

Jeremy Swann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3102051/publications.pdf>

Version: 2024-02-01

17
papers

1,123
citations

840119

11
h-index

996533

15
g-index

29
all docs

29
docs citations

29
times ranked

2455
citing authors

#	ARTICLE	IF	CITATIONS
1	An Observational Cohort Study on the Incidence of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Infection and B.1.1.7 Variant Infection in Healthcare Workers by Antibody and Vaccination Status. <i>Clinical Infectious Diseases</i> , 2022, 74, 1208-1219.	2.9	64
2	ReadItAndKeep: rapid decontamination of SARS-CoV-2 sequencing reads. <i>Bioinformatics</i> , 2022, 38, 3291-3293.	1.8	5
3	Genomic network analysis of environmental and livestock F-type plasmid populations. <i>ISME Journal</i> , 2021, 15, 2322-2335.	4.4	24
4	Niche and local geography shape the pangenome of wastewater- and livestock-associated Enterobacteriaceae. <i>Science Advances</i> , 2021, 7, .	4.7	47
5	Population-level faecal metagenomic profiling as a tool to predict antimicrobial resistance in Enterobacterales isolates causing invasive infections: An exploratory study across Cambodia, Kenya, and the UK. <i>EClinicalMedicine</i> , 2021, 36, 100910.	3.2	10
6	Epidemiological data and genome sequencing reveals that nosocomial transmission of SARS-CoV-2 is underestimated and mostly mediated by a small number of highly infectious individuals. <i>Journal of Infection</i> , 2021, 83, 473-482.	1.7	55
7	The Duration, Dynamics, and Determinants of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Antibody Responses in Individual Healthcare Workers. <i>Clinical Infectious Diseases</i> , 2021, 73, e699-e709.	2.9	235
8	High precision <i>Neisseria gonorrhoeae</i> variant and antimicrobial resistance calling from metagenomic Nanopore sequencing. <i>Genome Research</i> , 2020, 30, 1354-1363.	2.4	27
9	Reconciling the Potentially Irreconcilable? Genotypic and Phenotypic Amoxicillin-Clavulanate Resistance in <i>Escherichia coli</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	1.4	33
10	Optimized use of Oxford Nanopore flowcells for hybrid assemblies. <i>Microbial Genomics</i> , 2020, 6, .	1.0	14
11	Differential occupational risks to healthcare workers from SARS-CoV-2 observed during a prospective observational study. <i>ELife</i> , 2020, 9, .	2.8	196
12	Scalable Pathogen Pipeline Platform (SP ³): Enabling Unified Genomic Data Analysis with Elastic Cloud Computing. , 2019, , .		1
13	The impact of sequencing depth on the inferred taxonomic composition and AMR gene content of metagenomic samples. <i>Environmental Microbiomes</i> , 2019, 14, 7.	2.2	69
14	Comparison of long-read sequencing technologies in the hybrid assembly of complex bacterial genomes. <i>Microbial Genomics</i> , 2019, 5, .	1.0	171
15	An Open-Source Azure Solution for Scalable Genomics Workflows. , 2018, , .		2
16	Real-time analysis of nanopore-based metagenomic sequencing from infected orthopaedic devices. <i>BMC Genomics</i> , 2018, 19, 714.	1.2	128
17	Quantitative fat and R2* mapping in vivo to measure lipid-rich necrotic core and intraplaque hemorrhage in carotid atherosclerosis. <i>Magnetic Resonance in Medicine</i> , 2017, 78, 285-296.	1.9	9