Zhaolei Zhang

List of Publications by Year
in descending order

80 papers	3,672 citations	186265 28 h-index	144013 57 g-index
85 all docs	85 docs citations	85 times ranked	6574 citing authors

#	Article	IF	Citations
1	N6-methyladenosine modification destabilizes developmental regulators in embryonic stem cells. Nature Cell Biology, 2014, 16, 191-198.	10.3	1,063
2	N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. Nature Neuroscience, 2018, 21, 195-206.	14.8	317
3	PseudoPipe: an automated pseudogene identification pipeline. Bioinformatics, 2006, 22, 1437-1439.	4.1	169
4	Comprehensive Transcriptome Analysis Reveals Accelerated Genic Evolution in a Tibet Fish, Gymnodiptychus pachycheilus. Genome Biology and Evolution, 2015, 7, 251-261.	2.5	112
5	Long Noncoding RNAs and Repetitive Elements: Junk or Intimate Evolutionary Partners?. Trends in Genetics, 2019, 35, 892-902.	6.7	107
6	The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. Genome Research, 2008, 18, 1092-1099.	5.5	105
7	Gene Expression Variability within and between Human Populations and Implications toward Disease Susceptibility. PLoS Computational Biology, 2010, 6, e1000910.	3.2	85
8	Next-generation sequencing–based posttransplant monitoring of acute myeloid leukemia identifies patients at high risk of relapse. Blood, 2018, 132, 1604-1613.	1.4	84
9	Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. Bioinformatics, 2014, 30, 2627-2635.	4.1	79
10	Evidence for Positive Selection on a Number of MicroRNA Regulatory Interactions during Recent Human Evolution. PLoS Genetics, 2012, 8, e1002578.	3.5	63
11	Regression Analysis of Combined Gene Expression Regulation in Acute Myeloid Leukemia. PLoS Computational Biology, 2014, 10, e1003908.	3.2	62
12	Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. Nucleic Acids Research, 2016, 44, 669-682.	14.5	59
13	The Cellular Robustness by Genetic Redundancy in Budding Yeast. PLoS Genetics, 2010, 6, e1001187.	3.5	58
14	SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. Bioinformatics, 2014, 30, 1112-1119.	4.1	57
15	Inferring probabilistic miRNA–mRNA interaction signatures in cancers: a role-switch approach. Nucleic Acids Research, 2014, 42, e76-e76.	14.5	55
16	DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153.	14.5	53
17	Integrating exosomal microRNAs and electronic health data improved tuberculosis diagnosis. EBioMedicine, 2019, 40, 564-573.	6.1	53
18	Rad5 Recruits Error-Prone DNA Polymerases for Mutagenic Repair of ssDNA Gaps on Undamaged Templates. Molecular Cell, 2019, 73, 900-914.e9.	9.7	49

#	Article	IF	Citations
19	A Deep Non-linear Feature Mapping for Large-Margin kNN Classification. , 2009, , .		43
20	CRISPRâ€Net: A Recurrent Convolutional Network Quantifies CRISPR Offâ€Target Activities with Mismatches and Indels. Advanced Science, 2020, 7, 1903562.	11.2	43
21	Retention of protein complex membership by ancient duplicated gene products in budding yeast. Trends in Genetics, 2007, 23, 266-269.	6.7	42
22	Identification of Human Neuronal Protein Complexes Reveals Biochemical Activities and Convergent Mechanisms of Action in Autism Spectrum Disorders. Cell Systems, 2015, 1, 361-374.	6.2	42
23	RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. Nucleic Acids Research, 2013, 41, e94-e94.	14.5	41
24	Assembly of Slx4 signaling complexes behind <scp>DNA</scp> replication forks. EMBO Journal, 2015, 34, 2182-2197.	7.8	40
25	SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. Bioinformatics, 2015, 31, 17-24.	4.1	39
26	Computational Biology in <scp>microRNA</scp>. Wiley Interdisciplinary Reviews RNA, 2015, 6, 435-452.	6.4	39
27	A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. Bioinformatics, 2014, 30, 621-628.	4.1	37
28	miRNA regulatory variation in human evolution. Trends in Genetics, 2013, 29, 116-124.	6.7	34
29	Both Male-Biased and Female-Biased Genes Evolve Faster in Fish Genomes. Genome Biology and Evolution, 2016, 8, 3433-3445.	2.5	34
30	Exploiting the determinants of stochastic gene expression in <i>Saccharomyces cerevisiae</i> for genome-wide prediction of expression noise. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10472-10477.	7.1	30
31	A novel motif-discovery algorithm to identify co-regulatory motifs in large transcription factor and microRNA co-regulatory networks in human. Bioinformatics, 2015, 31, 2348-2355.	4.1	30
32	Exome sequencing reveals DNMT3A and ASXL1 variants associate with progression of chronic myeloid leukemia after tyrosine kinase inhibitor therapy. Leukemia Research, 2017, 59, 142-148.	0.8	27
33	Potential microRNA-mediated oncogenic intercellular communication revealed by pan-cancer analysis. Scientific Reports, 2015, 4, 7097.	3.3	26
34	Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. Cell Systems, 2016, 3, 264-277.e10.	6.2	26
35	G9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. Stem Cell Reports, 2016, 7, 454-470.	4.8	24
36	Cholinergic neuron gene expression differences captured by translational profiling in a mouse model of Alzheimer's disease. Neurobiology of Aging, 2017, 57, 104-119.	3.1	24

