Michael Q Zhang

List of Publications by Year
in descending order

115 papers	17,120 citations	71102 41 h-index	24258 110 g-index
151 all docs	151 docs citations	151 times ranked	32814 citing authors

#	Article	IF	Citations
1	A data-driven method to learn a jump diffusion process from aggregate biological gene expression data. Journal of Theoretical Biology, 2022, 532, 110923.	1.7	2
2	Integration of single cell data by disentangled representation learning. Nucleic Acids Research, 2022, 50, e8-e8.	14.5	4
3	MyoD is a 3D genome structure organizer for muscle cell identity. Nature Communications, 2022, 13, 205.	12.8	50
4	HPVMD-C: a disease-based mutation database of human papillomavirus in China. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	19
5	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. Cell Reports, 2022, 39, 110626.	6.4	22
6	MarkovHC: Markov hierarchical clustering for the topological structure of high-dimensional single-cell omics data with transition pathway and critical point detection. Nucleic Acids Research, 2022, 50, 46-56.	14.5	9
7	Computational modeling and analysis of the morphogenetic domain signaling networks regulating C. elegans embryogenesis. Computational and Structural Biotechnology Journal, 2022, 20, 3653-3666.	4.1	0
8	A personal journey on cracking the genomic codes. Quantitative Biology, 2021, 9, 8-22.	0.5	1
9	Deciphering hierarchical organization of topologically associated domains through change-point testing. BMC Bioinformatics, 2021, 22, 183.	2.6	12
10	3D genome alterations associated with dysregulated HOXA13 expression in high-risk T-lineage acute lymphoblastic leukemia. Nature Communications, 2021, 12, 3708.	12.8	24
11	The loss of heterochromatin is associated with multiscale three-dimensional genome reorganization and aberrant transcription during cellular senescence. Genome Research, 2021, 31, 1121-1135.	5.5	36
12	DAGM: A novel modelling framework to assess the risk of HER2-negative breast cancer based on germline rare coding mutations. EBioMedicine, 2021, 69, 103446.	6.1	4
13	Single-cell alternative polyadenylation analysis delineates GABAergic neuron types. BMC Biology, 2021, 19, 144.	3.8	12
14	Quantifying the phase separation property of chromatin-associated proteins under physiological conditions using an anti-1,6-hexanediol index. Genome Biology, 2021, 22, 229.	8.8	24
15	Characterizing microRNA-mediated modulation of gene expression noise and its effect on synthetic gene circuits. Cell Reports, 2021, 36, 109573.	6.4	11
16	SEAM is a spatial single nuclear metabolomics method for dissecting tissue microenvironment. Nature Methods, 2021, 18, 1223-1232.	19.0	78
17	ScaffComb: A Phenotype‐Based Framework for Drug Combination Virtual Screening in Large‐Scale Chemical Datasets. Advanced Science, 2021, 8, e2102092.	11.2	7
18	Highly diversified core promoters in the human genome and their effects on gene expression and disease predisposition. BMC Genomics, 2020, 21, 842.	2.8	3

