

# Sheng Zhong

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/679159/publications.pdf>

Version: 2024-02-01

44  
papers

3,877  
citations

304743

22  
h-index

276875

41  
g-index

57  
all docs

57  
docs citations

57  
times ranked

8009  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.  | 27.8 | 1,444     |
| 2  | The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.   | 27.8 | 579       |
| 3  | Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. <i>Genome Research</i> , 2014, 24, 1787-1796.   | 5.5  | 263       |
| 4  | Rewirable gene regulatory networks in the preimplantation embryonic development of three mammalian species. <i>Genome Research</i> , 2010, 20, 804-815.  | 5.5  | 204       |
| 5  | Comparative Epigenomic Annotation of Regulatory DNA. <i>Cell</i> , 2012, 149, 1381-1392.   | 28.9 | 188       |
| 6  | Lens regeneration using endogenous stem cells with gain of visual function. <i>Nature</i> , 2016, 531, 323-328.  | 27.8 | 171       |
| 7  | Systematic Mapping of RNA-Chromatin Interactions In Vivo. <i>Current Biology</i> , 2017, 27, 602-609.  | 3.9  | 144       |
| 8  | Mapping RNA-RNA interactome and RNA structure in vivo by MARIO. <i>Nature Communications</i> , 2016, 7, 12023.   | 12.8 | 135       |
| 9  | Genome-wide colocalization of RNA-DNA interactions and fusion RNA pairs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 3328-3337.                        | 7.1  | 52        |
| 10 | Extracellular RNA in a single droplet of human serum reflects physiologic and disease states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19200-19208. | 7.1  | 46        |
| 11 | Suppression of Endothelial AGO1 Promotes Adipose Tissue Browning and Improves Metabolic Dysfunction. <i>Circulation</i> , 2020, 142, 365-379.  | 1.6  | 44        |
| 12 | SMARCD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. <i>Cell Reports</i> , 2017, 18, 3117-3128.   | 6.4  | 40        |
| 13 | Stress-induced RNA-chromatin interactions promote endothelial dysfunction. <i>Nature Communications</i> , 2020, 11, 5211.  | 12.8 | 39        |
| 14 | Mapping RNA-chromatin interactions by sequencing with iMARGI. <i>Nature Protocols</i> , 2019, 14, 3243-3272.   | 12.0 | 36        |
| 15 | RNA, Action through Interactions. <i>Trends in Genetics</i> , 2018, 34, 867-882.   | 6.7  | 33        |
| 16 | Presymptomatic Increase of an Extracellular RNA in Blood Plasma Associates with the Development of Alzheimer's Disease. <i>Current Biology</i> , 2020, 30, 1771-1782.e3.                                       | 3.9  | 32        |
| 17 | Cross-species de novo identification of cis-regulatory modules with GibbsModule: Application to gene regulation in embryonic stem cells. <i>Genome Research</i> , 2008, 18, 1325-1335.                         | 5.5  | 29        |
| 18 | Time-variant clustering model for understanding cell fate decisions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4797-806.                            | 7.1  | 29        |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 19 | RNAs as Proximity-Labeling Media for Identifying Nuclear Speckle Positions Relative to the Genome. <i>IScience</i> , 2018, 4, 204-215.   | 4.1  | 29        |
| 20 | GITAR: An Open Source Tool for Analysis and Visualization of Hi-C Data. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 365-372.  | 6.9  | 28        |
| 21 | Revealing protein-protein interactions at the transcriptome scale by sequencing. <i>Molecular Cell</i> , 2021, 81, 4091-4103.e9.   | 9.7  | 28        |
| 22 | Natural display of nuclear-encoded RNA on the cell surface and its impact on cell interaction. <i>Genome Biology</i> , 2020, 21, 225.  | 8.8  | 27        |
| 23 | The Relationship between Gene Network Structure and Expression Variation among Individuals and Species. <i>PLoS Genetics</i> , 2015, 11, e1005398.   | 3.5  | 25        |
| 24 | Modeling Co-Expression across Species for Complex Traits: Insights to the Difference of Human and Mouse Embryonic Stem Cells. <i>PLoS Computational Biology</i> , 2010, 6, e1000707.                         | 3.2  | 24        |
| 25 | Pivotal Role of Fatty Acid Synthase in c-MYC Driven Hepatocarcinogenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8467.   | 4.1  | 20        |
| 26 | Transcriptomic insights into the genetic basis of mammalian limb diversity. <i>BMC Evolutionary Biology</i> , 2017, 17, 86.  | 3.2  | 19        |
| 27 | GIVE: portable genome browsers for personal websites. <i>Genome Biology</i> , 2018, 19, 92.  | 8.8  | 15        |
| 28 | Alpelisib combination treatment as novel targeted therapy against hepatocellular carcinoma. <i>Cell Death and Disease</i> , 2021, 12, 920.   | 6.3  | 13        |
| 29 | GeNemo: a search engine for web-based functional genomic data. <i>Nucleic Acids Research</i> , 2016, 44, W122-W127.  | 14.5 | 11        |
| 30 | PHGDH expression increases with progression of Alzheimer's disease pathology and symptoms. <i>Cell Metabolism</i> , 2022, 34, 651-653.   | 16.2 | 11        |
| 31 | Towards an Evolutionary Model of Transcription Networks. <i>PLoS Computational Biology</i> , 2011, 7, e1002064.  | 3.2  | 10        |
| 32 | Comparative epigenomics: defining and utilizing epigenomic variations across species, time-course, and individuals. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2014, 6, 345-352. | 6.6  | 10        |
| 33 | Integration of FRET and sequencing to engineer kinase biosensors from mammalian cell libraries. <i>Nature Communications</i> , 2021, 12, 5031.   | 12.8 | 10        |
| 34 | Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. <i>IScience</i> , 2018, 7, 16-29.  | 4.1  | 9         |
| 35 | From genomes to societies: a holistic view of determinants of human health. <i>Current Opinion in Biotechnology</i> , 2014, 28, 134-142.   | 6.6  | 7         |
| 36 | A likelihood approach to testing hypotheses on the co-evolution of epigenome and genome. <i>PLoS Computational Biology</i> , 2018, 14, e1006673.   | 3.2  | 4         |

