

Anton Bankevich

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7472877/publications.pdf>

Version: 2024-02-01

16
papers

22,333
citations

932766

10
h-index

940134

16
g-index

18
all docs

18
docs citations

18
times ranked

29029
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads. <i>Nature Biotechnology</i> , 2022, 40, 1075-1081.	9.4	41
2	ORFograph: search for novel insecticidal protein genes in genomic and metagenomic assembly graphs. <i>Microbiome</i> , 2021, 9, 149.	4.9	3
3	cloudSPAdes: assembly of synthetic long reads using de Bruijn graphs. <i>Bioinformatics</i> , 2019, 35, i61-i70.	1.8	22
4	Optimizing sequencing protocols for leaderboard metagenomics by combining long and short reads. <i>Genome Biology</i> , 2019, 20, 226.	3.8	47
5	Long Reads Enable Accurate Estimates of Complexity of Metagenomes. <i>Lecture Notes in Computer Science</i> , 2018, , 1-20.	1.0	1
6	Joint Analysis of Long and Short Reads Enables Accurate Estimates of Microbiome Complexity. <i>Cell Systems</i> , 2018, 7, 192-200.e3.	2.9	9
7	Comparison of carnivore, omnivore, and herbivore mammalian genomes with a new leopard assembly. <i>Genome Biology</i> , 2016, 17, 211.	3.8	101
8	TruSPAdes: barcode assembly of TruSeq synthetic long reads. <i>Nature Methods</i> , 2016, 13, 248-250.	9.0	40
9	dipSPAdes: Assembler for Highly Polymorphic Diploid Genomes. <i>Journal of Computational Biology</i> , 2015, 22, 528-545.	0.8	69
10	ExSPAnDer: a universal repeat resolver for DNA fragment assembly. <i>Bioinformatics</i> , 2014, 30, i293-i301.	1.8	103
11	dipSPAdes: Assembler for Highly Polymorphic Diploid Genomes. <i>Lecture Notes in Computer Science</i> , 2014, , 265-279.	1.0	10
12	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.0	439
13	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	0.8	1,235
14	SPAdes: A New Genome Assembly Algorithm and Its Applications to Single-Cell Sequencing. <i>Journal of Computational Biology</i> , 2012, 19, 455-477.	0.8	20,193
15	Bounds of the number of leaves of spanning trees in graphs without triangles. <i>Journal of Mathematical Sciences</i> , 2012, 184, 557-563.	0.1	4
16	Bounds of the number of leaves of spanning trees. <i>Journal of Mathematical Sciences</i> , 2012, 184, 564-572.	0.1	4