

# Michael Q Zhang

## List of Publications by Year in descending order

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115  
papers

17,120  
citations

71061

41  
h-index

24232

110  
g-index

151  
all docs

151  
docs citations

151  
times ranked

32814  
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative analysis of 111 reference human epigenomes. <i>Nature</i> , 2015, 518, 317-330.	13.7	5,653
2	Combinatorial patterns of histone acetylations and methylations in the human genome. <i>Nature Genetics</i> , 2008, 40, 897-903.	9.4	2,034
3	Analysis of the Vertebrate Insulator Protein CTCF-Binding Sites in the Human Genome. <i>Cell</i> , 2007, 128, 1231-1245.	13.5	910
4	CRISPR Inversion of CTCF Sites Alters Genome Topology and Enhancer/Promoter Function. <i>Cell</i> , 2015, 162, 900-910.	13.5	846
5	Network-based global inference of human disease genes. <i>Molecular Systems Biology</i> , 2008, 4, 189.	3.2	583
6	NONCODE 2016: an informative and valuable data source of long non-coding RNAs. <i>Nucleic Acids Research</i> , 2016, 44, D203-D208.	6.5	574
7	NONCODEV5: a comprehensive annotation database for long non-coding RNAs. <i>Nucleic Acids Research</i> , 2018, 46, D308-D314.	6.5	434
8	Allelic reprogramming of 3D chromatin architecture during early mammalian development. <i>Nature</i> , 2017, 547, 232-235.	13.7	406
9	An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. <i>Nucleic Acids Research</i> , 2009, 37, 4587-4602.	6.5	400
10	HITS-CLIP and Integrative Modeling Define the Rbfox Splicing-Regulatory Network Linked to Brain Development and Autism. <i>Cell Reports</i> , 2014, 6, 1139-1152.	2.9	326
11	Recurrently deregulated lncRNAs in hepatocellular carcinoma. <i>Nature Communications</i> , 2017, 8, 14421.	5.8	279
12	Genome-wide map of regulatory interactions in the human genome. <i>Genome Research</i> , 2014, 24, 1905-1917.	2.4	259
13	In Situ Capture of Chromatin Interactions by Biotinylated dCas9. <i>Cell</i> , 2017, 170, 1028-1043.e19.	13.5	236
14	Pervasive Chromatin-RNA Binding Protein Interactions Enable RNA-Based Regulation of Transcription. <i>Cell</i> , 2019, 178, 107-121.e18.	13.5	224
15	Integrative analysis of haplotype-resolved epigenomes across human tissues. <i>Nature</i> , 2015, 518, 350-354.	13.7	201
16	CGmapTools improves the precision of heterozygous SNV calls and supports allele-specific methylation detection and visualization in bisulfite-sequencing data. <i>Bioinformatics</i> , 2018, 34, 381-387.	1.8	152
17	Co-inhibitory Molecule B7 Superfamily Member 1 Expressed by Tumor-Infiltrating Myeloid Cells Induces Dysfunction of Anti-tumor CD8+ T Cells. <i>Immunity</i> , 2018, 48, 773-786.e5.	6.6	150
18	Histone Deacetylases Positively Regulate Transcription through the Elongation Machinery. <i>Cell Reports</i> , 2015, 13, 1444-1455.	2.9	138

