

Yong Zhang

List of Publications by Year in Descending Order

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Version: 2024-04-25

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

93
papers

17,047
citations

35
h-index

102
g-index

102
ext. papers

22,172
ext. citations

12.2
avg, IF

6.02
L-index

#	Paper	IF	Citations
93	MyoD is a 3D genome structure organizer for muscle cell identity.. <i>Nature Communications</i> , 2022 , 13, 205	17.4	3
92	Aberrant Epigenetic Reprogramming in the First Cell Cycle of Bovine Somatic Cell Nuclear Transfer Embryos. <i>Cellular Reprogramming</i> , 2021 , 23, 99-107	2.1	2
91	GLENER: a web server for GermLine cycle Expression ANalysis and Epigenetic Roadmap visualization. <i>BMC Bioinformatics</i> , 2021 , 22, 289	3.6	1
90	SUMO2, a small ubiquitin-like modifier, is essential for development of murine preimplantation embryos. <i>Theriogenology</i> , 2021 , 166, 29-37	2.8	
89	NUCOME: A comprehensive database of nucleosome organization referenced landscapes in mammalian genomes. <i>BMC Bioinformatics</i> , 2021 , 22, 321	3.6	0
88	HBO1 is a versatile histone acyltransferase critical for promoter histone acylations. <i>Nucleic Acids Research</i> , 2021 , 49, 8037-8059	20.1	5
87	Smarca5-mediated epigenetic programming facilitates fetal HSPC development in vertebrates. <i>Blood</i> , 2021 , 137, 190-202	2.2	5
86	ATACdb: a comprehensive human chromatin accessibility database. <i>Nucleic Acids Research</i> , 2021 , 49, D55-D64	20.1	4
85	SIRT1 reduces epigenetic and non-epigenetic changes to maintain the quality of postovulatory aged oocytes in mice. <i>Experimental Cell Research</i> , 2021 , 399, 112421	4.2	6
84	Aspirin inhibits prostaglandins to prevents colon tumor formation via down-regulating Wnt production. <i>European Journal of Pharmacology</i> , 2021 , 906, 174173	5.3	1
83	nChMR detector: a computational framework to systematically reveal non-classical functions of histone modification regulators. <i>Genome Biology</i> , 2020 , 21, 48	18.3	2
82	Transcriptional memory inherited from donor cells is a developmental defect of bovine cloned embryos. <i>FASEB Journal</i> , 2020 , 34, 1637-1651	0.9	12
81	A DNA methylation state transition model reveals the programmed epigenetic heterogeneity in human pre-implantation embryos. <i>Genome Biology</i> , 2020 , 21, 277	18.3	1
80	A Transcriptomic Analysis Reveals Diverse Regulatory Networks That Respond to Cold Stress in Strawberry (🍓) <i>International Journal of Genomics</i> , 2019 , 2019, 7106092	2.5	7
79	Esrrb plays important roles in maintaining self-renewal of trophoblast stem cells (TSCs) and reprogramming somatic cells to induced TSCs. <i>Journal of Molecular Cell Biology</i> , 2019 , 11, 463-473	6.3	7
78	Reprogramming of H3K9me3-dependent heterochromatin during mammalian embryo development. <i>Nature Cell Biology</i> , 2018 , 20, 620-631	23.4	152
77	H3K9 demethylase KDM4E is an epigenetic regulator for bovine embryonic development and a defective factor for nuclear reprogramming. <i>Development (Cambridge)</i> , 2018 , 145,	6.6	67

