# 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 | RNALigands: a database and web server for RNA–ligand interactions. Rna, 2022, 28, 115-122. | 3.5 | 12 |
| 2 | A configurable deep learning framework for medical image analysis. Neural Computing and Applications, 2022, 34, 7375-7392. | 5.6 | 11 |
| 3 | Inferring RNA-binding protein target preferences using adversarial domain adaptation. PLoS Computational Biology, 2022, 18, e1009863. | 3.2 | 2 |
| 4 | 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 |
| 5 | RNANetMotif: Identifying sequence-structure RNA network motifs in RNA-protein binding sites. PLoS Computational Biology, 2022, 18, e1010293. | 3.2 | 9 |
| 6 | 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 |
| 7 | Ion channel profiling of the Lymnaea stagnalis ganglia via transcriptome analysis. BMC Genomics, 2021, 22, 18. | 2.8 | 8 |
| 8 | 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 |
| 9 | ProTICS reveals prognostic impact of tumor infiltrating immune cells in different molecular subtypes. Briefings in Bioinformatics, 2021, 22, . | 6.5 | 11 |
| 10 | 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 |
| 11 | Deep Learning Classification of Unipolar Electrograms in Human Atrial Fibrillation: Application in Focal Source Mapping. Frontiers in Physiology, 2021, 12, 704122. | 2.8 | 7 |
| 12 | 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 |
| 13 | 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 |
| 14 | A Survey of Regulatory Interactions Among RNA Binding Proteins and MicroRNAs in Cancer. Frontiers in Genetics, 2020, 11, 515094. | 2.3 | 1 |
| 15 | 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 |
| 16 | CRISPR–Net: A Recurrent Convolutional Network Quantifies CRISPR Off–Target Activities with Mismatches and Indels. Advanced Science, 2020, 7, 1903562. | 11.2 | 43 |
| 17 | Long Noncoding RNA and Predictive Model To Improve Diagnosis of Clinically Diagnosed Pulmonary Tuberculosis. Journal of Clinical Microbiology, 2020, 58, . | 3.9 | 18 |
| 18 | Long Noncoding RNAs and Repetitive Elements: Junk or Intimate Evolutionary Partners?. Trends in Genetics, 2019, 35, 892-902. | 6.7 | 107 |

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|---|---------|-----|-----------|
| 19 | 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 |
| 20 | 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 |
| 21 | Integrating exosomal microRNAs and electronic health data improved tuberculosis diagnosis. EBioMedicine, 2019, 40, 564-573. | 6.1 | 53 |
| 22 | 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 |
| 23 | N6-methyladenosine RNA modification regulates embryonic neural stem cell self-renewal through histone modifications. Nature Neuroscience, 2018, 21, 195-206. | 14.8 | 317 |
| 24 | Dimension Reduction on Open Data Using Variational Autoencoder. , 2018, , . | | 0 |
| 25 | 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 |
| 26 | Assessment of a new genomic classification system in acute myeloid leukemia with a normal karyotype. Oncotarget, 2018, 9, 4961-4968. | 1.8 | 19 |
| 27 | Candida albicans Is Resistant to Polyglutamine Aggregation and Toxicity. G3: Genes, Genomes, Genetics, 2017, 7, 95-108. | 1.8 | 6 |
| 28 | 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 |
| 29 | 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 |
| 30 | Targeting synthetic lethality between the SRC kinase and the EPHB6 receptor may benefit cancer treatment. Oncotarget, 2016, 7, 50027-50042. | 1.8 | 17 |
| 31 | G9a and ZNF644 Physically Associate to Suppress Progenitor Gene Expression during Neurogenesis. Stem Cell Reports, 2016, 7, 454-470. | 4.8 | 24 |
| 32 | Unsupervised Learning in Genome Informatics. , 2016, , 405-448. | | 4 |
| 33 | *MTE1* Functions with *MPH1* in Double-Strand Break Repair. Genetics, 2016, 203, 147-157. | 2.9 | 13 |
| 34 | Exploring Quantitative Yeast Phenomics with Single-Cell Analysis of DNA Damage Foci. Cell Systems, 2016, 3, 264-277.e10. | 6.2 | 26 |
| 35 | Both Male-Biased and Female-Biased Genes Evolve Faster in Fish Genomes. Genome Biology and Evolution, 2016, 8, 3433-3445. | 2.5 | 34 |
| 36 | Enrichment analysis of Alu elements with different spatial chromatin proximity in the human genome. Protein and Cell, 2016, 7, 250-266. | 11.0 | 23 |

