

Yong Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

25,383
citations

87723

38
h-index

38300

95
g-index

102
all docs

102
docs citations

102
times ranked

43872
citing authors

#	ARTICLE	IF	CITATIONS
1	Model-based Analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008, 9, R137.	13.9	13,517
2	Identifying ChIP-seq enrichment using MACS. <i>Nature Protocols</i> , 2012, 7, 1728-1740.	5.5	1,471
3	FoxA1 Translates Epigenetic Signatures into Enhancer-Driven Lineage-Specific Transcription. <i>Cell</i> , 2008, 132, 958-970.	13.5	863
4	Androgen Receptor Regulates a Distinct Transcription Program in Androgen-Independent Prostate Cancer. <i>Cell</i> , 2009, 138, 245-256.	13.5	797
5	PPAR β and C/EBP factors orchestrate adipocyte biology via adjacent binding on a genome-wide scale. <i>Genes and Development</i> , 2008, 22, 2941-2952.	2.7	690
6	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , 2011, 12, R83.	13.9	598
7	Distinct features of H3K4me3 and H3K27me3 chromatin domains in pre-implantation embryos. <i>Nature</i> , 2016, 537, 558-562.	13.7	538
8	Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 908-913.	3.6	524
9	Target analysis by integration of transcriptome and ChIP-seq data with BETA. <i>Nature Protocols</i> , 2013, 8, 2502-2515.	5.5	428
10	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010, 42, 343-347.	9.4	426
11	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	2.8	406
12	GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2012, 28, 2782-2788.	1.8	376
13	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010, 464, 922-926.	13.7	340
14	Intrinsic histone-DNA interactions are not the major determinant of nucleosome positions in vivo. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 847-852.	3.6	324
15	A Transcriptional Signature and Common Gene Networks Link Cancer with Lipid Metabolism and Diverse Human Diseases. <i>Cancer Cell</i> , 2010, 17, 348-361.	7.7	309
16	Reprogramming of H3K9me3-dependent heterochromatin during mammalian embryo development. <i>Nature Cell Biology</i> , 2018, 20, 620-631.	4.6	292
17	NONCODE: an integrated knowledge database of non-coding RNAs. <i>Nucleic Acids Research</i> , 2004, 33, D112-D115.	6.5	270
18	Computational prediction of associations between long non-coding RNAs and proteins. <i>BMC Genomics</i> , 2013, 14, 651.	1.2	208

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19	Using MACS to Identify Peaks from ChIP-seq Data. <i>Current Protocols in Bioinformatics</i> , 2011, 34, Unit 2.14.	25.8	203
20	Identification of key factors conquering developmental arrest of somatic cell cloned embryos by combining embryo biopsy and single-cell sequencing. <i>Cell Discovery</i> , 2016, 2, 16010.	3.1	165
21	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , 2012, 9, 609-614.	9.0	156
22	Single Cas9 nickase induced generation of NRAMP1 knockin cattle with reduced off-target effects. <i>Genome Biology</i> , 2017, 18, 13.	3.8	155
23	Identifying Positioned Nucleosomes with Epigenetic Marks in Human from ChIP-Seq. <i>BMC Genomics</i> , 2008, 9, 537.	1.2	122
24	A Comprehensive View of Nuclear Receptor Cancer Cistromes. <i>Cancer Research</i> , 2011, 71, 6940-6947.	0.4	118
25	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 404.	1.2	100
26	H3K9 demethylase KDM4E is an epigenetic regulator for bovine embryonic development and a defective factor for nuclear reprogramming. <i>Development (Cambridge)</i> , 2018, 145, .	1.2	98
27	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006, 34, D150-D152.	6.5	93
28	Canonical nucleosome organization at promoters forms during genome activation. <i>Genome Research</i> , 2014, 24, 260-266.	2.4	87
29	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014, 15, 419.	3.8	87
30	Gene Expression Profiling of Liver Cancer Stem Cells by RNA-Sequencing. <i>PLoS ONE</i> , 2012, 7, e37159.	1.1	83
31	Nucleosome depletion at yeast terminators is not intrinsic and can occur by a transcriptional mechanism linked to 3'-end formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 17945-17950.	3.3	79
32	Inhibition of Aberrant DNA Re-methylation Improves Post-implantation Development of Somatic Cell Nuclear Transfer Embryos. <i>Cell Stem Cell</i> , 2018, 23, 426-435.e5.	5.2	72
33	Evidence against a genomic code for nucleosome positioning Reply to "Nucleosome sequence preferences influence in vivo nucleosome organization". <i>Nature Structural and Molecular Biology</i> , 2010, 17, 920-923.	3.6	63
34	Comprehensive profiling reveals mechanisms of SOX2-mediated cell fate specification in human ESCs and NPCs. <i>Cell Research</i> , 2016, 26, 171-189.	5.7	62
35	Inherited DNA methylation primes the establishment of accessible chromatin during genome activation. <i>Genome Research</i> , 2018, 28, 998-1007.	2.4	54
36	MyoD is a 3D genome structure organizer for muscle cell identity. <i>Nature Communications</i> , 2022, 13, 205.	5.8	50

