

Matthew D Clark

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

10,020
citations

430442

18
h-index

676716

22
g-index

29
all docs

29
docs citations

29
times ranked

15193
citing authors

#	ARTICLE	IF	CITATIONS
1	Nanopore adaptive sampling: a tool for enrichment of low abundance species in metagenomic samples. <i>Genome Biology</i> , 2022, 23, 11.	3.8	78
2	New approaches for metagenome assembly with short reads. <i>Briefings in Bioinformatics</i> , 2020, 21, 584-594.	3.2	140
3	Rapid MinION profiling of preterm microbiota and antimicrobial-resistant pathogens. <i>Nature Microbiology</i> , 2020, 5, 430-442.	5.9	113
4	Semi-quantitative characterisation of mixed pollen samples using MinION sequencing and Reverse Metagenomics (RevMet). <i>Methods in Ecology and Evolution</i> , 2019, 10, 1690-1701.	2.2	29
5	A critical comparison of technologies for a plant genome sequencing project. <i>GigaScience</i> , 2019, 8, .	3.3	41
6	Independent assessment and improvement of wheat genome sequence assemblies using Fosill jumping libraries. <i>GigaScience</i> , 2018, 7, .	3.3	12
7	Shifting the limits in wheat research and breeding using a fully annotated reference genome. <i>Science</i> , 2018, 361, .	6.0	2,424
8	Evolutionary genomics of the cold-adapted diatom <i>Fragilariopsis cylindrus</i> . <i>Nature</i> , 2017, 541, 536-540.	13.7	332
9	An improved assembly and annotation of the allohexaploid wheat genome identifies complete families of agronomic genes and provides genomic evidence for chromosomal translocations. <i>Genome Research</i> , 2017, 27, 885-896.	2.4	464
10	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
11	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
12	Genomic innovation for crop improvement. <i>Nature</i> , 2017, 543, 346-354.	13.7	301
13	Building a locally diploid genome and transcriptome of the diatom <i>Fragilariopsis cylindrus</i> . <i>Scientific Data</i> , 2017, 4, 170149.	2.4	14
14	A world of opportunities with nanopore sequencing. <i>Journal of Experimental Botany</i> , 2017, 68, 5419-5429.	2.4	158
15	Comparative analysis of targeted long read sequencing approaches for characterization of a plant's immune receptor repertoire. <i>BMC Genomics</i> , 2017, 18, 564.	1.2	51
16	NanoOK: multi-reference alignment analysis of nanopore sequencing data, quality and error profiles. <i>Bioinformatics</i> , 2016, 32, 142-144.	1.8	51
17	Targeted capture and sequencing of gene-sized DNA molecules. <i>BioTechniques</i> , 2016, 61, 315-322.	0.8	48
18	Accelerated cloning of a potato late blight resistance gene using RenSeq and SMRT sequencing. <i>Nature Biotechnology</i> , 2016, 34, 656-660.	9.4	248

#	ARTICLE	IF	CITATIONS
19	Zebrafish Rab5 proteins and a role for Rab5ab in nodal signalling. <i>Developmental Biology</i> , 2015, 397, 212-224.	0.9	15
20	NextClip: an analysis and read preparation tool for Nextera Long Mate Pair libraries. <i>Bioinformatics</i> , 2014, 30, 566-568.	1.8	218
21	The zebrafish reference genome sequence and its relationship to the human genome. <i>Nature</i> , 2013, 496, 498-503.	13.7	3,708