

Joshua C Quick

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

8,865
citations

361413

20
h-index

580821

25
g-index

30
all docs

30
docs citations

30
times ranked

15080
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic assessment of quarantine measures to prevent SARS-CoV-2 importation and transmission. <i>Nature Communications</i> , 2022, 13, 1012.	12.8	10
2	Recurrent emergence of SARS-CoV-2 spike deletion H69/V70 and its role in the Alpha variant B.1.1.7. <i>Cell Reports</i> , 2021, 35, 109292.	6.4	375
3	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
4	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
5	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. <i>Cell</i> , 2020, 181, 990-996.e5.	28.9	321
6	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
7	Importation and early local transmission of COVID-19 in Brazil, 2020. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2020, 62, e30.	1.1	80
8	Ultra-deep, long-read nanopore sequencing of mock microbial community standards. <i>GigaScience</i> , 2019, 8, .	6.4	209
9	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. <i>Genome Biology</i> , 2019, 20, 8.	8.8	712
10	Complete Closed Genome Sequence of Nontoxigenic Invasive <i>Corynebacterium diphtheriae</i> bv. mitis Strain ISS 3319. <i>Genome Announcements</i> , 2018, 6, .	0.8	3
11	Field investigation with real-time virus genetic characterisation support of a cluster of Ebola virus disease cases in Dubuque, Guinea, April to June 2015. <i>Eurosurveillance</i> , 2018, 23, .	7.0	11
12	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
13	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
14	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. <i>Nature Protocols</i> , 2017, 12, 1261-1276.	12.0	898
15	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
16	Extensive Modulation of the Fecal Metagenome in Children With Crohn's Disease During Exclusive Enteral Nutrition. <i>American Journal of Gastroenterology</i> , 2015, 110, 1718-1729.	0.4	229
17	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015, 12, 733-735.	19.0	1,176
18	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. <i>Genome Biology</i> , 2015, 16, 114.	8.8	271

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19	Eighteenth-century genomes show that mixed infections were common at time of peak tuberculosis in Europe. <i>Nature Communications</i> , 2015, 6, 6717.	12.8	165
20	Deletions in a ribosomal protein-coding gene are associated with tigecycline resistance in <i>Enterococcus faecium</i> . <i>International Journal of Antimicrobial Agents</i> , 2015, 46, 572-575.	2.5	32
21	Draft Genome Sequence of <i>Elizabethkingia meningoseptica</i> Isolated from a Traumatic Wound. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
22	Seeking the source of <i>Pseudomonas aeruginosa</i> infections in a recently opened hospital: an observational study using whole-genome sequencing. <i>BMJ Open</i> , 2014, 4, e006278.	1.9	104
23	A reference bacterial genome dataset generated on the MinION, a portable single-molecule nanopore sequencer. <i>GigaScience</i> , 2014, 3, 22.	6.4	208
24	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014, 11, 1144-1146.	19.0	1,709
25	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. <i>Wellcome Open Research</i> , 0, 6, 241.	1.8	10
26	First whole genome analysis of the novel coronavirus (SARS-CoV-2) obtained from COVID-19 patients from five districts in Western Serbia. <i>Epidemiology and Infection</i> , 0, , 1-31.	2.1	5