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19	Model-based analysis of chromatin interactions from dCas9-Based CAPTURE-3C-seq. PLoS ONE, 2020, 15, e0236666.	2.5	1
20	Molecular basis for histone H3 â€œK4me3-K9me3/2â€•methylation pattern readout by Spindlin1. Journal of Biological Chemistry, 2020, 295, 16877-16887.	3.4	15
21	Singleâ€‘cell RNA sequencing of t(8;21) acute myeloid leukemia for risk prediction. Oncology Reports, 2020, 43, 1278-1288.	2.6	2
22	Tn5-FISH, a novel cytogenetic method to image chromatin interactions with sub-kilobase resolution. Journal of Genetics and Genomics, 2020, 47, 727-734.	3.9	8
23	Multiplexed capture of spatial configuration and temporal dynamics of locus-specific 3D chromatin by biotinylated dCas9. Genome Biology, 2020, 21, 59.	8.8	27
24	Dynamic Alternative Splicing During Mouse Preimplantation Embryo Development. Frontiers in Bioengineering and Biotechnology, 2020, 8, 35.	4.1	17
25	2SigFinder: the combined use of small-scale and large-scale statistical testing for genomic island detection from a single genome. BMC Bioinformatics, 2020, 21, 159.	2.6	29
26	The landscape of RNA polymerase IIâ€“associated chromatin interactions in prostate cancer. Journal of Clinical Investigation, 2020, 130, 3987-4005.	8.2	37
27	Rathkeâ€™s cleft cyst with xanthogranulomatous change: A case report and review of the literature. , 2020, 11, 246.		2
28	A large-scale CRISPR screen and identification of essential genes in cellular senescence bypass. Aging, 2019, 11, 4011-4031.	3.1	8
29	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. Cell, 2019, 178, 107-121.e18.	28.9	224
30	Sox2 and Klf4 as the Functional Core in Pluripotency Induction without Exogenous Oct4. Cell Reports, 2019, 29, 1986-2000.e8.	6.4	32
31	Integrating Hi-C and FISH data for modeling of the 3D organization of chromosomes. Nature Communications, 2019, 10, 2049.	12.8	45
32	SuperCT: a supervised-learning framework for enhanced characterization of single-cell transcriptomic profiles. Nucleic Acids Research, 2019, 47, e48-e48.	14.5	52
33	Integrative molecular analysis of metastatic hepatocellular carcinoma. BMC Medical Genomics, 2019, 12, 164.	1.5	11
34	Single-cell stochastic gene expression kinetics with coupled positive-plus-negative feedback. Physical Review E, 2019, 100, 052406.	2.1	33
35	Relaxation rates of gene expression kinetics reveal the feedback signs of autoregulatory gene networks. Journal of Chemical Physics, 2018, 148, .	3.0	24
36	Co-inhibitory Molecule B7 Superfamily Member 1 Expressed by Tumor-Infiltrating Myeloid Cells Induces Dysfunction of Anti-tumor CD8+ T Cells. Immunity, 2018, 48, 773-786.e5.	14.3	150

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37	FIND: difFerential chromatin INteractions Detection using a spatial Poisson process. Genome Research, 2018, 28, 412-422.	5.5	69
38	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. Nucleic Acids Research, 2018, 46, D308-D314.	14.5	434
39	Alterations of specific chromatin conformation affect ATRA-induced leukemia cell differentiation. Cell Death and Disease, 2018, 9, 200.	6.3	29
40	Developing novel methods to image and visualize 3D genomes. Cell Biology and Toxicology, 2018, 34, 367-380.	5.3	24
41	CGmapTools improves the precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data. Bioinformatics, 2018, 34, 381-387.	4.1	152
42	DE MERVLs are Enriched Around Two-Cell-Specific Genes During Zygotic Genome Activation in Mouse. , 2018, , .		0
43	Regulatory RNA binding proteins contribute to the transcriptome-wide splicing alterations in human cellular senescence. Aging, 2018, 10, 1489-1505.	3.1	17
44	Global transcriptional activity dynamics reveal functional enhancer RNAs. Genome Research, 2018, 28, 1799-1811.	5.5	34
45	HiCDB: a sensitive and robust method for detecting contact domain boundaries. Nucleic Acids Research, 2018, 46, 11239-11250.	14.5	52
46	Synergistic co-regulation and competition by a SOX9-GLI-FOXA phasic transcriptional network coordinate chondrocyte differentiation transitions. PLoS Genetics, 2018, 14, e1007346.	3.5	56
47	CAPTURE: *In Situ* Analysis of Chromatin Composition of Endogenous Genomic Loci by Biotinylated dCas9. Current Protocols in Molecular Biology, 2018, 123, e64.	2.9	14
48	Inhibiting the integrated stress response pathway prevents aberrant chondrocyte differentiation thereby alleviating chondrodysplasia. ELife, 2018, 7, .	6.0	59
49	Recurrently deregulated lncRNAs in hepatocellular carcinoma. Nature Communications, 2017, 8, 14421.	12.8	279
50	Web3DMol: interactive protein structure visualization based on WebGL. Nucleic Acids Research, 2017, 45, W523-W527.	14.5	21
51	HCSGD: An integrated database of human cellular senescence genes. Journal of Genetics and Genomics, 2017, 44, 227-234.	3.9	15
52	Reconstructing cell cycle pseudo time-series via single-cell transcriptome data. Nature Communications, 2017, 8, 22.	12.8	121
53	Emergent LÃ©vy behavior in single-cell stochastic gene expression. Physical Review E, 2017, 96, 040402.	2.1	40
54	In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell, 2017, 170, 1028-1043.e19.	28.9	236

