

Ming Hu

List of Publications by Year in descending order

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Version: 2024-02-01

84
papers

14,373
citations

117625

34
h-index

56724

83
g-index

105
all docs

105
docs citations

105
times ranked

22497
citing authors

#	ARTICLE	IF	CITATIONS
1	Topological domains in mammalian genomes identified by analysis of chromatin interactions. <i>Nature</i> , 2012, 485, 376-380.	27.8	5,786
2	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	21.4	2,224
3	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
4	Integrative functional genomic analysis of human brain development and neuropsychiatric risks. <i>Science</i> , 2018, 362, .	12.6	516
5	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016, 167, 1145-1149.	28.9	404
6	The 3D Genome Browser: a web-based browser for visualizing 3D genome organization and long-range chromatin interactions. <i>Genome Biology</i> , 2018, 19, 151.	8.8	393
7	Circular ecDNA promotes accessible chromatin and high oncogene expression. <i>Nature</i> , 2019, 575, 699-703.	27.8	343
8	Genome-wide mapping and analysis of chromosome architecture. <i>Nature Reviews Molecular Cell Biology</i> , 2016, 17, 743-755.	37.0	324
9	Widespread Rearrangement of 3D Chromatin Organization Underlies Polycomb-Mediated Stress-Induced Silencing. <i>Molecular Cell</i> , 2015, 58, 216-231.	9.7	299
10	An ultra high-throughput method for single-cell joint analysis of open chromatin and transcriptome. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1063-1070.	8.2	239
11	HiCNorm: removing biases in Hi-C data via Poisson regression. <i>Bioinformatics</i> , 2012, 28, 3131-3133.	4.1	228
12	Emergency Departmentâ€œInitiated Palliative Care in Advanced Cancer. <i>JAMA Oncology</i> , 2016, 2, 591.	7.1	194
13	Bayesian Inference of Spatial Organizations of Chromosomes. <i>PLoS Computational Biology</i> , 2013, 9, e1002893.	3.2	188
14	Promoter-proximal CTCF binding promotes distal enhancer-dependent gene activation. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 152-161.	8.2	172
15	Enhancing Hi-C data resolution with deep convolutional neural network HiCPlus. <i>Nature Communications</i> , 2018, 9, 750.	12.8	132
16	Histone H3 lysine 4 monomethylation modulates long-range chromatin interactions at enhancers. <i>Cell Research</i> , 2018, 28, 204-220.	12.0	131
17	Cell-type-specific 3D epigenomes in the developing human cortex. <i>Nature</i> , 2020, 587, 644-649.	27.8	110
18	Robust Hi-C Maps of Enhancer-Promoter Interactions Reveal the Function of Non-coding Genome in Neural Development and Diseases. <i>Molecular Cell</i> , 2020, 79, 521-534.e15.	9.7	110

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19	HPeak: an HMM-based algorithm for defining read-enriched regions in ChIP-Seq data. BMC Bioinformatics, 2010, 11, 369.	2.6	94
20	MAPS: Model-based analysis of long-range chromatin interactions from PLAC-seq and HiChIP experiments. PLoS Computational Biology, 2019, 15, e1006982.	3.2	94
21	CTCF mediates dosage- and sequence-context-dependent transcriptional insulation by forming local chromatin domains. Nature Genetics, 2021, 53, 1064-1074.	21.4	90
22	Spatial heterogeneity modeling of water quality based on random forest regression and model interpretation. Environmental Research, 2021, 202, 111660.	7.5	75
23	Quantitative Ultra-Widefield Angiography and Diabetic Retinopathy Severity. Ophthalmology, 2019, 126, 1527-1532.	5.2	71
24	HUGIn: Hi-C Unifying Genomic Interrogator. Bioinformatics, 2017, 33, 3793-3795.	4.1	69
25	DIMM-SC: a Dirichlet mixture model for clustering droplet-based single cell transcriptomic data. Bioinformatics, 2018, 34, 139-146.	4.1	68
26	Sensory experience remodels genome architecture in neural circuit to drive motor learning. Nature, 2019, 569, 708-713.	27.8	66
27	Common DNA sequence variation influences 3-dimensional conformation of the human genome. Genome Biology, 2019, 20, 255.	8.8	65
28	Gene regulation in the 3D genome. Human Molecular Genetics, 2018, 27, R228-R233.	2.9	61
29	Automated quantitative characterisation of retinal vascular leakage and microaneurysms in ultra-widefield fluorescein angiography. British Journal of Ophthalmology, 2017, 101, 696-699.	3.9	58
30	A Bayesian mixture model for clustering droplet-based single-cell transcriptomic data from population studies. Nature Communications, 2019, 10, 1649.	12.8	56
31	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.	8.0	55
32	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.	7.0	48
33	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.	4.1	47
34	SnapHiC: a computational pipeline to identify chromatin loops from single-cell Hi-C data. Nature Methods, 2021, 18, 1056-1059.	19.0	46
35	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.	2.4	44
36	FastHiC: a fast and accurate algorithm to detect long-range chromosomal interactions from Hi-C data. Bioinformatics, 2016, 32, 2692-2695.	4.1	40

