Ming Hu

List of Publications by Year
in descending order

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Version: 2024-02-01

84	14,373	117453	56606
papers	citations	34	83
		h-index	g-index

105	105	105	22497
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	1.5	4
2	Understanding Regulatory Mechanisms of Brain Function and Disease through 3D Genome Organization. Genes, 2022, 13, 586.	1.0	7
3	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data. PLoS Genetics, 2022, 18, e1010102.	1.5	9
4	TWO-SIGMA-G: a new competitive gene set testing framework for scRNA-seq data accounting for inter-gene and cellâ€“cell correlation. Briefings in Bioinformatics, 2022, 23, .	3.2	5
5	Mapping chromatin loops in single cells. Trends in Genetics, 2022, 38, 637-640.	2.9	9
6	A systematic evaluation of Hi-C data enhancement methods for enhancing PLAC-seq and HiChIP data. Briefings in Bioinformatics, 2022, 23, .	3.2	3
7	Predictive Assessment of Quantitative Ultra-Widefield Angiographic Features for Future Need for Anti-VEGF Therapy in Diabetic Eye Disease. Journal of Personalized Medicine, 2022, 12, 608.	1.1	2
8	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. Computational and Structural Biotechnology Journal, 2022, 20, 2778-2783.	1.9	7
9	The Association of Fluid Volatility With Subretinal Hyperreflective Material and Ellipsoid Zone Integrity in Neovascular AMD. , 2022, 63, 17.		7
10	Machine Learningâ€“Based Automated Detection of Hydroxychloroquine Toxicity and Prediction of Future Toxicity Using Higher-Order OCT Biomarkers. Ophthalmology Retina, 2022, 6, 1241-1252.	1.2	6
11	Longitudinal panretinal microaneurysm dynamics on ultra-widefield fluorescein angiography in eyes treated with intravitreal aflibercept for proliferative diabetic retinopathy in the recovery study. British Journal of Ophthalmology, 2021, 105, 1111-1115.	2.1	11
12	Retinal Fluid Volatility Associated With Interval Tolerance and Visual Outcomes in Diabetic Macular Edema in the VISTA Phase III Trial. American Journal of Ophthalmology, 2021, 224, 217-227.	1.7	5
13	TWOâ€SIGMA: A novel twoâ€component single cell modelâ€based association method for singleâ€cell RNAâ€seq data. Genetic Epidemiology, 2021, 45, 142-153.	0.6	11
14	Aqueous Cytokine Expression and Higher Order OCT Biomarkers: Assessment of the Anatomic-Biologic Bridge in the IMAGINE DME Study. American Journal of Ophthalmology, 2021, 222, 328-339.	1.7	24
15	FIREcaller: Detecting frequently interacting regions from Hi-C data. Computational and Structural Biotechnology Journal, 2021, 19, 355-362.	1.9	22
16	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. American Journal of Human Genetics, 2021, 108, 257-268.	2.6	17
17	Longitudinal Assessment of Ellipsoid Zone Integrity, Subretinal Hyperreflective Material, and Subretinal Pigment Epithelium Disease in Neovascular Age-Related Macular Degeneration. Ophthalmology Retina, 2021, 5, 1204-1213.	1.2	28
18	Longitudinal Higher-Order OCT Assessment of Quantitative Fluid Dynamics and the Total Retinal Fluid Index in Neovascular AMD. Translational Vision Science and Technology, 2021, 10, 29.	1.1	15

