

Mikhail Kolmogorov

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

23
papers

1,820
citations

14
h-index

23
g-index

23
ext. papers

3,832
ext. citations

22
avg, IF

5.43
L-index

#	Paper	IF	Citations
23	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities.. <i>Nature Biotechnology</i> , 2022 ,	44.5	13
22	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads.. <i>Nature Biotechnology</i> , 2022 ,	44.5	5
21	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data.. <i>Genome Biology</i> , 2022 , 23, 57	18.3	1
20	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , 2022 ,	21.6	14
19	The complete sequence of a human genome.. <i>Science</i> , 2022 , 376, 44-53	33.3	107
18	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , 2021 , 18, 1322-1332	21.6	24
17	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , 2020 , 17, 1103-1110	21.6	101
16	Assembly of long, error-prone reads using repeat graphs. <i>Nature Biotechnology</i> , 2019 , 37, 540-546	44.5	897
15	Assembly Graph Browser: interactive visualization of assembly graphs. <i>Bioinformatics</i> , 2019 , 35, 3476-3478	9	9
14	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , 2018 , 28, 448-459	9.7	57
13	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , 2018 , 50, 1574-1583	36.3	91
12	High-quality genome sequences of uncultured microbes by assembly of read clouds. <i>Nature Biotechnology</i> , 2018 ,	44.5	60
11	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , 2018 , 28, 1720-1732	9.7	54
10	Single-molecule protein identification by sub-nanopore sensors. <i>PLoS Computational Biology</i> , 2017 , 13, e1005356	5	40
9	SpectroGene: A Tool for Proteogenomic Annotations Using Top-Down Spectra. <i>Journal of Proteome Research</i> , 2016 , 15, 144-51	5.6	12
8	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	11.5	120
7	Ragout-a reference-assisted assembly tool for bacterial genomes. <i>Bioinformatics</i> , 2014 , 30, i302-9	7.2	107

6	Assembling Long Accurate Reads Using de Bruijn Graphs	3
5	Assembly of Long Error-Prone Reads Using Repeat Graphs	28
4	metaFlye: scalable long-read metagenome assembly using repeat graphs	14
3	The complete sequence of a human genome	58
2	Generation of lineage-resolved complete metagenome-assembled genomes by precision phasing	2
1	Automated assembly of high-quality diploid human reference genomes	3