

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
citations

1163065

8
h-index

1199563

12
g-index

22
all docs

22
docs citations

22
times ranked

572
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell CUT&Tag analysis of chromatin modifications in differentiation and tumor progression. <i>Nature Biotechnology</i> , 2021, 39, 819-824.	17.5	121
2	Single-nucleotide human disease mutation inactivates a blood-regenerative GATA2 enhancer. <i>Journal of Clinical Investigation</i> , 2019, 129, 1180-1192.	8.2	47
3	Optimal therapeutic targeting by HDAC inhibition in biopsy-derived treatment-naïve diffuse midline glioma models. <i>Neuro-Oncology</i> , 2021, 23, 376-386.	1.2	43
4	GATA/Heme Multi-omics Reveals a Trace Metal-Dependent Cellular Differentiation Mechanism. <i>Developmental Cell</i> , 2018, 46, 581-594.e4.	7.0	31
5	Generative modeling of multi-mapping reads with mHi-C advances analysis of Hi-C studies. <i>ELife</i> , 2019, 8, .	6.0	28
6	Discovering How Heme Controls Genome Function Through Heme-omics. <i>Cell Reports</i> , 2020, 31, 107832.	6.4	21
7	FreeHi-C simulates high-fidelity Hi-C data for benchmarking and data augmentation. <i>Nature Methods</i> , 2020, 17, 37-40.	19.0	15
8	Transcriptome-wide transmission disequilibrium analysis identifies novel risk genes for autism spectrum disorder. <i>PLoS Genetics</i> , 2021, 17, e1009309.	3.5	14
9	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.	3.2	11
10	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, .	4.8	4
11	scGAD: single-cell gene associating domain scores for exploratory analysis of scHi-C data. <i>Bioinformatics</i> , 2022, 38, 3642-3644.	4.1	3
12	FreeHi-C spike-in simulations for benchmarking differential chromatin interaction detection. <i>Methods</i> , 2021, 189, 3-11.	3.8	1
13	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.	1.4	1