

Yunjiang Qiu

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

4,166
citations

331670

21
h-index

580821

25
g-index

35
all docs

35
docs citations

35
times ranked

9570
citing authors

#	ARTICLE	IF	CITATIONS
1	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. <i>Cell Reports</i> , 2016, 17, 2042-2059.	6.4	745
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. <i>Nature Communications</i> , 2019, 10, 1784.	12.8	636
3	RAP2 mediates mechanoresponses of the Hippo pathway. <i>Nature</i> , 2018, 560, 655-660.	27.8	266
4	An atlas of dynamic chromatin landscapes in mouse fetal development. <i>Nature</i> , 2020, 583, 744-751.	27.8	257
5	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. <i>Nature Genetics</i> , 2019, 51, 1380-1388.	21.4	236
6	Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates. <i>Cell Stem Cell</i> , 2015, 16, 386-399.	11.1	222
7	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. <i>Nature Methods</i> , 2017, 14, 629-635.	19.0	217
8	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	27.8	201
9	A single-cell atlas of chromatin accessibility in the human genome. <i>Cell</i> , 2021, 184, 5985-6001.e19.	28.9	194
10	The Hippo pathway effector proteins YAP and TAZ have both distinct and overlapping functions in the cell. <i>Journal of Biological Chemistry</i> , 2018, 293, 11230-11240.	3.4	164
11	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. <i>Cell Research</i> , 2018, 28, 204-220.	12.0	131
12	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 164-174.	8.2	123
13	Single-cell chromatin accessibility identifies pancreatic islet cell type-specific and state-specific regulatory programs of diabetes risk. <i>Nature Genetics</i> , 2021, 53, 455-466.	21.4	100
14	An atlas of gene regulatory elements in adult mouse cerebrum. <i>Nature</i> , 2021, 598, 129-136.	27.8	95
15	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. <i>PLoS Computational Biology</i> , 2019, 15, e1006982.	3.2	94
16	Systematic analysis of binding of transcription factors to noncoding variants. <i>Nature</i> , 2021, 591, 147-151.	27.8	89
17	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <i>Nature Communications</i> , 2019, 10, 2078.	12.8	82
18	Common DNA sequence variation influences 3-dimensional conformation of the human genome. <i>Genome Biology</i> , 2019, 20, 255.	8.8	65

#	ARTICLE	IF	CITATIONS
19	A common set of distinct features that characterize noncoding RNAs across multiple species. <i>Nucleic Acids Research</i> , 2015, 43, 104-114.	14.5	63
20	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. <i>Nature Communications</i> , 2021, 12, 6636.	12.8	31
21	FIREcaller: Detecting frequently interacting regions from Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 355-362.	4.1	22
22	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. <i>ELife</i> , 2021, 10, .	6.0	15
23	The Hippo pathway mediates Semaphorin signaling. <i>Science Advances</i> , 2022, 8, .	10.3	6
24	Inferring time series chromatin states for promoter-enhancer pairs based on Hi-C data. <i>BMC Genomics</i> , 2021, 22, 84.	2.8	3