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55	Network embedding-based representation learning for single cell RNA-seq data. Nucleic Acids Research, 2017, 45, e166-e166.	14.5	54
56	PAF1 regulation of promoter-proximal pause release via enhancer activation. Science, 2017, 357, 1294-1298.	12.6	95
57	Stochastic fluctuations can reveal the feedback signs of gene regulatory networks at the single-molecule level. Scientific Reports, 2017, 7, 16037.	3.3	22
58	BL-Hi-C is an efficient and sensitive approach for capturing structural and regulatory chromatin interactions. Nature Communications, 2017, 8, 1622.	12.8	60
59	Allelic reprogramming of 3D chromatin architecture during early mammalian development. Nature, 2017, 547, 232-235.	27.8	406
60	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. Nucleic Acids Research, 2017, 45, e4-e4.	14.5	104
61	Super-resolution imaging of a 2.5 kb non-repetitive DNA in situ in the nuclear genome using molecular beacon probes. ELife, 2017, 6, .	6.0	29
62	MTGIpick allows robust identification of genomic islands from a single genome. Briefings in Bioinformatics, 2016, 19, bbw118.	6.5	34
63	Super-resolution fluorescence dipole orientation microscopy. , 2016, , .		0
64	<i>De novo</i> deciphering three-dimensional chromatin interaction and topological domains by wavelet transformation of epigenetic profiles. Nucleic Acids Research, 2016, 44, e106-e106.	14.5	33
65	Advances in computational ChIA€PET data analysis. Quantitative Biology, 2016, 4, 217-225.	0.5	5
66	Analysis of<i>C. elegans</i>muscle transcriptome using trans-splicing-based RNA tagging (SRT). Nucleic Acids Research, 2016, 44, gkw734.	14.5	19
67	Super-resolution dipole orientation mapping via polarization demodulation. Light: Science and Applications, 2016, 5, e16166-e16166.	16.6	93
68	Mammalian non-CG methylations are conserved and cell-type specific and may have been involved in the evolution of transposon elements. Scientific Reports, 2016, 6, 32207.	3.3	8
69	FAT10 Is Critical in Influenza A Virus Replication by Inhibiting Type I IFN. Journal of Immunology, 2016, 197, 824-833.	0.8	16
70	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. Nucleic Acids Research, 2016, 44, D203-D208.	14.5	574
71	Engineering EMT using 3D micro-scaffold to promote hepatic functions for drug hepatotoxicity evaluation. Biomaterials, 2016, 91, 11-22.	11.4	45
72	Role of emergent palliative radiation therapy in the care of patients with cancer.. Journal of Clinical Oncology, 2016, 34, 201-201.	1.6	2

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73	Histone Deacetylases Positively Regulate Transcription through the Elongation Machinery. Cell Reports, 2015, 13, 1444-1455.	6.4	138
74	Fast dimension reduction and integrative clustering of multi-omics data using low-rank approximation: application to cancer molecular classification. BMC Genomics, 2015, 16, 1022.	2.8	124
75	Differential connectivity of splicing activators and repressors to the human spliceosome. Genome Biology, 2015, 16, 119.	9.6	33
76	Epigenome-Wide Association of Liver Methylation Patterns and Complex Metabolic Traits in Mice. Cell Metabolism, 2015, 21, 905-917.	16.2	98
77	MICC: an R package for identifying chromatin interactions from ChIA-PET data. Bioinformatics, 2015, 31, 3832-3834.	4.1	34
78	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. Nucleic Acids Research, 2015, 43, W264-W269.	14.5	19
79	3CPET: finding co-factor complexes from ChIA-PET data using a hierarchical Dirichlet process. Genome Biology, 2015, 16, 288.	8.8	20
80	Integrative analysis of haplotype-resolved epigenomes across human tissues. Nature, 2015, 518, 350-354.	27.8	201
81	Integrative analysis of 111 reference human epigenomes. Nature, 2015, 518, 317-330.	27.8	5,653
82	Model-guided quantitative analysis of microRNA-mediated regulation on competing endogenous RNAs using a synthetic gene circuit. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3158-3163.	7.1	117
83	Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic Acids Research, 2015, 43, 5263-5274.	14.5	65
84	Small C-terminal Domain Phosphatase 3 Dephosphorylates the Linker Sites of Receptor-regulated Smads (R-Smads) to Ensure Transforming Growth Factor β (TGFβ)-mediated Germ Layer Induction in Xenopus Embryos. Journal of Biological Chemistry, 2015, 290, 17239-17249.	3.4	6
85	A common set of distinct features that characterize noncoding RNAs across multiple species. Nucleic Acids Research, 2015, 43, 104-114.	14.5	63
86	Reconfigurable hybrid interface for molecular marker diagnostics and in-situ reporting. Biosensors and Bioelectronics, 2015, 74, 744-750.	10.1	7
87	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. Cell, 2015, 162, 900-910.	28.9	846
88	Quantitative combination of natural anti-oxidants prevents metabolic syndrome by reducing oxidative stress. Redox Biology, 2015, 6, 206-217.	9.0	39
89	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. IEEE Life Sciences Letters, 2015, 1, 30-33.	1.2	2
90	Genome-wide analysis of the response to nitric oxide in uropathogenic Escherichia coli CFT073. Microbial Genomics, 2015, 1, e000031.	2.0	21

