

Rebecca J Rockett

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9254416/publications.pdf>

Version: 2024-02-01

24
papers

1,129
citations

933447

10
h-index

642732

23
g-index

34
all docs

34
docs citations

34
times ranked

2186
citing authors

#	ARTICLE	IF	CITATIONS
1	Revealing COVID-19 transmission in Australia by SARS-CoV-2 genome sequencing and agent-based modeling. <i>Nature Medicine</i> , 2020, 26, 1398-1404.	30.7	283
2	Resistance Mutations in SARS-CoV-2 Delta Variant after Sotrovimab Use. <i>New England Journal of Medicine</i> , 2022, 386, 1477-1479.	27.0	134
3	An emergent clade of SARS-CoV-2 linked to returned travellers from Iran. <i>Virus Evolution</i> , 2020, 6, veaa027.	4.9	119
4	SARS-CoV-2 neutralizing antibodies: Longevity, breadth, and evasion by emerging viral variants. <i>PLoS Medicine</i> , 2021, 18, e1003656.	8.4	109
5	Epidemiologic Evidence for Airborne Transmission of SARS-CoV-2 during Church Singing, Australia, 2020. <i>Emerging Infectious Diseases</i> , 2021, 27, 1677-1680.	4.3	97
6	Co-infection with SARS-CoV-2 Omicron and Delta variants revealed by genomic surveillance. <i>Nature Communications</i> , 2022, 13, 2745.	12.8	64
7	Multidrug-Resistant <i>Salmonella enterica</i> [5],12:i:- Sequence Type 34, New South Wales, Australia, 2016–2017. <i>Emerging Infectious Diseases</i> , 2018, 24, 751-753.	4.3	52
8	Advances in Clinical Sample Preparation for Identification and Characterization of Bacterial Pathogens Using Metagenomics. <i>Frontiers in Public Health</i> , 2018, 6, 363.	2.7	48
9	SARS-CoV-2 Genome Sequencing Methods Differ in Their Abilities To Detect Variants from Low-Viral-Load Samples. <i>Journal of Clinical Microbiology</i> , 2021, 59, e0104621.	3.9	33
10	Whole Genome Sequencing of <i>Candida glabrata</i> for Detection of Markers of Antifungal Drug Resistance. <i>Journal of Visualized Experiments</i> , 2017, .	0.3	24
11	Genome-wide analysis of <i>Streptococcus pneumoniae</i> serogroup 19 in the decade after the introduction of pneumococcal conjugate vaccines in Australia. <i>Scientific Reports</i> , 2018, 8, 16969.	3.3	14
12	Genome Sequencing Links Persistent Outbreak of Legionellosis in Sydney (New South Wales, Australia) to an Emerging Clone of <i>Legionella pneumophila</i> Sequence Type 211. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	10
13	Bondi and beyond. Lessons from three waves of COVID-19 from 2020. <i>Public Health Research and Practice</i> , 2021, 31, .	1.5	10
14	Complete microbial genomes for public health in Australia and the Southwest Pacific. <i>Microbial Genomics</i> , 2020, 6, .	2.0	10
15	Optimization of sample preparation for culture-independent sequencing of <i>Bordetella pertussis</i> . <i>Microbial Genomics</i> , 2020, 6, .	2.0	8
16	Genome-wide networks reveal emergence of epidemic strains of <i>Salmonella Enteritidis</i> . <i>International Journal of Infectious Diseases</i> , 2022, 117, 65-73.	3.3	8
17	Genomic Surveillance Enables Suitability Assessment of <i>Salmonella</i> Gene Targets Used for Culture-Independent Diagnostic Testing. <i>Journal of Clinical Microbiology</i> , 2020, 58, .	3.9	5
18	Microbial Genomics as a Catalyst for Targeted Antivirulence Therapeutics. <i>Frontiers in Medicine</i> , 2021, 8, 641260.	2.6	4

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19	Documenting elimination of co-circulating COVID-19 clusters using genomics in New South Wales, Australia. BMC Research Notes, 2021, 14, 415.	1.4	4
20	Assessment of Inter-Laboratory Differences in SARS-CoV-2 Consensus Genome Assemblies between Public Health Laboratories in Australia. Viruses, 2022, 14, 185.	3.3	4
21	SARS-CoV-2 Within-Host and in vitro Genomic Variability and Sub-Genomic RNA Levels Indicate Differences in Viral Expression Between Clinical Cohorts and in vitro Culture. Frontiers in Microbiology, 2022, 13, .	3.5	4
22	Risk factors leading to COVID-19 cases in a Sydney restaurant. Australian and New Zealand Journal of Public Health, 2021, 45, 512-516.	1.8	3
23	Complete Genome Sequences, Derived by Next-Generation Sequencing, of JC Polyomavirus Strains Isolated from Vietnamese Renal Transplant Recipients. Microbiology Resource Announcements, 2020, 9, .	0.6	1
24	Deep Sequencing of Urine Specimens Detects Two BK Polyomavirus Genotypes in a Hematopoietic Stem Cell Transplant Recipient. Microbiology Resource Announcements, 2020, 9, .	0.6	0