

Mikhail Kolmogorov

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5024092/publications.pdf>

Version: 2024-02-01

17
papers

5,970
citations

623734

14
h-index

888059

17
g-index

23
all docs

23
docs citations

23
times ranked

6352
citing authors

#	ARTICLE	IF	CITATIONS
1	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities. <i>Nature Biotechnology</i> , 2022, 40, 711-719.	17.5	99
2	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads. <i>Nature Biotechnology</i> , 2022, 40, 1075-1081.	17.5	41
3	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data. <i>Genome Biology</i> , 2022, 23, 57.	8.8	11
4	Critical Assessment of Metagenome Interpretation: the second round of challenges. <i>Nature Methods</i> , 2022, 19, 429-440.	19.0	133
5	The complete sequence of a human genome. <i>Science</i> , 2022, 376, 44-53.	12.6	1,222
6	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , 2021, 18, 1322-1332.	19.0	139
7	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020, 17, 1103-1110.	19.0	430
8	Assembly of long, error-prone reads using repeat graphs. <i>Nature Biotechnology</i> , 2019, 37, 540-546.	17.5	2,730
9	Assembly Graph Browser: interactive visualization of assembly graphs. <i>Bioinformatics</i> , 2019, 35, 3476-3478.	4.1	12
10	Repeat associated mechanisms of genome evolution and function revealed by the <i>Mus caroli</i> and <i>Mus pahari</i> genomes. <i>Genome Research</i> , 2018, 28, 448-459.	5.5	99
11	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018, 50, 1574-1583.	21.4	169
12	High-quality genome sequences of uncultured microbes by assembly of read clouds. <i>Nature Biotechnology</i> , 2018, 36, 1067-1075.	17.5	103
13	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , 2018, 28, 1720-1732.	5.5	94
14	Single-molecule protein identification by sub-nanopore sensors. <i>PLoS Computational Biology</i> , 2017, 13, e1005356.	3.2	52
15	Assembly of long error-prone reads using de Bruijn graphs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8396-E8405.	7.1	230
16	SpectroGene: A Tool for Proteogenomic Annotations Using Top-Down Spectra. <i>Journal of Proteome Research</i> , 2016, 15, 144-151.	3.7	14
17	Ragout—a reference-assisted assembly tool for bacterial genomes. <i>Bioinformatics</i> , 2014, 30, i302-i309.	4.1	169