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19	Fast dimension reduction and integrative clustering of multi-omics data using low-rank approximation: application to cancer molecular classification. <i>BMC Genomics</i> , 2015, 16, 1022.	1.2	124
20	Reconstructing cell cycle pseudo time-series via single-cell transcriptome data. <i>Nature Communications</i> , 2017, 8, 22.	5.8	121
21	Model-guided quantitative analysis of microRNA-mediated regulation on competing endogenous RNAs using a synthetic gene circuit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3158-3163.	3.3	117
22	Activity-dependent FUS dysregulation disrupts synaptic homeostasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4769-78.	3.3	116
23	DNA motifs in human and mouse proximal promoters predict tissue-specific expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6275-6280.	3.3	114
24	Identifying tissue-selective transcription factor binding sites in vertebrate promoters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1560-1565.	3.3	113
25	ChIA-PET2: a versatile and flexible pipeline for ChIA-PET data analysis. <i>Nucleic Acids Research</i> , 2017, 45, e4-e4.	6.5	104
26	Epigenome-Wide Association of Liver Methylation Patterns and Complex Metabolic Traits in Mice. <i>Cell Metabolism</i> , 2015, 21, 905-917.	7.2	98
27	Similarity of position frequency matrices for transcription factor binding sites. <i>Bioinformatics</i> , 2005, 21, 307-313.	1.8	97
28	PAF1 regulation of promoter-proximal pause release via enhancer activation. <i>Science</i> , 2017, 357, 1294-1298.	6.0	95
29	Super-resolution dipole orientation mapping via polarization demodulation. <i>Light: Science and Applications</i> , 2016, 5, e16166-e16166.	7.7	93
30	Chd5 orchestrates chromatin remodelling during sperm development. <i>Nature Communications</i> , 2014, 5, 3812.	5.8	82
31	SEAM is a spatial single nuclear metabolomics method for dissecting tissue microenvironment. <i>Nature Methods</i> , 2021, 18, 1223-1232.	9.0	78
32	FIND: diffERential chromatin INteractions Detection using a spatial Poisson process. <i>Genome Research</i> , 2018, 28, 412-422.	2.4	69
33	Statistical significance of cis-regulatory modules. <i>BMC Bioinformatics</i> , 2007, 8, 19.	1.2	68
34	Design and bioinformatics analysis of genome-wide CLIP experiments. <i>Nucleic Acids Research</i> , 2015, 43, 5263-5274.	6.5	65
35	A common set of distinct features that characterize noncoding RNAs across multiple species. <i>Nucleic Acids Research</i> , 2015, 43, 104-114.	6.5	63
36	BL-Hi-C is an efficient and sensitive approach for capturing structural and regulatory chromatin interactions. <i>Nature Communications</i> , 2017, 8, 1622.	5.8	60

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37	Inhibiting the integrated stress response pathway prevents aberrant chondrocyte differentiation thereby alleviating chondrodysplasia. <i>ELife</i> , 2018, 7, .	2.8	59
38	Synergistic co-regulation and competition by a SOX9-GLI-FOXA phasic transcriptional network coordinate chondrocyte differentiation transitions. <i>PLoS Genetics</i> , 2018, 14, e1007346.	1.5	56
39	Network embedding-based representation learning for single cell RNA-seq data. <i>Nucleic Acids Research</i> , 2017, 45, e166-e166.	6.5	54
40	Tissue-specific regulatory elements in mammalian promoters. <i>Molecular Systems Biology</i> , 2007, 3, 73.	3.2	52
41	HiCDB: a sensitive and robust method for detecting contact domain boundaries. <i>Nucleic Acids Research</i> , 2018, 46, 11239-11250.	6.5	52
42	SuperCT: a supervised-learning framework for enhanced characterization of single-cell transcriptomic profiles. <i>Nucleic Acids Research</i> , 2019, 47, e48-e48.	6.5	52
43	MyoD is a 3D genome structure organizer for muscle cell identity. <i>Nature Communications</i> , 2022, 13, 205.	5.8	50
44	Engineering EMT using 3D micro-scaffold to promote hepatic functions for drug hepatotoxicity evaluation. <i>Biomaterials</i> , 2016, 91, 11-22.	5.7	45
45	Integrating Hi-C and FISH data for modeling of the 3D organization of chromosomes. <i>Nature Communications</i> , 2019, 10, 2049.	5.8	45
46	Emergent Lévy behavior in single-cell stochastic gene expression. <i>Physical Review E</i> , 2017, 96, 040402.	0.8	40
47	Distinct and Predictive Histone Lysine Acetylation Patterns at Promoters, Enhancers, and Gene Bodies. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2051-2063.	0.8	39
48	Quantitative combination of natural anti-oxidants prevents metabolic syndrome by reducing oxidative stress. <i>Redox Biology</i> , 2015, 6, 206-217.	3.9	39
49	The landscape of RNA polymerase II-associated chromatin interactions in prostate cancer. <i>Journal of Clinical Investigation</i> , 2020, 130, 3987-4005.	3.9	37
50	The loss of heterochromatin is associated with multiscale three-dimensional genome reorganization and aberrant transcription during cellular senescence. <i>Genome Research</i> , 2021, 31, 1121-1135.	2.4	36
51	MICC: an R package for identifying chromatin interactions from ChIA-PET data. <i>Bioinformatics</i> , 2015, 31, 3832-3834.	1.8	34
52	MTGpick allows robust identification of genomic islands from a single genome. <i>Briefings in Bioinformatics</i> , 2016, 19, bbw118.	3.2	34
53	Global transcriptional activity dynamics reveal functional enhancer RNAs. <i>Genome Research</i> , 2018, 28, 1799-1811.	2.4	34
54	Differential connectivity of splicing activators and repressors to the human spliceosome. <i>Genome Biology</i> , 2015, 16, 119.	13.9	33

