

Nadine McCallum

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1182648/publications.pdf>

Version: 2024-02-01

13
papers

1,591
citations

1163117

8
h-index

1058476

14
g-index

22
all docs

22
docs citations

22
times ranked

2933
citing authors

#	ARTICLE	IF	CITATIONS
1	Telomere-to-telomere assembly of a complete human X chromosome. <i>Nature</i> , 2020, 585, 79-84.	27.8	549
2	Nanopore native RNA sequencing of a human poly(A) transcriptome. <i>Nature Methods</i> , 2019, 16, 1297-1305.	19.0	411
3	BulkVis: a graphical viewer for Oxford nanopore bulk FAST5 files. <i>Bioinformatics</i> , 2019, 35, 2193-2198.	4.1	204
4	Readfish enables targeted nanopore sequencing of gigabase-sized genomes. <i>Nature Biotechnology</i> , 2021, 39, 442-450.	17.5	197
5	The Impact of Real-Time Whole-Genome Sequencing in Controlling Healthcare-Associated SARS-CoV-2 Outbreaks. <i>Journal of Infectious Diseases</i> , 2022, 225, 10-18.	4.0	25
6	Rapid-CNS2: rapid comprehensive adaptive nanopore-sequencing of CNS tumors, a proof-of-concept study. <i>Acta Neuropathologica</i> , 2022, 143, 609-612.	7.7	19
7	Stat3 oxidation-dependent regulation of gene expression impacts on developmental processes and involves cooperation with Hif-1 α . <i>PLoS ONE</i> , 2020, 15, e0244255.	2.5	11
8	Genetic variation at mouse and human ribosomal DNA influences associated epigenetic states. <i>Genome Biology</i> , 2022, 23, 54.	8.8	11
9	Retrospective screening of routine respiratory samples revealed undetected community transmission and missed intervention opportunities for SARS-CoV-2 in the United Kingdom. <i>Journal of General Virology</i> , 2021, 102, .	2.9	10
10	minoTour, real-time monitoring and analysis for nanopore sequencers. <i>Bioinformatics</i> , 2022, 38, 1133-1135.	4.1	8
11	Use of Bulk Segregant Analysis for Determining the Genetic Basis of Azole Resistance in the Opportunistic Pathogen <i>Aspergillus fumigatus</i> . <i>Frontiers in Cellular and Infection Microbiology</i> , 2022, 12, 841138.	3.9	6
12	Extensive Homoplasmy but No Evidence of Convergent Evolution of Repeat Numbers at MIRU Loci in Modern <i>Mycobacterium tuberculosis</i> Lineages. <i>Frontiers in Public Health</i> , 2020, 8, 455.	2.7	2
13	The UK Leicester COVID-19 "exceedance"™ May-July 2020: An analysis of hospitalised cases. <i>Journal of Infection</i> , 2021, 83, e5-e7.	3.3	1