#	Article	IF	Citations
37	Enrichment analysis of Alu elements with different spatial chromatin proximity in the human genome. Protein and Cell, 2016, 7, 250-266.	11.0	23
38	Alternative signaling pathways: When, where and why?. FEBS Letters, 2005, 579, 5265-5274.	2.8	21
39	Spindle Checkpoint Factors Bub1 and Bub2 Promote DNA Double-Strand Break Repair by Nonhomologous End Joining. Molecular and Cellular Biology, 2015, 35, 2448-2463.	2.3	21
40	Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. Genetics, 2015, 201, 937-949.	2.9	21
41	Computational learning on specificity-determining residue-nucleotide interactions. Nucleic Acids Research, 2015, 43, gkv1134.	14.5	20
42	Assessment of a new genomic classification system in acute myeloid leukemia with a normal karyotype. Oncotarget, 2018, 9, 4961-4968.	1.8	19
43	Long Noncoding RNA and Predictive Model To Improve Diagnosis of Clinically Diagnosed Pulmonary Tuberculosis. Journal of Clinical Microbiology, 2020, 58, .	3.9	18
44	Comparative analysis of genome tiling array data reveals many novel primate-specific functional RNAs in human. BMC Evolutionary Biology, 2007, 7, S14.	3.2	17
45	A PROBABILISTIC FRAMEWORK TO IMPROVE MICRORNA TARGET PREDICTION BY INCORPORATING PROTEOMICS DATA. Journal of Bioinformatics and Computational Biology, 2009, 07, 955-972.	0.8	17
46	Targeting synthetic lethality between the SRC kinase and the EPHB6 receptor may benefit cancer treatment. Oncotarget, 2016, 7, 50027-50042.	1.8	17
47	Reconstructing genetic networks in yeast. Nature Biotechnology, 2003, 21, 1295-1297.	17.5	14
48	New Tricks for â€œOldâ€Domains: How Novel Architectures and Promiscuous Hubs Contributed to the Organization and Evolution of the ECM. Genome Biology and Evolution, 2014, 6, 2897-2917.	2.5	14
49	Functional characterization of RebL1 highlights the evolutionary conservation of oncogenic activities of the RBBP4/7 orthologue in *Tetrahymena thermophila*. Nucleic Acids Research, 2021, 49, 6196-6212.	14.5	14
50	A hybrid model for robust detection of transcription factor binding sites. Bioinformatics, 2008, 24, 484-491.	4.1	13
51	*MTE1* Functions with *MPH1* in Double-Strand Break Repair. Genetics, 2016, 203, 147-157.	2.9	13
52	Genome-wide detection of high abundance N^6-methyladenosine sites by microarray. Rna, 2015, 21, 1511-1518.	3.5	12
53	RNALigands: a database and web server for RNAâ€"ligand interactions. Rna, 2022, 28, 115-122.	3.5	12
54	Global Robustness and Identifiability of Random, Scaleâ€Free, and Smallâ€World Networks. Annals of the New York Academy of Sciences, 2009, 1158, 82-92.	3.8	11

