

Chandler C Roe

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

897
citations

933447

10
h-index

940533

16
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18
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18
docs citations

18
times ranked

1226
citing authors

#	ARTICLE	IF	CITATIONS
1	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , 2016, 2, e000074.	2.0	237
2	Valley Fever: Finding New Places for an Old Disease: <i>Coccidioides immitis</i> Found in Washington State Soil Associated With Recent Human Infection. <i>Clinical Infectious Diseases</i> , 2015, 60, e1-e3.	5.8	153
3	<i>Cryptococcus gattii</i> in North American Pacific Northwest: Whole-Population Genome Analysis Provides Insights into Species Evolution and Dispersal. <i>MBio</i> , 2014, 5, e01464-14.	4.1	126
4	Update on the Epidemiology of coccidioidomycosis in the United States. <i>Medical Mycology</i> , 2019, 57, S30-S40.	0.7	104
5	Local Population Structure and Patterns of Western Hemisphere Dispersal for <i>Coccidioides</i> spp., the Fungal Cause of Valley Fever. <i>MBio</i> , 2016, 7, e00550-16.	4.1	71
6	Whole-Genome Analysis of <i>Exserohilum rostratum</i> from an Outbreak of Fungal Meningitis and Other Infections. <i>Journal of Clinical Microbiology</i> , 2014, 52, 3216-3222.	3.9	52
7	Genome Sequence of <i>Staphylococcus aureus</i> Strain CA-347, a USA600 Methicillin-Resistant Isolate. <i>Genome Announcements</i> , 2013, 1, .	0.8	40
8	Population Structure and Genetic Diversity among Isolates of <i>Coccidioides posadasii</i> in Venezuela and Surrounding Regions. <i>MBio</i> , 2019, 10, .	4.1	28
9	<i>Burkholderia pseudomallei</i> , the causative agent of melioidosis, is rare but ecologically established and widely dispersed in the environment in Puerto Rico. <i>PLoS Neglected Tropical Diseases</i> , 2019, 13, e0007727.	3.0	26
10	Coyotes as Reservoirs for <i>Onchocerca lupi</i> , United States, 2015–2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 2989-2993.	4.3	17
11	Identification of novel, cryptic <i>Clostridioides</i> species isolates from environmental samples collected from diverse geographical locations. <i>Microbial Genomics</i> , 2022, 8, .	2.0	11
12	Whole genome SNP typing to investigate methicillin-resistant <i>Staphylococcus aureus</i> carriage in a health-care provider as the source of multiple surgical site infections. <i>Hereditas</i> , 2016, 153, 11.	1.4	10
13	A global to local genomics analysis of <i>Clostridioides difficile</i> ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , 2019, 5, .	2.0	7
14	Complete mitochondrial genome of <i>Onchocerca lupi</i> (Nematoda, Onchocercidae). <i>Mitochondrial DNA Part B: Resources</i> , 2021, 6, 2572-2574.	0.4	6
15	Genomic analyses of <i>Staphylococcus aureus</i> clonal complex 45 isolates does not distinguish nasal carriage from bacteraemia. <i>Microbial Genomics</i> , 2020, 6, .	2.0	6
16	Multiple phylogenetically-diverse, differentially-virulent <i>Burkholderia pseudomallei</i> isolated from a single soil sample collected in Thailand. <i>PLoS Neglected Tropical Diseases</i> , 2022, 16, e0010172.	3.0	3