

# Joshua Quick

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10816720/publications.pdf>

Version: 2024-02-01

19  
papers

8,367  
citations

516710

16  
h-index

839539

18  
g-index

26  
all docs

26  
docs citations

26  
times ranked

13726  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Testing in the Community: Testing Positive Samples with the TaqMan SARS-CoV-2 Mutation Panel To Find Variants in Real Time. <i>Journal of Clinical Microbiology</i> , 2022, 60, e0240821.	3.9	7
2	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. <i>Nature</i> , 2021, 597, 539-543.	27.8	113
3	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016–2018. <i>PLoS Pathogens</i> , 2020, 16, e1008699.	4.7	39
4	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
5	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. <i>Cell Reports</i> , 2020, 30, 2275-2283.e7.	6.4	37
6	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
7	Field investigation with real-time virus genetic characterisation support of a cluster of Ebola virus disease cases in Dubréka, Guinea, April to June 2015. <i>Eurosurveillance</i> , 2018, 23, .	7.0	11
8	Virus genomes reveal factors that spread and sustained the Ebola epidemic. <i>Nature</i> , 2017, 544, 309-315.	27.8	346
9	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. <i>Nature</i> , 2017, 546, 401-405.	27.8	298
10	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
11	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014–2015. <i>Emerging Infectious Diseases</i> , 2016, 22, 2149-2152.	4.3	21
12	Real-time, portable genome sequencing for Ebola surveillance. <i>Nature</i> , 2016, 530, 228-232.	27.8	1,179
13	A complete bacterial genome assembled de novo using only nanopore sequencing data. <i>Nature Methods</i> , 2015, 12, 733-735.	19.0	1,176
14	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. <i>Genome Biology</i> , 2015, 16, 114.	8.8	271
15	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
16	A reference bacterial genome dataset generated on the MinION, a portable single-molecule nanopore sequencer. <i>GigaScience</i> , 2014, 3, 22.	6.4	208
17	Binning metagenomic contigs by coverage and composition. <i>Nature Methods</i> , 2014, 11, 1144-1146.	19.0	1,709
18	A Culture-Independent Sequence-Based Metagenomics Approach to the Investigation of an Outbreak of Shiga-Toxigenic <i>Escherichia coli</i> O104:H4. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1502.	7.4	290

#	ARTICLE	IF	CITATIONS
19	Rapid viral metagenomics using SMART-9N amplification and nanopore sequencing. Wellcome Open Research, 0, 6, 241.	1.8	10