Zhichao Miao

List of Publications by Year
in descending order

37 papers	3,002 citations	279487 23 h-index	344852 36 g-index
44 all docs	44 docs citations	44 times ranked	5772 citing authors

#	Article	IF	Citations
1	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	6.5	78
2	Evaluation of the stereochemical quality of predicted RNA 3D models in the RNA-Puzzles submissions. Rna, 2022, 28, 250-262.	1.6	12
3	Single-cell genomics identifies distinct B1 cell developmental pathways and reveals aging-related changes in the B-cell receptor repertoire. Cell and Bioscience, 2022, 12, 57.	2.1	7
4	Identification of TPBG-Expressing Amacrine Cells in DAT-tdTomato Mouse. , 2022, 63, 13.		2
5	Single-cell transcriptomics of adult macaque hippocampus reveals neural precursor cell populations. Nature Neuroscience, 2022, 25, 805-817.	7.1	47
6	Secondary structure of the SARS-CoV-2 5â€™-UTR. RNA Biology, 2021, 18, 447-456.	1.5	104
7	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. Nature Methods, 2021, 18, 327-328.	9.0	26
8	High-throughput full-length single-cell RNA-seq automation. Nature Protocols, 2021, 16, 2886-2915.	5.5	13
9	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	1.1	29
10	Longevity, clonal relationship, and transcriptional program of celiac diseaseâ€"specific plasma cells. Journal of Experimental Medicine, 2021, 218, .	4.2	25
11	Meta-analysis of COVID-19 single-cell studies confirms eight key immune responses. Scientific Reports, 2021, 11, 20833.	1.6	11
12	Single-Cell Analysis Reveals the Immune Characteristics of Myeloid Cells and Memory T Cells in Recovered COVID-19 Patients With Different Severities. Frontiers in Immunology, 2021, 12, 781432.	2.2	13
13	BBKNN: fast batch alignment of single cell transcriptomes. Bioinformatics, 2020, 36, 964-965.	1.8	517
14	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. Nucleic Acids Research, 2020, 48, 576-588.	6.5	44
15	Advances in RNA 3D Structure Modeling Using Experimental Data. Frontiers in Genetics, 2020, 11, 574485.	1.1	56
16	<i>NCKAP1L</i> defects lead to a novel syndrome combining immunodeficiency, lymphoproliferation, and hyperinflammation. Journal of Experimental Medicine, 2020, 217, .	4.2	48
17	Two Cases of Recessive Intellectual Disability Caused by NDST1 and METTL23 Variants. Genes, 2020, 11, 1021.	1.0	9
18	Putative cell type discovery from single-cell gene expression data. Nature Methods, 2020, 17, 621-628.	9.0	91

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19	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	1.6	100
20	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	13.7	392
21	Exome sequencing identifies a novel missense variant in CTSC causing nonsyndromic aggressive periodontitis. Journal of Human Genetics, 2019, 64, 689-694.	1.1	8
22	AbRSA: A robust tool for antibody numbering. Protein Science, 2019, 28, 1524-1531.	3.1	29
23	Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, 2019, 20, 70.	3.8	82
24	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	9.0	278
25	Evaluation of Protein–Ligand Docking by Cyscore. Methods in Molecular Biology, 2018, 1762, 233-243.	0.4	3
26	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	1.6	158
27	RNA Structure: Advances and Assessment of 3D Structure Prediction. Annual Review of Biophysics, 2017, 46, 483-503.	4.5	166
28	Mutations in signal recognition particle SRP54 cause syndromic neutropenia with Shwachman-Diamond–like features. Journal of Clinical Investigation, 2017, 127, 4090-4103.	3.9	126
29	Quantifying side-chain conformational variations in protein structure. Scientific Reports, 2016, 6, 37024.	1.6	30
30	RBscore&NBench: a high-level web server for nucleic acid binding residues prediction with a large-scale benchmarking database. Nucleic Acids Research, 2016, 44, W562-W567.	6.5	26
31	A Large-Scale Assessment of Nucleic Acids Binding Site Prediction Programs. PLoS Computational Biology, 2015, 11, e1004639.	1.5	62
32	Prediction of nucleic acid binding probability in proteins: a neighboring residue network based score. Nucleic Acids Research, 2015, 43, 5340-5351.	6.5	50
33	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	1.6	161
34	Modeling of Protein Side-Chain Conformations with RASP. Methods in Molecular Biology, 2014, 1137, 43-53.	0.4	3
35	RNA structure analysis of human spliceosomes reveals a compact 3D arrangement of snRNAs at the catalytic core. EMBO Journal, 2013, 32, 2804-2818.	3.5	57
36	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	1.8	52

#	Article	IF	Citations
37	RASP: rapid modeling of protein side chain conformations. Bioinformatics, 2011, 27, 3117-3122.	1.8	55