

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