76	Treating donor cells with 2-PCPA corrects aberrant histone H3K4 dimethylation and improves cloned goat embryo development. <i>Systems Biology in Reproductive Medicine</i> , 2018 , 64, 174-182	2.9	7
75	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	18	43
74	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018 , 93, 515-533	6.9	176
73	Inherited DNA methylation primes the establishment of accessible chromatin during genome activation. <i>Genome Research</i> , 2018 , 28, 998-1007	9.7	29
72	Overexpression of Tet3 in donor cells enhances goat somatic cell nuclear transfer efficiency. <i>FEBS Journal</i> , 2018 , 285, 2708-2723	5.7	10
71	Histone H3K27 methylation modulates the dynamics of FANCD2 on chromatin to facilitate NHEJ and genome stability. <i>Journal of Cell Science</i> , 2018 , 131,	5.3	18
70	Unique molecular events during reprogramming of human somatic cells to induced pluripotent stem cells (iPSCs) at naïve state. <i>ELife</i> , 2018 , 7,	8.9	18
69	Single Cas9 nickase induced generation of NRAMP1 knockin cattle with reduced off-target effects. <i>Genome Biology</i> , 2017 , 18, 13	18.3	119
68	CSTEA: a webserver for the Cell State Transition Expression Atlas. <i>Nucleic Acids Research</i> , 2017 , 45, W103-W108	10.1	108
67	Maternal Sall4 Is Indispensable for Epigenetic Maturation of Mouse Oocytes. <i>Journal of Biological Chemistry</i> , 2017 , 292, 1798-1807	5.4	27
66	Direct induction of neural progenitor cells transiently passes through a partially reprogrammed state. <i>Biomaterials</i> , 2017 , 119, 53-67	15.6	6
65	Dr.seq2: A quality control and analysis pipeline for parallel single cell transcriptome and epigenome data. <i>PLoS ONE</i> , 2017 , 12, e0180583	3.7	21
64	MicroRNA-125b is a key epigenetic regulatory factor that promotes nuclear transfer reprogramming. <i>Journal of Biological Chemistry</i> , 2017 , 292, 15916-15926	5.4	29
63	Using local chromatin structure to improve CRISPR/Cas9 efficiency in zebrafish. <i>PLoS ONE</i> , 2017 , 12, e0182528	10.37	20
62	CAM: A quality control pipeline for MNase-seq data. <i>PLoS ONE</i> , 2017 , 12, e0182771	3.7	3
61	Distinct features of H3K4me3 and H3K27me3 chromatin domains in pre-implantation embryos. <i>Nature</i> , 2016 , 537, 558-562	50.4	341
60	Histone Demethylase LSD1 Promotes Adipocyte Differentiation through Repressing Wnt Signaling. <i>Cell Chemical Biology</i> , 2016 , 23, 1228-1240	8.2	27
59	H3K4 Methyltransferase Set1a Is A Key Oct4 Coactivator Essential for Generation of Oct4 Positive Inner Cell Mass. <i>Stem Cells</i> , 2016 , 34, 565-80	5.8	32