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37	H3K4 Methyltransferase Set1a Is A Key Oct4 Coactivator Essential for Generation of Oct4 Positive Inner Cell Mass. <i>Stem Cells</i> , 2016, 34, 565-580.	1.4	49
38	BSeQC: quality control of bisulfite sequencing experiments. <i>Bioinformatics</i> , 2013, 29, 3227-3229.	1.8	45
39	The interactome as a tree—an attempt to visualize the protein-protein interaction network in yeast. <i>Nucleic Acids Research</i> , 2004, 32, 4804-4811.	6.5	43
40	CR Cistrome: a ChIP-Seq database for chromatin regulators and histone modification linkages in human and mouse. <i>Nucleic Acids Research</i> , 2014, 42, D450-D458.	6.5	42
41	Histone Demethylase LSD1 Promotes Adipocyte Differentiation through Repressing Wnt Signaling. <i>Cell Chemical Biology</i> , 2016, 23, 1228-1240.	2.5	41
42	The Combination of Tet1 with Oct4 Generates High-Quality Mouse-Induced Pluripotent Stem Cells. <i>Stem Cells</i> , 2015, 33, 686-698.	1.4	39
43	MicroRNA-125b is a key epigenetic regulatory factor that promotes nuclear transfer reprogramming. <i>Journal of Biological Chemistry</i> , 2017, 292, 15916-15926.	1.6	39
44	Maternal Sall4 Is Indispensable for Epigenetic Maturation of Mouse Oocytes. <i>Journal of Biological Chemistry</i> , 2017, 292, 1798-1807.	1.6	37
45	CistromeMap: a knowledgebase and web server for ChIP-Seq and DNase-Seq studies in mouse and human. <i>Bioinformatics</i> , 2012, 28, 1411-1412.	1.8	35
46	Unique molecular events during reprogramming of human somatic cells to induced pluripotent stem cells (iPSCs) at naïve state. <i>ELife</i> , 2018, 7, .	2.8	35
47	Conservation analysis of small RNA genes in <i>Escherichia coli</i> . <i>Bioinformatics</i> , 2004, 20, 599-603.	1.8	33
48	Integrated analysis of multiple data sources reveals modular structure of biological networks. <i>Biochemical and Biophysical Research Communications</i> , 2006, 345, 302-309.	1.0	33
49	SETDB1 modulates PRC2 activity at developmental genes independently of H3K9 trimethylation in mouse ES cells. <i>Genome Research</i> , 2015, 25, 1325-1335.	2.4	33
50	HBO1 is a versatile histone acyltransferase critical for promoter histone acylations. <i>Nucleic Acids Research</i> , 2021, 49, 8037-8059.	6.5	30
51	Using local chromatin structure to improve CRISPR/Cas9 efficiency in zebrafish. <i>PLoS ONE</i> , 2017, 12, e0182528.	1.1	29
52	Phylogenetic properties of metabolic pathway topologies as revealed by global analysis. <i>BMC Bioinformatics</i> , 2006, 7, 252.	1.2	27
53	Transcriptional memory inherited from donor cells is a developmental defect of bovine cloned embryos. <i>FASEB Journal</i> , 2020, 34, 1637-1651.	0.2	27
54	ATACdb: a comprehensive human chromatin accessibility database. <i>Nucleic Acids Research</i> , 2021, 49, D55-D64.	6.5	27

