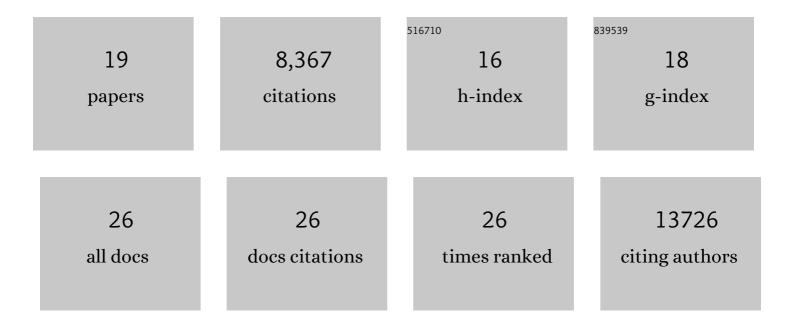
Joshua Quick

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10816720/publications.pdf Version: 2024-02-01



Іознил Ошск

#	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. Journal of Clinical Microbiology, 2022, 60, e0240821.	3.9	7
2	Resurgence of Ebola virus in 2021 in Guinea suggests a new paradigm for outbreaks. Nature, 2021, 597, 539-543.	27.8	113
3	Genomic Surveillance of Yellow Fever Virus Epizootic in São Paulo, Brazil, 2016 – 2018. PLoS Pathogens, 2020, 16, e1008699.	4.7	39
4	Coast-to-Coast Spread of SARS-CoV-2 during the Early Epidemic in the United States. Cell, 2020, 181, 990-996.e5.	28.9	321
5	Genomic and Epidemiological Surveillance of Zika Virus in the Amazon Region. Cell Reports, 2020, 30, 2275-2283.e7.	6.4	37
6	An amplicon-based sequencing framework for accurately measuring intrahost virus diversity using PrimalSeq and iVar. Genome Biology, 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. Eurosurveillance, 2018, 23, .	7.0	11
8	Virus genomes reveal factors that spread and sustained the Ebola epidemic. Nature, 2017, 544, 309-315.	27.8	346
9	Genomic epidemiology reveals multiple introductions of Zika virus into the United States. Nature, 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. Nature Protocols, 2017, 12, 1261-1276.	12.0	898
11	Unusual Ebola Virus Chain of Transmission, Conakry, Guinea, 2014–2015. Emerging Infectious Diseases, 2016, 22, 2149-2152.	4.3	21
12	Real-time, portable genome sequencing for Ebola surveillance. Nature, 2016, 530, 228-232.	27.8	1,179
13	A complete bacterial genome assembled de novo using only nanopore sequencing data. Nature Methods, 2015, 12, 733-735.	19.0	1,176
14	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. Genome Biology, 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. BMJ Open, 2014, 4, e006278.	1.9	104
16	A reference bacterial genome dataset generated on the MinIONâ"¢ portable single-molecule nanopore sequencer. GigaScience, 2014, 3, 22.	6.4	208
17	Binning metagenomic contigs by coverage and composition. Nature Methods, 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 Escherichia coli O104:H4. JAMA - Journal of the American Medical Association, 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