

Daniel J Park

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1065618/publications.pdf>

Version: 2024-02-01

25
papers

2,987
citations

567281

15
h-index

794594

19
g-index

26
all docs

26
docs citations

26
times ranked

5520
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak. <i>Science</i> , 2014, 345, 1369-1372.	12.6	1,083
2	Zika virus evolution and spread in the Americas. <i>Nature</i> , 2017, 546, 411-415.	27.8	323
3	Ebola Virus Epidemiology, Transmission, and Evolution during Seven Months in Sierra Leone. <i>Cell</i> , 2015, 161, 1516-1526.	28.9	275
4	Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events. <i>Science</i> , 2021, 371, .	12.6	226
5	Analysis of 6.4 million SARS-CoV-2 genomes identifies mutations associated with fitness. <i>Science</i> , 2022, 376, 1327-1332.	12.6	172
6	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
7	Genomic Analysis of Lassa Virus during an Increase in Cases in Nigeria in 2018. <i>New England Journal of Medicine</i> , 2018, 379, 1745-1753.	27.0	135
8	Multiplexed CRISPR-based microfluidic platform for clinical testing of respiratory viruses and identification of SARS-CoV-2 variants. <i>Nature Medicine</i> , 2022, 28, 1083-1094.	30.7	127
9	Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time. <i>Nature Communications</i> , 2020, 11, 4131.	12.8	101
10	Capturing sequence diversity in metagenomes with comprehensive and scalable probe design. <i>Nature Biotechnology</i> , 2019, 37, 160-168.	17.5	96
11	Monitoring of Ebola Virus Makona Evolution through Establishment of Advanced Genomic Capability in Liberia. <i>Emerging Infectious Diseases</i> , 2015, 21, 1135-1143.	4.3	79
12	Evaluation of the Potential Impact of Ebola Virus Genomic Drift on the Efficacy of Sequence-Based Candidate Therapeutics. <i>MBio</i> , 2015, 6, .	4.1	62
13	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. <i>Viruses</i> , 2014, 6, 3663-3682.	3.3	49
14	Combining genomics and epidemiology to track mumps virus transmission in the United States. <i>PLoS Biology</i> , 2020, 18, e3000611.	5.6	37
15	An Outbreak of Ebola Virus Disease in the Lassa Fever Zone. <i>Journal of Infectious Diseases</i> , 2016, 214, S110-S121.	4.0	34
16	Future-proofing and maximizing the utility of metadata: The PHA4GE SARS-CoV-2 contextual data specification package. <i>GigaScience</i> , 2022, 11, .	6.4	18
17	SARS-CoV-2 Reinfection in a Liver Transplant Recipient. <i>Annals of Internal Medicine</i> , 2021, 174, 1178-1180.	3.9	10
18	The Origins and Future of Sentinel: An Early-Warning System for Pandemic Preemption and Response. <i>Viruses</i> , 2021, 13, 1605.	3.3	8

#	ARTICLE	IF	CITATIONS
19	Synthetic DNA spike-ins (SDSIs) enable sample tracking and detection of inter-sample contamination in SARS-CoV-2 sequencing workflows. <i>Nature Microbiology</i> , 2022, 7, 108-119.	13.3	6
20	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
21	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
22	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
23	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
24	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0
25	Combining genomics and epidemiology to track mumps virus transmission in the United States. , 2020, 18, e3000611.		0