Medhat Mahmoud

List of Publications by Year
in descending order

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

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

#	Article	IF	Citations
19	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
20	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