	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. <i>ELife</i> , 2019, 8, .	2.8	28
11	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. <i>Developmental Cell</i> , 2018, 46, 581-594.e4.	3.1	31
12	Perm-seq: Mapping Protein-DNA Interactions in Segmental Duplication and Highly Repetitive Regions of Genomes with Prior-Enhanced Read Mapping. <i>PLoS Computational Biology</i> , 2015, 11, e1004491.	1.5	11
13	Regulatory Architecture of the RCA Gene Cluster Captures an Intragenic TAD Boundary, CTCF-Mediated Chromatin Looping and a Long-Range Intergenic Enhancer. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	4