

# Medhat Mahmoud

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3618226/publications.pdf>

Version: 2024-02-01

20  
papers

2,195  
citations

840776

11  
h-index

794594

19  
g-index

30  
all docs

30  
docs citations

30  
times ranked

3312  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accurate circular consensus long-read sequencing improves variant detection and assembly of a human genome. <i>Nature Biotechnology</i> , 2019, 37, 1155-1162.	17.5	1,010
2	Structural variant calling: the long and the short of it. <i>Genome Biology</i> , 2019, 20, 246.	8.8	409
3	Chromosome-scale, haplotype-resolved assembly of human genomes. <i>Nature Biotechnology</i> , 2021, 39, 309-312.	17.5	109
4	Curated variation benchmarks for challenging medically relevant autosomal genes. <i>Nature Biotechnology</i> , 2022, 40, 672-680.	17.5	90
5	Benchmarking challenging small variants with linked and long reads. <i>Cell Genomics</i> , 2022, 2, 100128.	6.5	77
6	Performance assessment of DNA sequencing platforms in the ABRF Next-Generation Sequencing Study. <i>Nature Biotechnology</i> , 2021, 39, 1129-1140.	17.5	69
7	Parliament2: Accurate structural variant calling at scale. <i>GigaScience</i> , 2020, 9, .	6.4	51
8	Efficiency of PacBio long read correction by 2nd generation Illumina sequencing. <i>Genomics</i> , 2019, 111, 43-49.	2.9	47
9	SARS-CoV-2 genomic diversity and the implications for qRT-PCR diagnostics and transmission. <i>Genome Research</i> , 2021, 31, 635-644.	5.5	39
10	PRINCESS: comprehensive detection of haplotype resolved SNVs, SVs, and methylation. <i>Genome Biology</i> , 2021, 22, 268.	8.8	28
11	Vulcan: Improved long-read mapping and structural variant calling via dual-mode alignment. <i>GigaScience</i> , 2021, 10, .	6.4	14
12	Approaches to Whole Mitochondrial Genome Sequencing on the Oxford Nanopore MinION. <i>Current Protocols in Human Genetics</i> , 2019, 104, e94.	3.5	13
13	Rescuing low frequency variants within intra-host viral populations directly from Oxford Nanopore sequencing data. <i>Nature Communications</i> , 2022, 13, 1321.	12.8	11
14	Fully resolved assembly of <i>Cryptosporidium parvum</i> . <i>GigaScience</i> , 2022, 11, .	6.4	8
15	A strategy for building and using a human reference pangenome. <i>F1000Research</i> , 2019, 8, 1751.	1.6	5
16	Identification of Structural Variants in Two Novel Genomes of Maize Inbred Lines Possibly Related to Glyphosate Tolerance. <i>Plants</i> , 2020, 9, 523.	3.5	4
17	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	3
18	An international virtual hackathon to build tools for the analysis of structural variants within species ranging from coronaviruses to vertebrates. <i>F1000Research</i> , 2021, 10, 246.	1.6	2

#	ARTICLE	IF	CITATIONS
19	The third international hackathon for applying insights into large-scale genomic composition to use cases in a wide range of organisms. F1000Research, 0, 11, 530.	1.6	1
20	Methods developed during the first National Center for Biotechnology Information Structural Variation Codeathon at Baylor College of Medicine. F1000Research, 0, 9, 1141.	1.6	0