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37	Using Poisson mixed-effects model to quantify transcript-level gene expression in RNA-Seq. <i>Bioinformatics</i> , 2012, 28, 63-68.	4.1	29
38	Understanding spatial organizations of chromosomes via statistical analysis of Hi-C data. <i>Quantitative Biology</i> , 2013, 1, 156-174.	0.5	29
39	Longitudinal Assessment of Ellipsoid Zone Integrity, Subretinal Hyperreflective Material, and Subretinal Pigment Epithelium Disease in Neovascular Age-Related Macular Degeneration. <i>Ophthalmology Retina</i> , 2021, 5, 1204-1213.	2.4	28
40	Transcriptional network orchestrating regional patterning of cortical progenitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
41	The Distribution of Genomic Variations in Human iPSCs Is Related to Replication-Timing Reorganization during Reprogramming. <i>Cell Reports</i> , 2014, 7, 70-78.	6.4	24
42	Aqueous Cytokine Expression and Higher Order OCT Biomarkers: Assessment of the Anatomic-Biologic Bridge in the IMAGINE DME Study. <i>American Journal of Ophthalmology</i> , 2021, 222, 328-339.	3.3	24
43	Polycomb-Mediated Disruption of an Androgen Receptor Feedback Loop Drives Castration-Resistant Prostate Cancer. <i>Cancer Research</i> , 2017, 77, 412-422.	0.9	23
44	Predictive Model for Macular Hole Closure Speed: Insights From Intraoperative Optical Coherence Tomography. <i>Translational Vision Science and Technology</i> , 2019, 8, 18.	2.2	23
45	FIREcaller: Detecting frequently interacting regions from Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 355-362.	4.1	22
46	Altered chromatin recruitment by FOXA1 mutations promotes androgen independence and prostate cancer progression. <i>Cell Research</i> , 2019, 29, 773-775.	12.0	20
47	Joint analyses of multi-tissue Hi-C and eQTL data demonstrate close spatial proximity between eQTLs and their target genes. <i>BMC Genetics</i> , 2019, 20, 43.	2.7	20
48	Quantitative assessment of outer retinal layers and ellipsoid zone mapping in hydroxychloroquine retinopathy. <i>British Journal of Ophthalmology</i> , 2019, 103, 3-7.	3.9	20
49	Quantitative Ultra-Widefield Angiographic Features and Associations with Diabetic Macular Edema. <i>Ophthalmology Retina</i> , 2020, 4, 49-56.	2.4	19
50	Longitudinal Panretinal Leakage and Ischemic Indices in Retinal Vascular Disease after Aflibercept Therapy. <i>Ophthalmology Retina</i> , 2020, 4, 154-163.	2.4	19
51	Assessment of inner and outer retinal layer metrics on the Cirrus HD-OCT Platform in normal eyes. <i>PLoS ONE</i> , 2018, 13, e0203324.	2.5	18
52	HiC-ACT: improved detection of chromatin interactions from Hi-C data via aggregated Cauchy test. <i>American Journal of Human Genetics</i> , 2021, 108, 257-268.	6.2	17
53	Repeatability of automated leakage quantification and microaneurysm identification utilising an analysis platform for ultra-widefield fluorescein angiography. <i>British Journal of Ophthalmology</i> , 2020, 104, 500-503.	3.9	16
54	Parallel characterization of cis-regulatory elements for multiple genes using CRISPRpath. <i>Science Advances</i> , 2021, 7, eabi4360.	10.3	16