58	Comprehensive profiling reveals mechanisms of SOX2-mediated cell fate specification in human ESCs and NPCs. <i>Cell Research</i> , 2016 , 26, 171-89	24.7	40
57	ChiLin: a comprehensive ChIP-seq and DNase-seq quality control and analysis pipeline. <i>BMC Bioinformatics</i> , 2016 , 17, 404	3.6	72
56	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	22.3	111
55	Dr.seq: a quality control and analysis pipeline for droplet sequencing. <i>Bioinformatics</i> , 2016 , 32, 2221-3	7.2	4
54	SETDB1 modulates PRC2 activity at developmental genes independently of H3K9 trimethylation in mouse ES cells. <i>Genome Research</i> , 2015 , 25, 1325-35	9.7	23
53	The combination of Tet1 with Oct4 generates high-quality mouse-induced pluripotent stem cells. <i>Stem Cells</i> , 2015 , 33, 686-98	5.8	32
52	Histone methylation mediates plasticity of human FOXP3(+) regulatory T cells by modulating signature gene expressions. <i>Immunology</i> , 2014 , 141, 362-76	7.8	12
51	CR Cistrome: a ChIP-Seq database for chromatin regulators and histone modification linkages in human and mouse. <i>Nucleic Acids Research</i> , 2014 , 42, D450-8	20.1	31
50	MethylPurify: tumor purity deconvolution and differential methylation detection from single tumor DNA methylomes. <i>Genome Biology</i> , 2014 , 15, 419	18.3	55
49	Transcription factor-pathway coexpression analysis reveals cooperation between SP1 and ESR1 on dysregulating cell cycle arrest in non-hyperdiploid multiple myeloma. <i>Leukemia</i> , 2014 , 28, 894-903	10.7	18
48	Canonical nucleosome organization at promoters forms during genome activation. <i>Genome Research</i> , 2014 , 24, 260-6	9.7	69
47	Computational methodology for ChIP-seq analysis. <i>Quantitative Biology</i> , 2013 , 1, 54-70	3.9	20
46	BSeQC: quality control of bisulfite sequencing experiments. <i>Bioinformatics</i> , 2013 , 29, 3227-9	7.2	35
45	Target analysis by integration of transcriptome and ChIP-seq data with BETA. <i>Nature Protocols</i> , 2013 , 8, 2502-15	18.8	255
44	Integrative genomic analyses reveal clinically relevant long noncoding RNAs in human cancer. <i>Nature Structural and Molecular Biology</i> , 2013 , 20, 908-13	17.6	432
43	Computational prediction of associations between long non-coding RNAs and proteins. <i>BMC Genomics</i> , 2013 , 14, 651	4.5	157
42	CistromeFinder for ChIP-seq and DNase-seq data reuse. <i>Bioinformatics</i> , 2013 , 29, 1352-4	7.2	15
41	Multiple metastases in a novel LNCaP model of human prostate cancer. <i>Oncology Reports</i> , 2013 , 30, 615-23	3.3	5

40	Classify hyperdiploidy status of multiple myeloma patients using gene expression profiles. <i>PLoS ONE</i> , 2013 , 8, e58809	3.7	9
39	GFOLD: a generalized fold change for ranking differentially expressed genes from RNA-seq data. <i>Bioinformatics</i> , 2012 , 28, 2782-8	7.2	273
38	CistromeMap: a knowledgebase and web server for ChIP-Seq and DNase-Seq studies in mouse and human. <i>Bioinformatics</i> , 2012 , 28, 1411-2	7.2	29
37	GeSICA: genome segmentation from intra-chromosomal associations. <i>BMC Genomics</i> , 2012 , 13, 164	4.5	5
36	Identifying ChIP-seq enrichment using MACS. <i>Nature Protocols</i> , 2012 , 7, 1728-40	18.8	857
35	Systematic evaluation of factors influencing ChIP-seq fidelity. <i>Nature Methods</i> , 2012 , 9, 609-14	21.6	112
34	DiNuP: a systematic approach to identify regions of differential nucleosome positioning. <i>Bioinformatics</i> , 2012 , 28, 1965-71	7.2	13
33	Computational inference of mRNA stability from histone modification and transcriptome profiles. <i>Nucleic Acids Research</i> , 2012 , 40, 6414-23	20.1	16
32	Local chromatin dynamics of transcription factors imply cell-lineage specific functions during cellular differentiation. <i>Epigenetics</i> , 2012 , 7, 55-62	5.7	4
31	Gene expression profiling of liver cancer stem cells by RNA-sequencing. <i>PLoS ONE</i> , 2012 , 7, e37159	3.7	62
30	Using MACS to identify peaks from ChIP-Seq data. <i>Current Protocols in Bioinformatics</i> , 2011 , Chapter 2, Unit 2.14	24.2	149
29	Cistrome: an integrative platform for transcriptional regulation studies. <i>Genome Biology</i> , 2011 , 12, R83	18.3	461
28	Epigenome sequencing comes of age in development, differentiation and disease mechanism research. <i>Epigenomics</i> , 2011 , 3, 207-20	4.4	5
27	A comprehensive view of nuclear receptor cancer cistromes. <i>Cancer Research</i> , 2011 , 71, 6940-7	10.1	99
26	CaSNP: a database for interrogating copy number alterations of cancer genome from SNP array data. <i>Nucleic Acids Research</i> , 2011 , 39, D968-74	20.1	20
25	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, 920-3	17.6	60
24	Chromatin signature of embryonic pluripotency is established during genome activation. <i>Nature</i> , 2010 , 464, 922-6	50.4	285
23	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010 , 42, 343-7	36.3	382