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19	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. Nature Genetics, 2021, 53, 1064-1074.	9.4	90
20	MUNIn: A statistical framework for identifying long-range chromatin interactions from multiple samples. Human Genetics and Genomics Advances, 2021, 2, 100036.	1.0	0
21	Exploring the angiographic-biologic phenotype in the IMAGINE study: quantitative UWFA and cytokine expression. British Journal of Ophthalmology, 2021, , bjophthalmol-2020-318726.	2.1	4
22	Determining and forecasting drought susceptibility in southwestern Iran using multi-criteria decision-making (MCDM) coupled with CA-Markov model. Science of the Total Environment, 2021, 781, 146703.	3.9	55
23	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	9.0	46
24	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. Current Issues in Molecular Biology, 2021, 43, 1156-1170.	1.0	4
25	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. Science Advances, 2021, 7, eabi4360.	4.7	16
26	Characterization of Ultra-Widefield Angiographic Vascular Features in Diabetic Retinopathy with Automated Severity Classification. Ophthalmology Science, 2021, 1, 100049.	1.0	4
27	Spatial heterogeneity modeling of water quality based on random forest regression and model interpretation. Environmental Research, 2021, 202, 111660.	3.7	75
28	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). Methods in Molecular Biology, 2021, 2351, 181-199.	0.4	6
29	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. Nature Structural and Molecular Biology, 2021, 28, 152-161.	3.6	172
30	The 2-Year Leakage Index and Quantitative Microaneurysm Results of the RECOVERY Study: Quantitative Ultra-Widefield Findings in Proliferative Diabetic Retinopathy Treated with Intravitreal Aflibercept. Journal of Personalized Medicine, 2021, 11, 1126.	1.1	4
31	Transcriptional network orchestrating regional patterning of cortical progenitors. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	25
32	Repeatability of automated leakage quantification and microaneurysm identification utilising an analysis platform for ultra-widefield fluorescein angiography. British Journal of Ophthalmology, 2020, 104, 500-503.	2.1	16
33	Quantitative Ultra-Widefield Angiographic Features and Associations with Diabetic Macular Edema. Ophthalmology Retina, 2020, 4, 49-56.	1.2	19
34	Longitudinal Panretinal Leakage and Ischemic Indices in Retinal Vascular Disease after Aflibercept Therapy. Ophthalmology Retina, 2020, 4, 154-163.	1.2	19
35	IMPACT OF OPTICAL COHERENCE TOMOGRAPHY ANGIOGRAPHY REVIEW STRATEGY ON DETECTION OF CHOROIDAL NEOVASCULARIZATION. Retina, 2020, 40, 672-678.	1.0	8
36	Cell-type-specific 3D epigenomes in the developing human cortex. Nature, 2020, 587, 644-649.	13.7	110

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37	RETINAL LEAKAGE INDEX DYNAMICS ON ULTRA-WIDEFIELD FLUORESCEIN ANGIOGRAPHY IN EYES TREATED WITH INTRAVITREAL AFLIBERCEPT FOR PROLIFERATIVE DIABETIC RETINOPATHY IN THE RECOVERY STUDY. Retina, 2020, 40, 2175-2183.	1.0	10
38	Global analysis of histone modifications and long-range chromatin interactions revealed the differential cistrome changes and novel transcriptional players in human dilated cardiomyopathy. Journal of Molecular and Cellular Cardiology, 2020, 145, 30-42.	0.9	11
39	Quantitative Analysis of Ellipsoid Zone in Acute Posterior Multifocal Placoid Pigment Epitheliopathy. Journal of Vitreoretinal Diseases, 2020, 4, 192-201.	0.2	2
40	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. Molecular Cell, 2020, 79, 521-534.e15.	4.5	110
41	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	1.9	1
42	Altered chromatin recruitment by FOXA1 mutations promotes androgen independence and prostate cancer progression. Cell Research, 2019, 29, 773-775.	5.7	20
43	Optical coherence tomography angiography characteristics of choroidal neovascularization requiring varied dosing frequencies in treat-and-extend management: An analysis of the AVATAR study. PLoS ONE, 2019, 14, e0218889.	1.1	14
44	Higher-Order Assessment of OCT in Diabetic Macular Edema from the VISTA Study: Ellipsoid Zone Dynamics and the Retinal Fluid Index. Ophthalmology Retina, 2019, 3, 1056-1066.	1.2	44
45	Quantitative Ultra-Widefield Angiography and Diabetic Retinopathy Severity. Ophthalmology, 2019, 126, 1527-1532.	2.5	71
46	A general result on complete convergence for weighted sums of linear processes and its statistical applications. Statistics, 2019, 53, 903-920.	0.3	8
47	Sensory experience remodels genome architecture in neural circuit to drive motor learning. Nature, 2019, 569, 708-713.	13.7	66
48	Joint analyses of multi-tissue Hi-C and eQTL data demonstrate close spatial proximity between eQTLs and their target genes. BMC Genetics, 2019, 20, 43.	2.7	20
49	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	1.5	94
50	Predictive Model for Macular Hole Closure Speed: Insights From Intraoperative Optical Coherence Tomography. Translational Vision Science and Technology, 2019, 8, 18.	1.1	23
51	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. Nature Communications, 2019, 10, 1649.	5.8	56
52	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	3.8	65
53	Circular ecDNA promotes accessible chromatin and high oncogene expression. Nature, 2019, 575, 699-703.	13.7	343
54	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. Nature Structural and Molecular Biology, 2019, 26, 1063-1070.	3.6	239

