

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	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads. <i>Nature Biotechnology</i> , 2022, 40, 1075-1081.	17.5	41
2	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data. <i>Genome Biology</i> , 2022, 23, 57.	8.8	11
3	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
4	Thousands of previously unknown phages discovered in whole-community human gut metagenomes. <i>Microbiome</i> , 2021, 9, 78.	11.1	101
5	Analysis of metagenome-assembled viral genomes from the human gut reveals diverse putative CrAss-like phages with unique genomic features. <i>Nature Communications</i> , 2021, 12, 1044.	12.8	80
6	SPAligner: alignment of long diverged molecular sequences to assembly graphs. <i>BMC Bioinformatics</i> , 2020, 21, 306.	2.6	13
7	Extending rnaSPAdes functionality for hybrid transcriptome assembly. <i>BMC Bioinformatics</i> , 2020, 21, 302.	2.6	17
8	Using SPAdes De Novo Assembler. <i>Current Protocols in Bioinformatics</i> , 2020, 70, e102.	25.8	1,113
9	<scp>Metaviral</scp> <scp>SPAdes</scp>: assembly of viruses from metagenomic data. <i>Bioinformatics</i> , 2020, 36, 4126-4129.	4.1	149
10	rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. <i>GigaScience</i> , 2019, 8, .	6.4	428
11	Plasmid detection and assembly in genomic and metagenomic data sets. <i>Genome Research</i> , 2019, 29, 961-968.	5.5	108
12	Versatile genome assembly evaluation with QUAST-LG. <i>Bioinformatics</i> , 2018, 34, i142-i150.	4.1	732
13	rnaQUAST: a quality assessment tool for <i>de novo</i> transcriptome assemblies. <i>Bioinformatics</i> , 2016, 32, 2210-2212.	4.1	106
14	plasmidSPAdes: assembling plasmids from whole genome sequencing data. <i>Bioinformatics</i> , 2016, 32, 3380-3387.	4.1	468
15	<scp>hybrid</scp>SPA<scp>des</scp>: an algorithm for hybrid assembly of short and long reads. <i>Bioinformatics</i> , 2016, 32, 1009-1015.	4.1	463
16	Assembling Genomes and Mini-metagenomes from Highly Chimeric Reads. <i>Lecture Notes in Computer Science</i> , 2013, , 158-170.	1.3	439
17	Assembling Single-Cell Genomes and Mini-Metagenomes From Chimeric MDA Products. <i>Journal of Computational Biology</i> , 2013, 20, 714-737.	1.6	1,235
18	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. <i>Journal of Computational Biology</i> , 2013, 20, 359-371.	1.6	14

#	ARTICLE	IF	CITATIONS
19	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
20	Pathset Graphs: A Novel Approach for Comprehensive Utilization of Paired Reads in Genome Assembly. Lecture Notes in Computer Science, 2012, , 200-212.	1.3	3