#	Article	IF	Citations
55	ProTICS reveals prognostic impact of tumor infiltrating immune cells in different molecular subtypes. Briefings in Bioinformatics, 2021, 22, .	6.5	11
56	A configurable deep learning framework for medical image analysis. Neural Computing and Applications, 2022, 34, 7375-7392.	5.6	11
57	Allogeneic transplant can abrogate the risk of relapse in the patients of first remission acute myeloid leukemia with detectable measurable residual disease by next-generation sequencing. Bone Marrow Transplantation, 2021, 56, 1159-1170.	2.4	10
58	Prognostic impact of the adverse molecular-genetic profile on long-term outcomes following allogeneic hematopoietic stem cell transplantation in acute myeloid leukemia. Bone Marrow Transplantation, 2021, 56, 1908-1918.	2.4	10
59	RNANetMotif: Identifying sequence-structure RNA network motifs in RNA-protein binding sites. PLoS Computational Biology, 2022, 18, e1010293.	3.2	9
60	Ion channel profiling of the Lymnaea stagnalis ganglia via transcriptome analysis. BMC Genomics, 2021, 22, 18.	2.8	8
61	Enhancing the Prediction of Transcription Factor Binding Sites by Incorporating Structural Properties and Nucleotide Covariations. Journal of Computational Biology, 2006, 13, 929-945.	1.6	7
62	Deep Learning Classification of Unipolar Electrograms in Human Atrial Fibrillation: Application in Focal Source Mapping. Frontiers in Physiology, 2021, 12, 704122.	2.8	7
63	Candida albicans Is Resistant to Polyglutamine Aggregation and Toxicity. G3: Genes, Genomes, Genetics, 2017, 7, 95-108.	1.8	6
64	RNA sequencing as an alternative tool for detecting measurable residual disease in core-binding factor acute myeloid leukemia. Scientific Reports, 2020, 10, 20119.	3.3	6
65	Schizophrenia Risk Mediated by microRNA Target Genes Overlapped by Genome-Wide Rare Copy Number Variation in 22q11.2 Deletion Syndrome. Frontiers in Genetics, 2022, 13, 812183.	2.3	5
66	Alternative Pathway Approach for Automating Analysis and Validation of Cell Perturbation Networks and Design of Perturbation Experiments. Annals of the New York Academy of Sciences, 2007, 1115, 267-285.	3.8	4
67	Bichir microRNA repertoire suggests a ray-finned fish affinity of Polypteriforme. Gene, 2015, 566, 242-247.	2.2	4
68	Unsupervised Learning in Genome Informatics. , 2016, , 405-448.		4
69	CellFrame: A Data Structure for Abstraction of Cell Biology Experiments and Construction of Perturbation Networks. Annals of the New York Academy of Sciences, 2007, 1115, 249-266.	3.8	3
70	Improving domain adaptation in de-identification of electronic health records through self-training. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 2093-2100.	4.4	3
71	Inferring RNA-binding protein target preferences using adversarial domain adaptation. PLoS Computational Biology, 2022, 18, e1009863.	3.2	2
72	Remission clone in acute myeloid leukemia shows growth advantage after chemotherapy but is distinct from leukemic clone. Experimental Hematology, 2019, 75, 26-30.	0.4	1

#	Article	IF	Citations
73	A Survey of Regulatory Interactions Among RNA Binding Proteins and MicroRNAs in Cancer. Frontiers in Genetics, 2020, 11, 515094.	2.3	1
74	Single-Cell Proteogenomic Sequencing Allows Early Detection of Relapse Clone with CN-LOH at FLT3-ITD Locus from Initial Diagnosis in AML. Blood, 2021, 138, 3428-3428.	1.4	1
75	Single cell proteogenomic sequencing identifies a relapseâ€fated AML subclone carrying <i>FLT3</i> â€ITD with CNâ€LOH at chr13q. EJHaem, 0, , .	1.0	1
76	Network Robustness Due to Multiple Positive Feedback Loops: A Systematic Study of a Th Cell Differentiation Model. Signal Transduction Insights, 2010, 2, STI.S3534.	2.0	0
77	Dimension Reduction on Open Data Using Variational Autoencoder. , 2018, , .		0
78	A Novel Micro RNA Signature Identifies a Patient Subset with Poor Prognosis in Core Binding Factor AML. Blood, 2016, 128, 1686-1686.	1.4	0
79	Replication of New Genomic Classification System in Acute Myeloid Leukemia with Normal Karyotype. Blood, 2016, 128, 2876-2876.	1.4	0
80	No Impact of Donor's Age-Related Clonal Hematopoiesis (ARCH) Observed on Graft-Versus-Host Disease Following Allogeneic Hematopoietic Stem Cell Transplantation: Result from Bar-Coded Error Corrected Sequencing in 33 Gene Mutations on 372 Pairs of Donor and Recipient. Blood, 2019, 134, 4514-4514.	1.4	0