

# Mikhail Kolmogorov

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/5024092/mikhail-kolmogorov-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Assembly of long, error-prone reads using repeat graphs. <i>Nature Biotechnology</i> , <b>2019</b> , 37, 540-546	44.5	897
22	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> , <b>2016</b> , 113, E8396-E8405	11.5	120
21	Ragout-a reference-assisted assembly tool for bacterial genomes. <i>Bioinformatics</i> , <b>2014</b> , 30, i302-9	7.2	107
20	The complete sequence of a human genome.. <i>Science</i> , <b>2022</b> , 376, 44-53	33.3	107
19	metaFlye: scalable long-read metagenome assembly using repeat graphs. <i>Nature Methods</i> , <b>2020</b> , 17, 1103-1110	21.6	101
18	Sixteen diverse laboratory mouse reference genomes define strain-specific haplotypes and novel functional loci. <i>Nature Genetics</i> , <b>2018</b> , 50, 1574-1583	36.3	91
17	High-quality genome sequences of uncultured microbes by assembly of read clouds. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	60
16	The complete sequence of a human genome		58
15	Repeat associated mechanisms of genome evolution and function revealed by the and genomes. <i>Genome Research</i> , <b>2018</b> , 28, 448-459	9.7	57
14	Chromosome assembly of large and complex genomes using multiple references. <i>Genome Research</i> , <b>2018</b> , 28, 1720-1732	9.7	54
13	Single-molecule protein identification by sub-nanopore sensors. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005356	5	40
12	Assembly of Long Error-Prone Reads Using Repeat Graphs		28
11	Haplotype-aware variant calling with PEPPER-Margin-DeepVariant enables high accuracy in nanopore long-reads. <i>Nature Methods</i> , <b>2021</b> , 18, 1322-1332	21.6	24
10	metaFlye: scalable long-read metagenome assembly using repeat graphs		14
9	Critical Assessment of Metagenome Interpretation: the second round of challenges.. <i>Nature Methods</i> , <b>2022</b> ,	21.6	14
8	Generating lineage-resolved, complete metagenome-assembled genomes from complex microbial communities.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44.5	13
7	SpectroGene: A Tool for Proteogenomic Annotations Using Top-Down Spectra. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 144-51	5.6	12

6	Assembly Graph Browser: interactive visualization of assembly graphs. <i>Bioinformatics</i> , <b>2019</b> , 35, 3476-3478	9
5	Multiplex de Bruijn graphs enable genome assembly from long, high-fidelity reads.. <i>Nature Biotechnology</i> , <b>2022</b> ,	44-5 5
4	Assembling Long Accurate Reads Using de Bruijn Graphs	3
3	Automated assembly of high-quality diploid human reference genomes	3
2	Generation of lineage-resolved complete metagenome-assembled genomes by precision phasing	2
1	viralFlye: assembling viruses and identifying their hosts from long-read metagenomics data.. <i>Genome Biology</i> , <b>2022</b> , 23, 57	18-3 1