Andrey D Prjibelski

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	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
2	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. Journal of Computational Biology, 2013, 20, 714-737.	1.6	1,235
3	Using SPAdes De Novo Assembler. Current Protocols in Bioinformatics, 2020, 70, e102.	25.8	1,113
4	Versatile genome assembly evaluation with QUAST-LG. Bioinformatics, 2018, 34, i142-i150.	4.1	732
5	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 2019, 8, .	6.4	428
6	Icarus: visualizer for <i>de novo</i> assembly evaluation. Bioinformatics, 2016, 32, 3321-3323.	4.1	115
7	A spatially resolved brain region- and cell type-specific isoform atlas of the postnatal mouse brain. Nature Communications, 2021, 12, 463.	12.8	109
8	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. Bioinformatics, 2016, 32, 2210-2212.	4.1	106
9	ExSPAnder: a universal repeat resolver for DNA fragment assembly. Bioinformatics, 2014, 30, i293-i301.	4.1	103
10	Single-nuclei isoform RNA sequencing unlocks barcoded exon connectivity in frozen brain tissue. Nature Biotechnology, 2022, 40, 1082-1092.	17.5	52
11	Assembling short reads from jumping libraries with large insert sizes. Bioinformatics, 2015, 31, 3262-3268.	4.1	40
12	De Novo Peptide Sequencing Reveals Many Cyclopeptides in the Human Gut and Other Environments. Cell Systems, 2020, 10, 99-108.e5.	6.2	28
13	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
14	Hybrid transcriptome sequencing approach improved assembly and gene annotation in Cynara cardunculus (L.). BMC Genomics, 2020, 21, 317.	2.8	18
15	Extending rnaSPAdes functionality for hybrid transcriptome assembly. BMC Bioinformatics, 2020, 21, 302.	2.6	17
16	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
17	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
18	Pattern of TAAR5 Expression in the Human Brain Based on Transcriptome Datasets Analysis. International Journal of Molecular Sciences, 2021, 22, 8802.	4.1	10

#	Article	IF	Citations
19	Sequence Analysis. , 2019, , 292-322.		8
20	SGTK: a toolkit for visualization and assessment of scaffold graphs. Bioinformatics, 2019, 35, 2303-2305.	4.1	8
21	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