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55	<i>De novo</i> deciphering three-dimensional chromatin interaction and topological domains by wavelet transformation of epigenetic profiles. <i>Nucleic Acids Research</i> , 2016, 44, e106-e106.	6.5	33
56	Single-cell stochastic gene expression kinetics with coupled positive-plus-negative feedback. <i>Physical Review E</i> , 2019, 100, 052406.	0.8	33
57	Sox2 and Klf4 as the Functional Core in Pluripotency Induction without Exogenous Oct4. <i>Cell Reports</i> , 2019, 29, 1986-2000.e8.	2.9	32
58	Alterations of specific chromatin conformation affect ATRA-induced leukemia cell differentiation. <i>Cell Death and Disease</i> , 2018, 9, 200.	2.7	29
59	2SigFinder: the combined use of small-scale and large-scale statistical testing for genomic island detection from a single genome. <i>BMC Bioinformatics</i> , 2020, 21, 159.	1.2	29
60	Super-resolution imaging of a 2.5 kb non-repetitive DNA in situ in the nuclear genome using molecular beacon probes. <i>ELife</i> , 2017, 6, .	2.8	29
61	Hsa-miR-1246, hsa-miR-320a and hsa-miR-196b-5p inhibitors can reduce the cytotoxicity of Ebola virus glycoprotein in vitro. <i>Science China Life Sciences</i> , 2014, 57, 959-972.	2.3	28
62	Multiplexed capture of spatial configuration and temporal dynamics of locus-specific 3D chromatin by biotinylated dCas9. <i>Genome Biology</i> , 2020, 21, 59.	3.8	27
63	FastDMA: An Infinium HumanMethylation450 Beadchip Analyzer. <i>PLoS ONE</i> , 2013, 8, e74275.	1.1	25
64	Relaxation rates of gene expression kinetics reveal the feedback signs of autoregulatory gene networks. <i>Journal of Chemical Physics</i> , 2018, 148, .	1.2	24
65	Developing novel methods to image and visualize 3D genomes. <i>Cell Biology and Toxicology</i> , 2018, 34, 367-380.	2.4	24
66	3D genome alterations associated with dysregulated HOXA13 expression in high-risk T-lineage acute lymphoblastic leukemia. <i>Nature Communications</i> , 2021, 12, 3708.	5.8	24
67	Quantifying the phase separation property of chromatin-associated proteins under physiological conditions using an anti-1,6-hexanediol index. <i>Genome Biology</i> , 2021, 22, 229.	3.8	24
68	Population dynamics of cancer cells with cell state conversions. <i>Quantitative Biology</i> , 2013, 1, 201-208.	0.3	22
69	Stochastic fluctuations can reveal the feedback signs of gene regulatory networks at the single-molecule level. <i>Scientific Reports</i> , 2017, 7, 16037.	1.6	22
70	CTCF functions as an insulator for somatic genes and a chromatin remodeler for pluripotency genes during reprogramming. <i>Cell Reports</i> , 2022, 39, 110626.	2.9	22
71	Web3DMol: interactive protein structure visualization based on WebGL. <i>Nucleic Acids Research</i> , 2017, 45, W523-W527.	6.5	21
72	Genome-wide analysis of the response to nitric oxide in uropathogenic <i>Escherichia coli</i> CFT073. <i>Microbial Genomics</i> , 2015, 1, e000031.	1.0	21