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55	Dr.seq2: A quality control and analysis pipeline for parallel single cell transcriptome and epigenome data. PLoS ONE, 2017, 12, e0180583.	1.1	25
56	Histone H3K27 methylation is required for NHEJ and genome stability by modulating the dynamics of FANCD2 on chromatin. Journal of Cell Science, 2018, 131, .	1.2	25
57	Computational methodology for ChIP-seq analysis. Quantitative Biology, 2013, 1, 54-70.	0.3	24
58	Smarca5-mediated epigenetic programming facilitates fetal HSPC development in vertebrates. Blood, 2021, 137, 190-202.	0.6	24
59	CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. Nucleic Acids Research, 2011, 39, D968-D974.	6.5	22
60	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. FEBS Letters, 2006, 580, 1891-1896.	1.3	20
61	SIRT1 reduces epigenetic and non-epigenetic changes to maintain the quality of postovulatory aged oocytes in mice. Experimental Cell Research, 2021, 399, 112421.	1.2	20
62	DiNuP: a systematic approach to identify regions of differential nucleosome positioning. Bioinformatics, 2012, 28, 1965-1971.	1.8	19
63	Transcription factor-pathway coexpression analysis reveals cooperation between SP1 and ESR1 on dysregulating cell cycle arrest in non-hyperdiploid multiple myeloma. Leukemia, 2014, 28, 894-903.	3.3	19
64	Esrrb plays important roles in maintaining self-renewal of trophoblast stem cells (TSCs) and reprogramming somatic cells to induced TSCs. Journal of Molecular Cell Biology, 2019, 11, 463-473.	1.5	19
65	Identification and Characterization of Human snoRNA Core Promoters. Genomics, 2010, 96, 50-56.	1.3	18
66	CistromeFinder for ChIP-seq and DNase-seq data reuse. Bioinformatics, 2013, 29, 1352-1354.	1.8	18
67	Histone methylation mediates plasticity of human FOXP3 ⁺ regulatory T cells by modulating signature gene expressions. Immunology, 2014, 141, 362-376.	2.0	17
68	Computational inference of mRNA stability from histone modification and transcriptome profiles. Nucleic Acids Research, 2012, 40, 6414-6423.	6.5	16
69	A Transcriptomic Analysis Reveals Diverse Regulatory Networks That Respond to Cold Stress in Strawberry (<i>Fragaria ananassa</i>). International Journal of Genomics, 2019, 2019, 1-13.	0.8	16
70	Dynamic Changes in Subgraph Preference Profiles of Crucial Transcription Factors. PLoS Computational Biology, 2006, 2, e47.	1.5	14
71	Dynamic nucleosome organization after fertilization reveals regulatory factors for mouse zygotic genome activation. Cell Research, 2022, 32, 801-813.	5.7	14
72	Allele-specific H3K9me3 and DNA methylation co-marked CpG-rich regions serve as potential imprinting control regions in pre-implantation embryo. Nature Cell Biology, 2022, 24, 783-792.	4.6	14

