

# Sheng Zhong

## List of Publications by Year in descending order

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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	Isolation and Profiling of Human Primary Mesenteric Arterial Endothelial Cells at the Transcriptome Level. <i>Journal of Visualized Experiments</i> , 2022, , .	0.3	3
2	PHGDH expression increases with progression of Alzheimer's disease pathology and symptoms. <i>Cell Metabolism</i> , 2022, 34, 651-653.	16.2	11
3	Integration of FRET and sequencing to engineer kinase biosensors from mammalian cell libraries. <i>Nature Communications</i> , 2021, 12, 5031.	12.8	10
4	Revealing protein-protein interactions at the transcriptome scale by sequencing. <i>Molecular Cell</i> , 2021, 81, 4091-4103.e9.	9.7	28
5	Alpelisib combination treatment as novel targeted therapy against hepatocellular carcinoma. <i>Cell Death and Disease</i> , 2021, 12, 920.	6.3	13
6	Stress-induced RNA-chromatin interactions promote endothelial dysfunction. <i>Nature Communications</i> , 2020, 11, 5211.	12.8	39
7	Pivotal Role of Fatty Acid Synthase in c-MYC Driven Hepatocarcinogenesis. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8467.	4.1	20
8	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
9	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
10	Suppression of Endothelial AGO1 Promotes Adipose Tissue Browning and Improves Metabolic Dysfunction. <i>Circulation</i> , 2020, 142, 365-379.	1.6	44
11	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
12	CDK9 is dispensable for YAP-driven hepatoblastoma development. <i>Pediatric Blood and Cancer</i> , 2020, 67, e28221.	1.5	3
13	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
14	Mapping RNA-chromatin interactions by sequencing with iMARGI. <i>Nature Protocols</i> , 2019, 14, 3243-3272.	12.0	36
15	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
16	EpiAlignment: alignment with both DNA sequence and epigenomic data. <i>Nucleic Acids Research</i> , 2019, 47, W11-W19.	14.5	3
17	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
18	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

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19	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
20	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. <i>IScience</i> , 2018, 7, 16-29.	4.1	9
21	RNA, Action through Interactions. <i>Trends in Genetics</i> , 2018, 34, 867-882.	6.7	33
22	RNAs as Proximity-Labeling Media for Identifying Nuclear Speckle Positions Relative to the Genome. <i>IScience</i> , 2018, 4, 204-215.	4.1	29
23	GIVE: portable genome browsers for personal websites. <i>Genome Biology</i> , 2018, 19, 92.	8.8	15
24	Localized Single Transcript Detection of Eml4â€Alk in NSCLC using Co-localization Quantum Dot Fluorescent In Situ Hybridization (CoQFISH). <i>FASEB Journal</i> , 2018, 32, 532.7.	0.5	0
25	A System for Global Analysis of Correlation between Protein Expression and mRNA. <i>FASEB Journal</i> , 2018, 32, 651.10.	0.5	0
26	Systematic Mapping of RNA-Chromatin Interactions InÂVivo. <i>Current Biology</i> , 2017, 27, 602-609.	3.9	144
27	Transcriptomic insights into the genetic basis of mammalian limb diversity. <i>BMC Evolutionary Biology</i> , 2017, 17, 86.	3.2	19
28	SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. <i>Cell Reports</i> , 2017, 18, 3117-3128.	6.4	40
29	Pattern-based Search of Epigenomic Data Using GeNemo. <i>Journal of Visualized Experiments</i> , 2017, , .	0.3	0
30	The 4D nucleome project. <i>Nature</i> , 2017, 549, 219-226.	27.8	579
31	GeNemo: a search engine for web-based functional genomic data. <i>Nucleic Acids Research</i> , 2016, 44, W122-W127.	14.5	11
32	Mapping RNAâ€RNA interactome and RNA structure in vivo by MARIO. <i>Nature Communications</i> , 2016, 7, 12023.	12.8	135
33	Lens regeneration using endogenous stem cells with gain of visual function. <i>Nature</i> , 2016, 531, 323-328.	27.8	171
34	The Relationship between Gene Network Structure and Expression Variation among Individuals and Species. <i>PLoS Genetics</i> , 2015, 11, e1005398.	3.5	25
35	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
36	A comparative encyclopedia of DNA elements in the mouse genome. <i>Nature</i> , 2014, 515, 355-364.	27.8	1,444

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37	Time-variant clustering model for understanding cell fate decisions. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E4797-806.	7.1	29
38	Cell fate inclination within 2-cell and 4-cell mouse embryos revealed by single-cell RNA sequencing. Genome Research, 2014, 24, 1787-1796.	5.5	263
39	From genomes to societies: a holistic view of determinants of human health. Current Opinion in Biotechnology, 2014, 28, 134-142.	6.6	7
40	Comparative Epigenomic Annotation of Regulatory DNA. Cell, 2012, 149, 1381-1392.	28.9	188
41	Towards an Evolutionary Model of Transcription Networks. PLoS Computational Biology, 2011, 7, e1002064.	3.2	10
42	Modeling Co-Expression across Species for Complex Traits: Insights to the Difference of Human and Mouse Embryonic Stem Cells. PLoS Computational Biology, 2010, 6, e1000707.	3.2	24
43	Rewirable gene regulatory networks in the preimplantation embryonic development of three mammalian species. Genome Research, 2010, 20, 804-815.	5.5	204
44	Cross-species de novo identification of cis-regulatory modules with GibbsModule: Application to gene regulation in embryonic stem cells. Genome Research, 2008, 18, 1325-1335.	5.5	29