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55	Longitudinal Higher-Order OCT Assessment of Quantitative Fluid Dynamics and the Total Retinal Fluid Index in Neovascular AMD. <i>Translational Vision Science and Technology</i> , 2021, 10, 29.	2.2	15
56	Optical coherence tomography angiography characteristics of choroidal neovascularization requiring varied dosing frequencies in treat-and-extend management: An analysis of the AVATAR study. <i>PLoS ONE</i> , 2019, 14, e0218889.	2.5	14
57	Longitudinal panretinal microaneurysm dynamics on ultra-widefield fluorescein angiography in eyes treated with intravitreal aflibercept for proliferative diabetic retinopathy in the recovery study. <i>British Journal of Ophthalmology</i> , 2021, 105, 1111-1115.	3.9	11
58	Global analysis of histone modifications and long-range chromatin interactions revealed the differential cistrome changes and novel transcriptional players in human dilated cardiomyopathy. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 145, 30-42.	1.9	11
59	TWO-SIGMA: A novel two-component single cell model-based association method for single-cell RNA-seq data. <i>Genetic Epidemiology</i> , 2021, 45, 142-153.	1.3	11
60	HiView: an integrative genome browser to leverage Hi-C results for the interpretation of GWAS variants. <i>BMC Research Notes</i> , 2016, 9, 159.	1.4	10
61	RETINAL LEAKAGE INDEX DYNAMICS ON ULTRA-WIDEFIELD FLUORESCHEIN ANGIOGRAPHY IN EYES TREATED WITH INTRAVITREAL AFLIBERCEPT FOR PROLIFERATIVE DIABETIC RETINOPATHY IN THE RECOVERY STUDY. <i>Retina</i> , 2020, 40, 2175-2183.	1.7	10
62	Statistical Challenges in Analyzing Methylation and Long-Range Chromosomal Interaction Data. <i>Statistics in Biosciences</i> , 2016, 8, 284-309.	1.2	9
63	THUNDER: A reference-free deconvolution method to infer cell type proportions from bulk Hi-C data. <i>PLoS Genetics</i> , 2022, 18, e1010102.	3.5	9
64	Mapping chromatin loops in single cells. <i>Trends in Genetics</i> , 2022, 38, 637-640.	6.7	9
65	A general result on complete convergence for weighted sums of linear processes and its statistical applications. <i>Statistics</i> , 2019, 53, 903-920.	0.6	8
66	IMPACT OF OPTICAL COHERENCE TOMOGRAPHY ANGIOGRAPHY REVIEW STRATEGY ON DETECTION OF CHOROIDAL NEOVASCULARIZATION. <i>Retina</i> , 2020, 40, 672-678.	1.7	8
67	Understanding Regulatory Mechanisms of Brain Function and Disease through 3D Genome Organization. <i>Genes</i> , 2022, 13, 586.	2.4	7
68	SnapHiC2: A computationally efficient loop caller for single cell Hi-C data. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 2778-2783.	4.1	7
69	The Association of Fluid Volatility With Subretinal Hyperreflective Material and Ellipsoid Zone Integrity in Neovascular AMD. , 2022, 63, 17.		7
70	Proximity Ligation-Assisted ChIP-Seq (PLAC-Seq). <i>Methods in Molecular Biology</i> , 2021, 2351, 181-199.	0.9	6
71	Machine Learning-Based Automated Detection of Hydroxychloroquine Toxicity and Prediction of Future Toxicity Using Higher-Order OCT Biomarkers. <i>Ophthalmology Retina</i> , 2022, 6, 1241-1252.	2.4	6
72	LAIT: a local ancestry inference toolkit. <i>BMC Genetics</i> , 2017, 18, 83.	2.7	5

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73	Retinal Fluid Volatility Associated With Interval Tolerance and Visual Outcomes in Diabetic Macular Edema in the VISTA Phase III Trial. <i>American Journal of Ophthalmology</i> , 2021, 224, 217-227.	3.3	5
74	TWO-SIGMA-G: a new competitive gene set testing framework for scRNA-seq data accounting for inter-gene and cell-cell correlation. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	5
75	Exploring the angiographic-biologic phenotype in the IMAGINE study: quantitative UWFA and cytokine expression. <i>British Journal of Ophthalmology</i> , 2021, , bjophthalmol-2020-318726.	3.9	4
76	HPRep: Quantifying Reproducibility in HiChIP and PLAC-Seq Datasets. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1156-1170.	2.4	4
77	Characterization of Ultra-Widefield Angiographic Vascular Features in Diabetic Retinopathy with Automated Severity Classification. <i>Ophthalmology Science</i> , 2021, 1, 100049.	2.5	4
78	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. <i>Journal of Personalized Medicine</i> , 2021, 11, 1126.	2.5	4
79	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. <i>PLoS Genetics</i> , 2022, 18, e1009984.	3.5	4
80	A systematic evaluation of Hi-C data enhancement methods for enhancing PLAC-seq and HiChIP data. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	3
81	Quantitative Analysis of Ellipsoid Zone in Acute Posterior Multifocal Placoid Pigment Epitheliopathy. <i>Journal of Vitreoretinal Diseases</i> , 2020, 4, 192-201.	0.7	2
82	Predictive Assessment of Quantitative Ultra-Widefield Angiographic Features for Future Need for Anti-VEGF Therapy in Diabetic Eye Disease. <i>Journal of Personalized Medicine</i> , 2022, 12, 608.	2.5	2
83	Inferring Spatial Organization of Individual Topologically Associated Domains via Piecewise Helical Model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 17, 1-1.	3.0	1
84	MUNIn: A statistical framework for identifying long-range chromatin interactions from multiple samples. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100036.	1.7	0