

# Dmitry Antipov

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10138028/publications.pdf>

Version: 2024-02-01

20  
papers

25,895  
citations

567281

15  
h-index

752698

20  
g-index

25  
all docs

25  
docs citations

25  
times ranked

30728  
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	plasmidSPAdes: assembling plasmids from whole genome sequencing data. Bioinformatics, 2016, 32, 3380-3387.	4.1	468
6	<sc>hybrid</sc>SPA<sc>des</sc>: an algorithm for hybrid assembly of short and long reads. Bioinformatics, 2016, 32, 1009-1015.	4.1	463
7	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. Lecture Notes in Computer Science, 2013, , 158-170.	1.3	439
8	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 2019, 8, .	6.4	428
9	<sc>Metaviral</sc> <sc>SPAdes</sc>: assembly of viruses from metagenomic data. Bioinformatics, 2020, 36, 4126-4129.	4.1	149
10	Critical Assessment of Metagenome Interpretation: the second round of challenges. Nature Methods, 2022, 19, 429-440.	19.0	133
11	Plasmid detection and assembly in genomic and metagenomic data sets. Genome Research, 2019, 29, 961-968.	5.5	108
12	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. Bioinformatics, 2016, 32, 2210-2212.	4.1	106
13	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. Microbiome, 2021, 9, 78.	11.1	101
14	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. Nature Communications, 2021, 12, 1044.	12.8	80
15	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads. Nature Biotechnology, 2022, 40, 1075-1081.	17.5	41
16	Extending rnaSPAdes functionality for hybrid transcriptome assembly. BMC Bioinformatics, 2020, 21, 302.	2.6	17
17	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. Journal of Computational Biology, 2013, 20, 359-371.	1.6	14
18	SPAligner: alignment of long diverged molecular sequences to assembly graphs. BMC Bioinformatics, 2020, 21, 306.	2.6	13

#	ARTICLE	IF	CITATIONS
19	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data. <i>Genome Biology</i> , 2022, 23, 57.	8.8	11
20	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. <i>Lecture Notes in Computer Science</i> , 2012, , 200-212.	1.3	3