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	BBKNN: fast batch alignment of single cell transcriptomes. Bioinformatics, 2020, 36, 964-965.	1.8	517
2	Decoding human fetal liver haematopoiesis. Nature, 2019, 574, 365-371.	13.7	392
3	A test metric for assessing single-cell RNA-seq batch correction. Nature Methods, 2019, 16, 43-49.	9.0	278
4	RNA Structure: Advances and Assessment of 3D Structure Prediction. Annual Review of Biophysics, 2017, 46, 483-503.	4.5	166
5	<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
6	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	1.6	158
7	Mutations in signal recognition particle SRP54 cause syndromic neutropenia with Shwachman-Diamondâ€"like features. Journal of Clinical Investigation, 2017, 127, 4090-4103.	3.9	126
8	Secondary structure of the SARS-CoV-2 5â€™-UTR. RNA Biology, 2021, 18, 447-456.	1.5	104
9	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	1.6	100
10	Putative cell type discovery from single-cell gene expression data. Nature Methods, 2020, 17, 621-628.	9.0	91
11	Comparative analysis of sequencing technologies for single-cell transcriptomics. Genome Biology, 2019, 20, 70.	3.8	82
12	Expression Atlas update: gene and protein expression in multiple species. Nucleic Acids Research, 2022, 50, D129-D140.	6.5	78
13	A Large-Scale Assessment of Nucleic Acids Binding Site Prediction Programs. PLoS Computational Biology, 2015, 11, e1004639.	1.5	62
14	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
15	Advances in RNA 3D Structure Modeling Using Experimental Data. Frontiers in Genetics, 2020, 11, 574485.	1.1	56
16	RASP: rapid modeling of protein side chain conformations. Bioinformatics, 2011, 27, 3117-3122.	1.8	55
17	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	1.8	52
18	Prediction of nucleic acid binding probability in proteins: a neighboring residue network based score. Nucleic Acids Research, 2015, 43, 5340-5351.	6.5	50

#	Article	IF	Citations
19	*NCKAP1L* defects lead to a novel syndrome combining immunodeficiency, lymphoproliferation, and hyperinflammation. Journal of Experimental Medicine, 2020, 217, .	4.2	48
20	Single-cell transcriptomics of adult macaque hippocampus reveals neural precursor cell populations. Nature Neuroscience, 2022, 25, 805-817.	7.1	47
21	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
22	Quantifying side-chain conformational variations in protein structure. Scientific Reports, 2016, 6, 37024.	1.6	30
23	AbRSA: A robust tool for antibody numbering. Protein Science, 2019, 28, 1524-1531.	3.1	29
24	Mapping Rora expression in resting and activated CD4+ T cells. PLoS ONE, 2021, 16, e0251233.	1.1	29
25	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
26	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. Nature Methods, 2021, 18, 327-328.	9.0	26
27	Longevity, clonal relationship, and transcriptional program of celiac disease–specific plasma cells. Journal of Experimental Medicine, 2021, 218, .	4.2	25
28	High-throughput full-length single-cell RNA-seq automation. Nature Protocols, 2021, 16, 2886-2915.	5.5	13
29	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
30	Evaluation of the stereochemical quality of predicted RNA 3D models in the RNA-Puzzles submissions. Rna, 2022, 28, 250-262.	1.6	12
31	Meta-analysis of COVID-19 single-cell studies confirms eight key immune responses. Scientific Reports, 2021, 11, 20833.	1.6	11
32	Two Cases of Recessive Intellectual Disability Caused by NDST1 and METTL23 Variants. Genes, 2020, 11, 1021.	1.0	9
33	Exome sequencing identifies a novel missense variant in CTSC causing nonsyndromic aggressive periodontitis. Journal of Human Genetics, 2019, 64, 689-694.	1.1	8
34	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
35	Evaluation of Protein–Ligand Docking by Cyscore. Methods in Molecular Biology, 2018, 1762, 233-243.	0.4	3
36	Modeling of Protein Side-Chain Conformations with RASP. Methods in Molecular Biology, 2014, 1137, 43-53.	0.4	3

#	ARTICLE	IF	CITATIONS
37	Identification of TPBG-Expressing Amacrine Cells in DAT-tdTomato Mouse. , 2022, 63, 13.		2