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73	3CPET: finding co-factor complexes from ChIA-PET data using a hierarchical Dirichlet process. <i>Genome Biology</i> , 2015, 16, 288.	3.8	20
74	ChIP-Array 2: integrating multiple omics data to construct gene regulatory networks. <i>Nucleic Acids Research</i> , 2015, 43, W264-W269.	6.5	19
75	Analysis of <i>C. elegans</i> muscle transcriptome using trans-splicing-based RNA tagging (SRT). <i>Nucleic Acids Research</i> , 2016, 44, gkw734.	6.5	19
76	HPVMD-C: a disease-based mutation database of human papillomavirus in China. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	19
77	Nucleosome eviction and multiple co-factor binding predict estrogen-receptor-alpha-associated long-range interactions. <i>Nucleic Acids Research</i> , 2014, 42, 6935-6944.	6.5	17
78	Regulatory RNA binding proteins contribute to the transcriptome-wide splicing alterations in human cellular senescence. <i>Aging</i> , 2018, 10, 1489-1505.	1.4	17
79	Dynamic Alternative Splicing During Mouse Preimplantation Embryo Development. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 35.	2.0	17
80	Resolving the genetic heterogeneity of prelingual hearing loss within one family: Performance comparison and application of two targeted next generation sequencing approaches. <i>Journal of Human Genetics</i> , 2014, 59, 599-607.	1.1	16
81	FAT10 Is Critical in Influenza A Virus Replication by Inhibiting Type I IFN. <i>Journal of Immunology</i> , 2016, 197, 824-833.	0.4	16
82	HCSGD: An integrated database of human cellular senescence genes. <i>Journal of Genetics and Genomics</i> , 2017, 44, 227-234.	1.7	15
83	Molecular basis for histone H3 $\text{K4me3-K9me3}$ methylation pattern readout by Spindlin1. <i>Journal of Biological Chemistry</i> , 2020, 295, 16877-16887.	1.6	15
84	CAPTURE: <i>In Situ</i> Analysis of Chromatin Composition of Endogenous Genomic Loci by Biotinylated dCas9. <i>Current Protocols in Molecular Biology</i> , 2018, 123, e64.	2.9	14
85	Computational prediction of novel components of lung transcriptional networks. <i>Bioinformatics</i> , 2007, 23, 21-29.	1.8	13
86	Deciphering hierarchical organization of topologically associated domains through change-point testing. <i>BMC Bioinformatics</i> , 2021, 22, 183.	1.2	12
87	Single-cell alternative polyadenylation analysis delineates GABAergic neuron types. <i>BMC Biology</i> , 2021, 19, 144.	1.7	12
88	Integrative molecular analysis of metastatic hepatocellular carcinoma. <i>BMC Medical Genomics</i> , 2019, 12, 164.	0.7	11
89	Characterizing microRNA-mediated modulation of gene expression noise and its effect on synthetic gene circuits. <i>Cell Reports</i> , 2021, 36, 109573.	2.9	11
90	Exome Sequencing Identifies a Novel Frameshift Mutation of <i>MYO6</i> as the Cause of Autosomal Dominant Nonsyndromic Hearing Loss in a Chinese Family. <i>Annals of Human Genetics</i> , 2014, 78, 410-423.	0.3	10

