

# Jason

## List of Publications by Citations

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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	<i>Yersinia pestis</i> and the plague of Justinian 541-543 AD: a genomic analysis. <i>Lancet Infectious Diseases, The</i> , <b>2014</b> , 14, 319-26	25.5	263
35	The large-scale blast score ratio (LS-BSR) pipeline: a method to rapidly compare genetic content between bacterial genomes. <i>PeerJ</i> , <b>2014</b> , 2, e332	3.1	154
34	NASP: an accurate, rapid method for the identification of SNPs in WGS datasets that supports flexible input and output formats. <i>Microbial Genomics</i> , <b>2016</b> , 2, e000074	4.4	132
33	17 Century Variola Virus Reveals the Recent History of Smallpox. <i>Current Biology</i> , <b>2016</b> , 26, 3407-3412	6.3	118
32	Best practices for evaluating single nucleotide variant calling methods for microbial genomics. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 235	4.5	109
31	Defining the phylogenomics of <i>Shigella</i> species: a pathway to diagnostics. <i>Journal of Clinical Microbiology</i> , <b>2015</b> , 53, 951-60	9.7	57
30	Comparative genomic analyses reveal broad diversity in botulinum-toxin-producing <i>Clostridia</i> . <i>BMC Genomics</i> , <b>2016</b> , 17, 180	4.5	56
29	More than 50% of <i>Clostridium difficile</i> Isolates from Pet Dogs in Flagstaff, USA, Carry Toxigenic Genotypes. <i>PLoS ONE</i> , <b>2016</b> , 11, e0164504	3.7	44
28	The Effects of Signal Erosion and Core Genome Reduction on the Identification of Diagnostic Markers. <i>MBio</i> , <b>2016</b> , 7,	7.8	37
27	A <i>Bacillus anthracis</i> Genome Sequence from the Sverdlovsk 1979 Autopsy Specimens. <i>MBio</i> , <b>2016</b> , 7,	7.8	35
26	Unprecedented <i>Melioidosis</i> Cases in Northern Australia Caused by an Asian <i>Burkholderia pseudomallei</i> Strain Identified by Using Large-Scale Comparative Genomics. <i>Applied and Environmental Microbiology</i> , <b>2016</b> , 82, 954-63	4.8	34
25	Phylogenetically typing bacterial strains from partial SNP genotypes observed from direct sequencing of clinical specimen metagenomic data. <i>Genome Medicine</i> , <b>2015</b> , 7, 52	14.4	32
24	<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> , <b>2017</b> , 83,	4.8	23
23	Genomic characterization of <i>Burkholderia pseudomallei</i> isolates selected for medical countermeasures testing: comparative genomics associated with differential virulence. <i>PLoS ONE</i> , <b>2015</b> , 10, e0121052	3.7	20
22	<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> , <b>2019</b> , 13, e0007727	4.8	16
21	Differentiating Botulinum Neurotoxin-Producing <i>Clostridia</i> with a Simple, Multiplex PCR Assay. <i>Applied and Environmental Microbiology</i> , <b>2017</b> , 83,	4.8	15
20	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> , <b>2019</b> , 58, 53-72	2.8	13

19	Diverse Burkholderia Species Isolated from Soils in the Southern United States with No Evidence of <i>B. pseudomallei</i> . <i>PLoS ONE</i> , <b>2015</b> , 10, e0143254	3.7	13
18	Population Structure and Genetic Diversity among Isolates of in Venezuela and Surrounding Regions. <i>MBio</i> , <b>2019</b> , 10,	7.8	8
17	Reorganized Genomic Taxonomy of Enables Design of Robust Environmental PCR Assays for Detection of. <i>Microorganisms</i> , <b>2021</b> , 9,	4.9	7
16	Pathogen to commensal? Longitudinal within-host population dynamics, evolution, and adaptation during a chronic >16-year Burkholderia pseudomallei infection. <i>PLoS Pathogens</i> , <b>2020</b> , 16, e1008298	7.6	6
15	Genome Sequence of Burkholderia pseudomallei NCTC 13392. <i>Genome Announcements</i> , <b>2013</b> , 1,		6
14	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> , <b>2015</b> , 1, e000039	4.4	5
13	A global to local genomics analysis of Clostridioides difficile ST1/RT027 identifies cryptic transmission events in a northern Arizona healthcare network. <i>Microbial Genomics</i> , <b>2019</b> , 5,	4.4	4
12	Evolutionary history and current distribution of the West Mediterranean lineage of in Italy. <i>Microbial Genomics</i> , <b>2020</b> , 6,	4.4	4
11	Draft Genome Sequence of the First Pathogenic Leptospira Isolates from Ecuador. <i>Genome Announcements</i> , <b>2016</b> , 4,		4
10	Developing Inclusivity and Exclusivity Panels for Testing Diagnostic and Detection Tools Targeting , the Causative Agent of Melioidosis. <i>Journal of AOAC INTERNATIONAL</i> , <b>2018</b> , 101, 1920-1926	1.7	4
9	Selective whole genome amplification and sequencing of Coxiella burnetii directly from environmental samples. <i>Genomics</i> , <b>2020</b> , 112, 1872-1878	4.3	3
8	Burkholderia ubonensis Meropenem Resistance: Insights into Distinct Properties of Class A $\beta$ -Lactamases in Burkholderia cepacia Complex and Burkholderia pseudomallei Complex Bacteria. <i>MBio</i> , <b>2020</b> , 11,	7.8	3
7	Expanding the complex with the addition of two novel species: sp. nov. and sp. nov. <i>Applied and Environmental Microbiology</i> , <b>2021</b> , AEM0158321	4.8	2
6	Burkholderia pseudomallei in Soil, US Virgin Islands, 2019. <i>Emerging Infectious Diseases</i> , <b>2020</b> , 26, 2773-2775		2
5	Burkholderia ubonensis High-Level Tetracycline Resistance Is Due to Efflux Pump Synergy Involving a Novel TetA(64) Resistance Determinant. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65,	5.9	2
4	A chromosomal-level reference genome of the widely utilized Coccidioides posadasii laboratory strain "Silveira".. <i>G3: Genes, Genomes, Genetics</i> , <b>2022</b> ,	3.2	1
3	Conservation of Resistance-Nodulation-Cell Division Efflux Pump-Mediated Antibiotic Resistance in Burkholderia cepacia Complex and Burkholderia pseudomallei Complex Species. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2021</b> , 65, e0092021	5.9	1
2	Multiple phylogenetically-diverse, differentially-virulent Burkholderia pseudomallei isolated from a single soil sample collected in Thailand.. <i>PLoS Neglected Tropical Diseases</i> , <b>2022</b> , 16, e0010172	4.8	

- 1 VNTR diversity in *Yersinia pestis* isolates from an animal challenge study reveals the potential for in vitro mutations during laboratory cultivation. *Infection, Genetics and Evolution*, **2016**, 45, 297-302 4.5