Andrey D Prjibelski

List of Publications by Year
in descending order

21 papers	24,392 citations	687363 13 h-index	752698 20 g-index
26 all docs	26 docs citations	26 times ranked	30080 citing authors

#	Article	IF	Citations
1	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. Nature Biotechnology, 2022, 40, 1082-1092.	17.5	52
2	Sequencing of individual barcoded cDNAs using Pacific Biosciences and Oxford Nanopore Technologies reveals platform-specific error patterns. Genome Research, 2022, 32, 726-737.	5.5	13
3	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	12.8	109
4	Pattern of TAAR5 Expression in the Human Brain Based on Transcriptome Datasets Analysis. International Journal of Molecular Sciences, 2021, 22, 8802.	4.1	10
5	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. Cell Systems, 2020, 10, 99-108.e5.	6.2	28
6	Liquid drop of DNA libraries reveals total genome information. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27300-27306.	7.1	4
7	Seed Transcriptome Annotation Reveals Enhanced Expression of Genes Related to ROS Homeostasis and Ethylene Metabolism at Alternating Temperatures in Wild Cardoon. Plants, 2020, 9, 1225.	3.5	10
8	Understanding complex dynamics of behavioral, neurochemical and transcriptomic changes induced by prolonged chronic unpredictable stress in zebrafish. Scientific Reports, 2020, 10, 19981.	3.3	24
9	Extending rnaSPAdes functionality for hybrid transcriptome assembly. BMC Bioinformatics, 2020, 21, 302.	2.6	17
10	Hybrid transcriptome sequencing approach improved assembly and gene annotation in Cynara cardunculus (L.). BMC Genomics, 2020, 21, 317.	2.8	18
11	Using SPAdes De Novo Assembler. Current Protocols in Bioinformatics, 2020, 70, e102.	25.8	1,113
12	Sequence Analysis. , 2019, , 292-322.		8
13	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 2019, 8, .	6.4	428
14	SGTK: a toolkit for visualization and assessment of scaffold graphs. Bioinformatics, 2019, 35, 2303-2305.	4.1	8
15	Versatile genome assembly evaluation with QUAST-LG. Bioinformatics, 2018, 34, i142-i150.	4.1	732
16	Icarus: visualizer for <i>de novo</i> assembly evaluation. Bioinformatics, 2016, 32, 3321-3323.	4.1	115
17	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. Bioinformatics, 2016, 32, 2210-2212.	4.1	106
18	Assembling short reads from jumping libraries with large insert sizes. Bioinformatics, 2015, 31, 3262-3268.	4.1	40

#	Article	IF	Citations
19	ExSPAnder: a universal repeat resolver for DNA fragment assembly. Bioinformatics, 2014, 30, i293-i301.	4.1	103
20	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. Journal of Computational Biology, 2013, 20, 714-737.	1.6	1,235
21	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. Journal of Computational Biology, 2012, 19, 455-477.	1.6	20,193