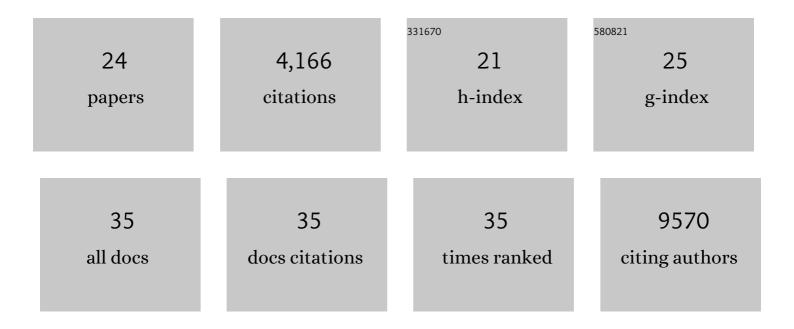
Yunjiang Qiu

List of Publications by Year in descending order

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ΥΠΝΠΑΝΟ ΟΠΙ

#	Article	IF	CITATIONS
1	The Hippo pathway mediates Semaphorin signaling. Science Advances, 2022, 8, .	10.3	6
2	Inferring time series chromatin states for promoter-enhancer pairs based on Hi-C data. BMC Genomics, 2021, 22, 84.	2.8	3
3	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	4.1	22
4	Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development. ELife, 2021, 10, .	6.0	15
5	Single-cell chromatin accessibility identifies pancreatic islet cell type– and state-specific regulatory programs of diabetes risk. Nature Genetics, 2021, 53, 455-466.	21.4	100
6	Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151.	27.8	89
7	An atlas of gene regulatory elements in adult mouse cerebrum. Nature, 2021, 598, 129-136.	27.8	95
8	Sequence logic at enhancers governs a dual mechanism of endodermal organ fate induction by FOXA pioneer factors. Nature Communications, 2021, 12, 6636.	12.8	31
9	A single-cell atlas of chromatin accessibility in the human genome. Cell, 2021, 184, 5985-6001.e19.	28.9	194
10	An atlas of dynamic chromatin landscapes in mouse fetal development. Nature, 2020, 583, 744-751.	27.8	257
11	Transcriptionally active HERV-H retrotransposons demarcate topologically associating domains in human pluripotent stem cells. Nature Genetics, 2019, 51, 1380-1388.	21.4	236
12	Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. Nature Communications, 2019, 10, 2078.	12.8	82
13	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	3.2	94
14	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
15	Dynamic reorganization of the genome shapes the recombination landscape in meiotic prophase. Nature Structural and Molecular Biology, 2019, 26, 164-174.	8.2	123
16	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	8.8	65
17	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. Cell Research, 2018, 28, 204-220.	12.0	131
18	The Hippo pathway effector proteins YAP and TAZ have both distinct and overlapping functions in the cell. Journal of Biological Chemistry, 2018, 293, 11230-11240.	3.4	164

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#	Article	IF	CITATIONS
19	RAP2 mediates mechanoresponses of the Hippo pathway. Nature, 2018, 560, 655-660.	27.8	266
20	A tiling-deletion-based genetic screen for cis-regulatory element identification in mammalian cells. Nature Methods, 2017, 14, 629-635.	19.0	217
21	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. Cell Reports, 2016, 17, 2042-2059.	6.4	745
22	Integrative analysis of haplotype-resolved epigenomes across human tissues. Nature, 2015, 518, 350-354.	27.8	201
23	A common set of distinct features that characterize noncoding RNAs across multiple species. Nucleic Acids Research, 2015, 43, 104-114.	14.5	63
24	Epigenetic Priming of Enhancers Predicts Developmental Competence of hESC-Derived Endodermal Lineage Intermediates. Cell Stem Cell, 2015, 16, 386-399.	11.1	222