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91	ModuleRole: A Tool for Modulization, Role Determination and Visualization in Protein-Protein Interaction Networks. PLoS ONE, 2014, 9, e94608.	2.5	5
92	Activity-dependent FUS dysregulation disrupts synaptic homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4769-78.	7.1	116
93	Genome wide mapping of Foxo1 binding-sites in murine T lymphocytes. Genomics Data, 2014, 2, 280-281.	1.3	5
94	Nucleosome eviction and multiple co-factor binding predict estrogen-receptor-alpha-associated long-range interactions. Nucleic Acids Research, 2014, 42, 6935-6944.	14.5	17
95	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. G3: Genes, Genomes, Genetics, 2014, 4, 2051-2063.	1.8	39
96	HITS-CLIP and Integrative Modeling Define the Rbfox Splicing-Regulatory Network Linked to Brain Development and Autism. Cell Reports, 2014, 6, 1139-1152.	6.4	326
97	Chd5 orchestrates chromatin remodelling during sperm development. Nature Communications, 2014, 5, 3812.	12.8	82
98	Hsa-miR-1246, hsa-miR-320a and hsa-miR-196b-5p inhibitors can reduce the cytotoxicity of Ebola virus glycoprotein in vitro. Science China Life Sciences, 2014, 57, 959-972.	4.9	28
99	Resolving the genetic heterogeneity of prelingual hearing loss within one family: Performance comparison and application of two targeted next generation sequencing approaches. Journal of Human Genetics, 2014, 59, 599-607.	2.3	16
100	Exome Sequencing Identifies a Novel Frameshift Mutation of<i>MYO6</i>as the Cause of Autosomal Dominant Nonsyndromic Hearing Loss in a Chinese Family. Annals of Human Genetics, 2014, 78, 410-423.	0.8	10
101	Genome-wide map of regulatory interactions in the human genome. Genome Research, 2014, 24, 1905-1917.	5.5	259
102	Assembly and Validation of Versatile Transcription Activator-Like Effector Libraries. Scientific Reports, 2014, 4, 4857.	3.3	7
103	Population dynamics of cancer cells with cell state conversions. Quantitative Biology, 2013, 1, 201-208.	0.5	22
104	FastDMA: An Infinium HumanMethylation450 Beadchip Analyzer. PLoS ONE, 2013, 8, e74275.	2.5	25
105	Bivalent-Like Chromatin Markers Are Predictive for Transcription Start Site Distribution in Human. PLoS ONE, 2012, 7, e38112.	2.5	3
106	An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. Nucleic Acids Research, 2009, 37, 4587-4602.	14.5	400
107	Combinatorial patterns of histone acetylations and methylations in the human genome. Nature Genetics, 2008, 40, 897-903.	21.4	2,034
108	Networkâ€based global inference of human disease genes. Molecular Systems Biology, 2008, 4, 189.	7.2	583

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109	Computational prediction of novel components of lung transcriptional networks. Bioinformatics, 2007, 23, 21-29.	4.1	13
110	Tissue‐specific regulatory elements in mammalian promoters. Molecular Systems Biology, 2007, 3, 73.	7.2	52
111	Analysis of the Vertebrate Insulator Protein CTCF-Binding Sites in the Human Genome. Cell, 2007, 128, 1231-1245.	28.9	910
112	Statistical significance of cis-regulatory modules. BMC Bioinformatics, 2007, 8, 19.	2.6	68
113	DNA motifs in human and mouse proximal promoters predict tissue-specific expression. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 6275-6280.	7.1	114
114	Identifying tissue-selective transcription factor binding sites in vertebrate promoters. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 1560-1565.	7.1	113
115	Similarity of position frequency matrices for transcription factor binding sites. Bioinformatics, 2005, 21, 307-313.	4.1	97