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 37 | EpiAlignment: alignment with both DNA sequence and epigenomic data. <i>Nucleic Acids Research</i> , 2019, 47, W11-W19.   | 14.5 | 3         |
| 38 | CDK9 is dispensable for YAP-driven hepatoblastoma development. <i>Pediatric Blood and Cancer</i> , 2020, 67, e28221.   | 1.5  | 3         |
| 39 | Isolation and Profiling of Human Primary Mesenteric Arterial Endothelial Cells at the Transcriptome Level. <i>Journal of Visualized Experiments</i> , 2022, , .  | 0.3  | 3         |
| 40 | Reply to Verwilt et al.: Experimental evidence against DNA contamination in SILVER-seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 18937-18938.                           | 7.1  | 2         |
| 41 | Pattern-based Search of Epigenomic Data Using GeNemo. <i>Journal of Visualized Experiments</i> , 2017, , .   | 0.3  | 0         |
| 42 | Reply to Hartl and Gao: Lack of between-batch difference in the distributions of measured extracellular RNA levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1851-1852. | 7.1  | 0         |
| 43 | Localized Single Transcript Detection of Eml4-Alk in NSCLC using Co-localization Quantum Dot Fluorescent In Situ Hybridization (CoQFISH). <i>FASEB Journal</i> , 2018, 32, 532.7.  | 0.5  | 0         |
| 44 | A System for Global Analysis of Correlation between Protein Expression and mRNA. <i>FASEB Journal</i> , 2018, 32, 651.10.  | 0.5  | 0         |