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|---|---------|----|-----------|
| 37 | Slx4 and Rtt107 control checkpoint signalling and DNA resection at double-strand breaks. Nucleic Acids Research, 2016, 44, 669-682. | 14.5 | 59 |
| 38 | 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 |
| 39 | Replication of New Genomic Classification System in Acute Myeloid Leukemia with Normal Karyotype. Blood, 2016, 128, 2876-2876. | 1.4 | 0 |
| 40 | Assembly of Slx4 signaling complexes behind <scp>DNA</scp> replication forks. EMBO Journal, 2015, 34, 2182-2197. | 7.8 | 40 |
| 41 | Bichir microRNA repertoire suggests a ray-finned fish affinity of Polypteriforme. Gene, 2015, 566, 242-247. | 2.2 | 4 |
| 42 | Computational learning on specificity-determining residue-nucleotide interactions. Nucleic Acids Research, 2015, 43, gkv1134. | 14.5 | 20 |
| 43 | 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 |
| 44 | SignalSpider: probabilistic pattern discovery on multiple normalized ChIP-Seq signal profiles. Bioinformatics, 2015, 31, 17-24. | 4.1 | 39 |
| 45 | Comprehensive Transcriptome Analysis Reveals Accelerated Genic Evolution in a Tibet Fish, Gymnodiptychus pachycheilus. Genome Biology and Evolution, 2015, 7, 251-261. | 2.5 | 112 |
| 46 | Potential microRNA-mediated oncogenic intercellular communication revealed by pan-cancer analysis. Scientific Reports, 2015, 4, 7097. | 3.3 | 26 |
| 47 | Genome-wide detection of high abundance $N^6$-methyladenosine sites by microarray. Rna, 2015, 21, 1511-1518. | 3.5 | 12 |
| 48 | 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 |
| 49 | Computational Biology in <scp>microRNA</scp>. Wiley Interdisciplinary Reviews RNA, 2015, 6, 435-452. | 6.4 | 39 |
| 50 | 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 |
| 51 | Termination of Replication Stress Signaling via Concerted Action of the Slx4 Scaffold and the PP4 Phosphatase. Genetics, 2015, 201, 937-949. | 2.9 | 21 |
| 52 | 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 |
| 53 | A probabilistic approach to explore human miRNA targetome by integrating miRNA-overexpression data and sequence information. Bioinformatics, 2014, 30, 621-628. | 4.1 | 37 |
| 54 | Regression Analysis of Combined Gene Expression Regulation in Acute Myeloid Leukemia. PLoS Computational Biology, 2014, 10, e1003908. | 3.2 | 62 |

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|---|---------|-----|-----------|
| 55 | Inferring probabilistic miRNA–mRNA interaction signatures in cancers: a role-switch approach. Nucleic Acids Research, 2014, 42, e76-e76. | 14.5 | 55 |
| 56 | N6-methyladenosine modification destabilizes developmental regulators in embryonic stem cells. Nature Cell Biology, 2014, 16, 191-198. | 10.3 | 1,063 |
| 57 | SNPdryad: predicting deleterious non-synonymous human SNPs using only orthologous protein sequences. Bioinformatics, 2014, 30, 1112-1119. | 4.1 | 57 |
| 58 | Mirsynergy: detecting synergistic miRNA regulatory modules by overlapping neighbourhood expansion. Bioinformatics, 2014, 30, 2627-2635. | 4.1 | 79 |
| 59 | miRNA regulatory variation in human evolution. Trends in Genetics, 2013, 29, 116-124. | 6.7 | 34 |
| 60 | DNA motif elucidation using belief propagation. Nucleic Acids Research, 2013, 41, e153-e153. | 14.5 | 53 |
| 61 | RIPSeeker: a statistical package for identifying protein-associated transcripts from RIP-seq experiments. Nucleic Acids Research, 2013, 41, e94-e94. | 14.5 | 41 |
| 62 | Evidence for Positive Selection on a Number of MicroRNA Regulatory Interactions during Recent Human Evolution. PLoS Genetics, 2012, 8, e1002578. | 3.5 | 63 |
| 63 | 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 |
| 64 | Gene Expression Variability within and between Human Populations and Implications toward Disease Susceptibility. PLoS Computational Biology, 2010, 6, e1000910. | 3.2 | 85 |
| 65 | The Cellular Robustness by Genetic Redundancy in Budding Yeast. PLoS Genetics, 2010, 6, e1001187. | 3.5 | 58 |
| 66 | 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 |
| 67 | 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 |
| 68 | Global Robustness and Identifiability of Random, Scale–Free, and Small–World Networks. Annals of the New York Academy of Sciences, 2009, 1158, 82-92. | 3.8 | 11 |
| 69 | A Deep Non-linear Feature Mapping for Large-Margin kNN Classification. , 2009, , . |  | 43 |
| 70 | A hybrid model for robust detection of transcription factor binding sites. Bioinformatics, 2008, 24, 484-491. | 4.1 | 13 |
| 71 | The extensive and condition-dependent nature of epistasis among whole-genome duplicates in yeast. Genome Research, 2008, 18, 1092-1099. | 5.5 | 105 |
| 72 | 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 |

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|---|---------|----|-----------|
| 73 | Retention of protein complex membership by ancient duplicated gene products in budding yeast. Trends in Genetics, 2007, 23, 266-269. | 6.7 | 42 |
| 74 | 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 |
| 75 | 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 |
| 76 | PseudoPipe: an automated pseudogene identification pipeline. Bioinformatics, 2006, 22, 1437-1439. | 4.1 | 169 |
| 77 | 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 |
| 78 | Alternative signaling pathways: When, where and why?. FEBS Letters, 2005, 579, 5265-5274. | 2.8 | 21 |
| 79 | Reconstructing genetic networks in yeast. Nature Biotechnology, 2003, 21, 1295-1297. | 17.5 | 14 |
| 80 | 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 |