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73	Identifying Hfq-binding small RNA targets in Escherichia coli. Biochemical and Biophysical Research Communications, 2006, 343, 950-955.	1.0	13
74	Overexpression of Tet3 in donor cells enhances goat somatic cell nuclear transfer efficiency. FEBS Journal, 2018, 285, 2708-2723.	2.2	13
75	A Novel Sulindac Derivative Lacking Cyclooxygenase-Inhibitory Activities Suppresses Carcinogenesis in the Transgenic Adenocarcinoma of Mouse Prostate Model. Cancer Prevention Research, 2010, 3, 885-895.	0.7	12
76	Classify Hyperdiploidy Status of Multiple Myeloma Patients Using Gene Expression Profiles. PLoS ONE, 2013, 8, e58809.	1.1	11
77	CSTEa: a webserver for the Cell State Transition Expression Atlas. Nucleic Acids Research, 2017, 45, W103-W108.	6.5	10
78	Direct induction of neural progenitor cells transiently passes through a partially reprogrammed state. Biomaterials, 2017, 119, 53-67.	5.7	10
79	CpG island reconfiguration for the establishment and synchronization of polycomb functions upon exit from naive pluripotency. Molecular Cell, 2022, 82, 1169-1185.e7.	4.5	10
80	Treating donor cells with 2-PCPA corrects aberrant histone H3K4 dimethylation and improves cloned goat embryo development. Systems Biology in Reproductive Medicine, 2018, 64, 174-182.	1.0	9
81	CAM: A quality control pipeline for MNase-seq data. PLoS ONE, 2017, 12, e0182771.	1.1	8
82	Epigenome sequencing comes of age in development, differentiation and disease mechanism research. Epigenomics, 2011, 3, 207-220.	1.0	7
83	ncHMR detector: a computational framework to systematically reveal non-classical functions of histone modification regulators. Genome Biology, 2020, 21, 48.	3.8	7
84	Aberrant Epigenetic Reprogramming in the First Cell Cycle of Bovine Somatic Cell Nuclear Transfer Embryos. Cellular Reprogramming, 2021, 23, 99-107.	0.5	7
85	Aspirin inhibits prostaglandins to prevents colon tumor formation via down-regulating Wnt production. European Journal of Pharmacology, 2021, 906, 174173.	1.7	7
86	GeSICA: Genome segmentation from intra-chromosomal associations. BMC Genomics, 2012, 13, 164.	1.2	6
87	Multiple metastases in a novel LNCaP model of human prostate cancer. Oncology Reports, 2013, 30, 615-622.	1.2	6
88	Dr.seq: a quality control and analysis pipeline for droplet sequencing. Bioinformatics, 2016, 32, 2221-2223.	1.8	6
89	Local chromatin dynamics of transcription factors imply cell-lineage specific functions during cellular differentiation. Epigenetics, 2012, 7, 55-62.	1.3	5
90	CStreet: a computed cell state trajectory inference method for time-series single-cell RNA sequencing data. Bioinformatics, 2021, 37, 3774-3780.	1.8	5

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91	Genome-wide analysis of mammalian DNA segment fusion/fission. <i>Journal of Theoretical Biology</i> , 2006, 240, 200-208.	0.8	4
92	Antibody-free profiling of transcription factor occupancy during early embryogenesis by FitCUT&RUN. <i>Genome Research</i> , 2022, 32, 378-388.	2.4	4
93	A DNA methylation state transition model reveals the programmed epigenetic heterogeneity in human pre-implantation embryos. <i>Genome Biology</i> , 2020, 21, 277.	3.8	3
94	SUMO2, a small ubiquitin-like modifier, is essential for development of murine preimplantation embryos. <i>Theriogenology</i> , 2021, 166, 29-37.	0.9	2
95	NUCOME: A comprehensive database of nucleosome organization referenced landscapes in mammalian genomes. <i>BMC Bioinformatics</i> , 2021, 22, 321.	1.2	2
96	GLENER: a web server for GermLine cycle Expression ANalysis and Epigenetic Roadmap visualization. <i>BMC Bioinformatics</i> , 2021, 22, 289.	1.2	1
97	Detecting chimeric 5'/3'UTRs with cross-chromosomal splicing by bioinformatics. <i>Science Bulletin</i> , 2004, 49, 1051.	1.7	0