22	Nucleosome depletion at yeast terminators is not intrinsic and can occur by a transcriptional mechanism linked to 3Rend formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17945-50	11.5	65
21	A novel sulindac derivative lacking cyclooxygenase-inhibitory activities suppresses carcinogenesis in the transgenic adenocarcinoma of mouse prostate model. <i>Cancer Prevention Research</i> , 2010 , 3, 885-95 ^{3,2}		9
20	Identification and characterization of human snoRNA core promoters. <i>Genomics</i> , 2010 , 96, 50-6	4.3	14
19	A transcriptional signature and common gene networks link cancer with lipid metabolism and diverse human diseases. <i>Cancer Cell</i> , 2010 , 17, 348-61	24.3	263
18	Intrinsic histone-DNA interactions are not the major determinant of nucleosome positions in vivo. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 847-52	17.6	293
17	Androgen receptor regulates a distinct transcription program in androgen-independent prostate cancer. <i>Cell</i> , 2009 , 138, 245-56	56.2	691
16	Identifying positioned nucleosomes with epigenetic marks in human from ChIP-Seq. <i>BMC Genomics</i> , 2008 , 9, 537	4.5	103
15	Model-based analysis of ChIP-Seq (MACS). <i>Genome Biology</i> , 2008 , 9, R137	18.3	8406
14	FoxA1 translates epigenetic signatures into enhancer-driven lineage-specific transcription. <i>Cell</i> , 2008 , 132, 958-70	56.2	746
13	PPARgamma and C/EBP factors orchestrate adipocyte biology via adjacent binding on a genome-wide scale. <i>Genes and Development</i> , 2008 , 22, 2941-52	12.6	582
12	Genome-wide analysis of mammalian DNA segment fusion/fission. <i>Journal of Theoretical Biology</i> , 2006 , 240, 200-8	2.3	3
11	Phylogenetic properties of metabolic pathway topologies as revealed by global analysis. <i>BMC Bioinformatics</i> , 2006 , 7, 252	3.6	23
10	NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. <i>Nucleic Acids Research</i> , 2006 , 34, D150-2	20.1	63
9	Dynamic changes in subgraph preference profiles of crucial transcription factors. <i>PLoS Computational Biology</i> , 2006 , 2, e47	5	12
8	Faster and more accurate global protein function assignment from protein interaction networks using the MFGO algorithm. <i>FEBS Letters</i> , 2006 , 580, 1891-6	3.8	16
7	Identifying Hfq-binding small RNA targets in Escherichia coli. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 343, 950-5	3.4	11
6	Integrated analysis of multiple data sources reveals modular structure of biological networks. <i>Biochemical and Biophysical Research Communications</i> , 2006 , 345, 302-9	3.4	25
5	NONCODE: an integrated knowledge database of non-coding RNAs. <i>Nucleic Acids Research</i> , 2005 , 33, D112-5	20.1	223

- 4 Conservation analysis of small RNA genes in Escherichia coli. *Bioinformatics*, **2004**, 20, 599-603 7.2 25
- 3 The interactome as a tree--an attempt to visualize the protein-protein interaction network in yeast. *Nucleic Acids Research*, **2004**, 32, 4804-11 20.1 36
- 2 Detecting chimeric 5'UTRs with cross-chromosomal splicing by bioinformatics. *Science Bulletin*, **2004**, 49, 1051
- 1 Dr.seq2: a quality control and analysis pipeline for parallel single cell transcriptome and epigenome data 1