

Jason

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

36
papers

1,233
citations

15
h-index

35
g-index

37
ext. papers

1,733
ext. citations

5.8
avg, IF

3.83
L-index

#	Paper	IF	Citations
36	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	4.8	
35	A chromosomal-level reference genome of the widely utilized <i>Coccidioides posadasii</i> laboratory strain "Silveira".. <i>G3: Genes, Genomes, Genetics</i> , 2022 ,	3.2	1
34	Expanding the complex with the addition of two novel species: sp. nov. and sp. nov. <i>Applied and Environmental Microbiology</i> , 2021 , AEM0158321	4.8	2
33	<i>Burkholderia ubonensis</i> High-Level Tetracycline Resistance Is Due to Efflux Pump Synergy Involving a Novel TetA(64) Resistance Determinant. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65,	5.9	2
32	Reorganized Genomic Taxonomy of Enables Design of Robust Environmental PCR Assays for Detection of. <i>Microorganisms</i> , 2021 , 9,	4.9	7
31	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , 2021 , 65, e0092021	5.9	1
30	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year <i>Burkholderia pseudomallei</i> infection. <i>PLoS Pathogens</i> , 2020 , 16, e1008298	7.6	6
29	Evolutionary history and current distribution of the West Mediterranean lineage of in Italy. <i>Microbial Genomics</i> , 2020 , 6,	4.4	4
28	Selective whole genome amplification and sequencing of <i>Coxiella burnetii</i> directly from environmental samples. <i>Genomics</i> , 2020 , 112, 1872-1878	4.3	3
27	<i>Burkholderia pseudomallei</i> in Soil, US Virgin Islands, 2019. <i>Emerging Infectious Diseases</i> , 2020 , 26, 2773-2775	7.5	2
26	<i>Burkholderia ubonensis</i> Meropenem Resistance: Insights into Distinct Properties of Class A β -Lactamases in <i>Burkholderia cepacia</i> Complex and <i>Burkholderia pseudomallei</i> Complex Bacteria. <i>MBio</i> , 2020 , 11,	7.8	3
25	<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	4.8	16
24	Domestic canines do not display evidence of gut microbial dysbiosis in the presence of <i>Clostridioides (Clostridium) difficile</i> , despite cellular susceptibility to its toxins. <i>Anaerobe</i> , 2019 , 58, 53-72	2.8	13
23	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,	4.4	4
22	Population Structure and Genetic Diversity among Isolates of in Venezuela and Surrounding Regions. <i>MBio</i> , 2019 , 10,	7.8	8
21	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , 2018 , 101, 1920-1926	1.7	4
20	<i>Burkholderia humptydoensis</i> sp. nov., a New Species Related to <i>Burkholderia thailandensis</i> and the Fifth Member of the <i>Burkholderia pseudomallei</i> Complex. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	23

19	Differentiating Botulinum Neurotoxin-Producing Clostridia with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	15
18	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , 2016 , 7,	7.8	37
17	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing Clostridia. <i>BMC Genomics</i> , 2016 , 17, 180	4.5	56
16	Unprecedented Melioidosis Cases in Northern Australia Caused by an Asian Burkholderia pseudomallei Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 954-63	4.8	34
15	More than 50% of Clostridium difficile Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. <i>PLoS ONE</i> , 2016 , 11, e0164504	3.7	44
14	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	4.4	132
13	17 Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , 2016 , 26, 3407-3412	6.3	118
12	Draft Genome Sequence of the First Pathogenic Leptospira Isolates from Ecuador. <i>Genome Announcements</i> , 2016 , 4,		4
11	A Bacillus anthracis Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , 2016 , 7,	7.8	35
10	VNTR diversity in Yersinia pestis isolates from an animal challenge study reveals the potential for in vitro mutations during laboratory cultivation. <i>Infection, Genetics and Evolution</i> , 2016 , 45, 297-302	4.5	
9	Defining the phylogenomics of Shigella species: a pathway to diagnostics. <i>Journal of Clinical Microbiology</i> , 2015 , 53, 951-60	9.7	57
8	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , 2015 , 7, 52	14.4	32
7	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , 2015 , 6, 235	4.5	109
6	Genomic characterization of Burkholderia pseudomallei isolates selected for medical countermeasures testing: comparative genomics associated with differential virulence. <i>PLoS ONE</i> , 2015 , 10, e0121052	3.7	20
5	Diverse Burkholderia Species Isolated from Soils in the Southern United States with No Evidence of B. pseudomallei. <i>PLoS ONE</i> , 2015 , 10, e0143254	3.7	13
4	Whole-genome sequencing investigation of animal-skin-drum-associated UK anthrax cases reveals evidence of mixed populations and relatedness to a US case. <i>Microbial Genomics</i> , 2015 , 1, e000039	4.4	5
3	Yersinia pestis and the plague of Justinian 541-543 AD: a genomic analysis. <i>Lancet Infectious Diseases</i> , 2014 , 14, 319-26	25.5	263
2	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. <i>PeerJ</i> , 2014 , 2, e332	3.1	154

1 Genome Sequence of *Burkholderia pseudomallei* NCTC 13392. *Genome Announcements*, **2013**, 1,

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