

# Zhang Yiming

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4837031/publications.pdf>

Version: 2024-02-01

14  
papers

333  
citations

1039880

9  
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1058333

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14  
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14  
docs citations

14  
times ranked

566  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic monitoring of SARS-CoV-2 uncovers an Nsp1 deletion variant that modulates type I interferon response. <i>Cell Host and Microbe</i> , 2021, 29, 489-502.e8.	5.1	95
2	Sequential fate-switches in stem-like cells drive the tumorigenic trajectory from human neural stem cells to malignant glioma. <i>Cell Research</i> , 2021, 31, 684-702.	5.7	41
3	EnhancerDB: a resource of transcriptional regulation in the context of enhancers. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	1.4	29
4	Differential immune responses in pregnant patients recovered from COVID-19. <i>Signal Transduction and Targeted Therapy</i> , 2021, 6, 289.	7.1	28
5	Comprehensive Expression Profiling and Functional Network Analysis of p53-Regulated MicroRNAs in HepG2 Cells Treated with Doxorubicin. <i>PLoS ONE</i> , 2016, 11, e0149227.	1.1	23
6	Integrated single-cell RNA sequencing analysis reveals distinct cellular and transcriptional modules associated with survival in lung cancer. <i>Signal Transduction and Targeted Therapy</i> , 2022, 7, 9.	7.1	23
7	Identification and Analysis of P53-Mediated Competing Endogenous RNA Network in Human Hepatocellular Carcinoma. <i>International Journal of Biological Sciences</i> , 2017, 13, 1213-1221.	2.6	20
8	Sustainable Electrocatalytic Oxidant-Free Syntheses of Thiosulfonates from Thiols. <i>ChemElectroChem</i> , 2018, 5, 3619-3623.	1.7	20
9	Paired rRNA-depleted and polyA-selected RNA sequencing data and supporting multi-omics data from human T cells. <i>Scientific Data</i> , 2020, 7, 376.	2.4	15
10	MeDAS: a Metazoan Developmental Alternative Splicing database. <i>Nucleic Acids Research</i> , 2021, 49, D144-D150.	6.5	13
11	SCAPE: a mixture model revealing single-cell polyadenylation diversity and cellular dynamics during cell differentiation and reprogramming. <i>Nucleic Acids Research</i> , 2022, 50, e66-e66.	6.5	13
12	Transcriptome profiling analysis of differentially expressed mRNAs and lncRNAs in HepG2 cells treated with peptide 9R-P201. <i>Biotechnology Letters</i> , 2017, 39, 1639-1647.	1.1	6
13	An overview of SNP-SNP microhaplotypes in the 26 populations of the 1000 Genomes Project. <i>International Journal of Legal Medicine</i> , 2022, 136, 1211-1226.	1.2	6
14	Short-read and long-read RNA sequencing of mouse hematopoietic stem cells at bulk and single-cell levels. <i>Scientific Data</i> , 2021, 8, 309.	2.4	1