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91	MarkovHC: Markov hierarchical clustering for the topological structure of high-dimensional single-cell omics data with transition pathway and critical point detection. <i>Nucleic Acids Research</i> , 2022, 50, 46-56.	6.5	9
92	Mammalian non-CG methylations are conserved and cell-type specific and may have been involved in the evolution of transposon elements. <i>Scientific Reports</i> , 2016, 6, 32207.	1.6	8
93	A large-scale CRISPR screen and identification of essential genes in cellular senescence bypass. <i>Aging</i> , 2019, 11, 4011-4031.	1.4	8
94	Tn5-FISH, a novel cytogenetic method to image chromatin interactions with sub-kilobase resolution. <i>Journal of Genetics and Genomics</i> , 2020, 47, 727-734.	1.7	8
95	Assembly and Validation of Versatile Transcription Activator-Like Effector Libraries. <i>Scientific Reports</i> , 2014, 4, 4857.	1.6	7
96	Reconfigurable hybrid interface for molecular marker diagnostics and in-situ reporting. <i>Biosensors and Bioelectronics</i> , 2015, 74, 744-750.	5.3	7
97	ScaffComb: A Phenotype-Based Framework for Drug Combination Virtual Screening in Large-Scale Chemical Datasets. <i>Advanced Science</i> , 2021, 8, e2102092.	5.6	7
98	Small C-terminal Domain Phosphatase 3 Dephosphorylates the Linker Sites of Receptor-regulated Smads (R-Smads) to Ensure Transforming Growth Factor $\beta^2$ (TGF $\beta^2$ )-mediated Germ Layer Induction in Xenopus Embryos. <i>Journal of Biological Chemistry</i> , 2015, 290, 17239-17249.	1.6	6
99	ModuleRole: A Tool for Modulization, Role Determination and Visualization in Protein-Protein Interaction Networks. <i>PLoS ONE</i> , 2014, 9, e94608.	1.1	5
100	Genome wide mapping of Foxo1 binding-sites in murine T lymphocytes. <i>Genomics Data</i> , 2014, 2, 280-281.	1.3	5
101	Advances in computational ChIA-PET data analysis. <i>Quantitative Biology</i> , 2016, 4, 217-225.	0.3	5
102	DAGM: A novel modelling framework to assess the risk of HER2-negative breast cancer based on germline rare coding mutations. <i>EBioMedicine</i> , 2021, 69, 103446.	2.7	4
103	Integration of single cell data by disentangled representation learning. <i>Nucleic Acids Research</i> , 2022, 50, e8-e8.	6.5	4
104	Bivalent-Like Chromatin Markers Are Predictive for Transcription Start Site Distribution in Human. <i>PLoS ONE</i> , 2012, 7, e38112.	1.1	3
105	Highly diversified core promoters in the human genome and their effects on gene expression and disease predisposition. <i>BMC Genomics</i> , 2020, 21, 842.	1.2	3
106	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. <i>IEEE Life Sciences Letters</i> , 2015, 1, 30-33.	1.2	2
107	Single-cell RNA sequencing of t(8;21) acute myeloid leukemia for risk prediction. <i>Oncology Reports</i> , 2020, 43, 1278-1288.	1.2	2
108	A data-driven method to learn a jump diffusion process from aggregate biological gene expression data. <i>Journal of Theoretical Biology</i> , 2022, 532, 110923.	0.8	2

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109	Role of emergent palliative radiation therapy in the care of patients with cancer.. Journal of Clinical Oncology, 2016, 34, 201-201.	0.8	2
110	Rathke's cleft cyst with xanthogranulomatous change: A case report and review of the literature. , 2020, 11, 246.		2
111	Model-based analysis of chromatin interactions from dCas9-Based CAPTURE-3C-seq. PLoS ONE, 2020, 15, e0236666.	1.1	1
112	A personal journey on cracking the genomic codes. Quantitative Biology, 2021, 9, 8-22.	0.3	1
113	Super-resolution fluorescence dipole orientation microscopy. , 2016, , .		0
114	DE MERVLs are Enriched Around Two-Cell-Specific Genes During Zygotic Genome Activation in Mouse. , 2018, , .		0
115	Computational modeling and analysis of the morphogenetic domain signaling networks regulating C. elegans embryogenesis. Computational and Structural Biotechnology Journal, 2022, 20, 3653-3666.	1.9	0