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55	Quantitative assessment of outer retinal layers and ellipsoid zone mapping in hydroxychloroquine retinopathy. British Journal of Ophthalmology, 2019, 103, 3-7.	2.1	20
56	Transcriptomic and Protein Analysis of Small-cell Bladder Cancer (SCBC) Identifies Prognostic Biomarkers and DLL3 as a Relevant Therapeutic Target. Clinical Cancer Research, 2019, 25, 210-221.	3.2	48
57	Enhancing Hi-C data resolution with deep convolutional neural network HiCPlus. Nature Communications, 2018, 9, 750.	5.8	132
58	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. Cell Research, 2018, 28, 204-220.	5.7	131
59	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
60	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. Bioinformatics, 2018, 34, 139-146.	1.8	68
61	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. Science, 2018, 362, .	6.0	516
62	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. Genome Biology, 2018, 19, 151.	3.8	393
63	Assessment of inner and outer retinal layer metrics on the Cirrus HD-OCT Platform in normal eyes. PLoS ONE, 2018, 13, e0203324.	1.1	18
64	Gene regulation in the 3D genome. Human Molecular Genetics, 2018, 27, R228-R233.	1.4	61
65	Automated quantitative characterisation of retinal vascular leakage and microaneurysms in ultra-widefield fluorescein angiography. British Journal of Ophthalmology, 2017, 101, 696-699.	2.1	58
66	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	1.8	69
67	Polycomb-Mediated Disruption of an Androgen Receptor Feedback Loop Drives Castration-Resistant Prostate Cancer. Cancer Research, 2017, 77, 412-422.	0.4	23
68	LAIT: a local ancestry inference toolkit. BMC Genetics, 2017, 18, 83.	2.7	5
69	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. Bioinformatics, 2016, 32, 2692-2695.	1.8	40
70	Genome-wide mapping and analysis of chromosome architecture. Nature Reviews Molecular Cell Biology, 2016, 17, 743-755.	16.1	324
71	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
72	A Compendium of Chromatin Contact Maps Reveals Spatially Active Regions in the Human Genome. Cell Reports, 2016, 17, 2042-2059.	2.9	745

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73	HiView: an integrative genome browser to leverage Hi-C results for the interpretation of GWAS variants. BMC Research Notes, 2016, 9, 159.	0.6	10
74	Emergency Departmentâ€“Initiated Palliative Care in Advanced Cancer. JAMA Oncology, 2016, 2, 591.	3.4	194
75	Statistical Challenges in Analyzing Methylation and Long-Range Chromosomal Interaction Data. Statistics in Biosciences, 2016, 8, 284-309.	0.6	9
76	A hidden Markov random field-based Bayesian method for the detection of long-range chromosomal interactions in Hi-C data. Bioinformatics, 2016, 32, 650-656.	1.8	47
77	Widespread Rearrangement of 3D Chromatin Organization Underlies Polycomb-Mediated Stress-Induced Silencing. Molecular Cell, 2015, 58, 216-231.	4.5	299
78	The Distribution of Genomic Variations in Human iPSCs Is Related to Replication-Timing Reorganization during Reprogramming. Cell Reports, 2014, 7, 70-78.	2.9	24
79	Understanding spatial organizations of chromosomes via statistical analysis of Hiâ€€ data. Quantitative Biology, 2013, 1, 156-174.	0.3	29
80	Bayesian Inference of Spatial Organizations of Chromosomes. PLoS Computational Biology, 2013, 9, e1002893.	1.5	188
81	Using Poisson mixed-effects model to quantify transcript-level gene expression in RNA-Seq. Bioinformatics, 2012, 28, 63-68.	1.8	29
82	HiCNorm: removing biases in Hi-C data via Poisson regression. Bioinformatics, 2012, 28, 3131-3133.	1.8	228
83	Topological domains in mammalian genomes identified by analysis of chromatin interactions. Nature, 2012, 485, 376-380.	13.7	5,786
84	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	1.2	94