

# Jolene R Bowers

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

790  
citations

759233

12  
h-index

839539

18  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1334  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic Analysis of the Emergence and Rapid Global Dissemination of the Clonal Group 258 <i>Klebsiella pneumoniae</i> Pandemic. <i>PLoS ONE</i> , 2015, 10, e0133727.	2.5	195
2	Phylogeography of <i>Francisella tularensis</i> : Global Expansion of a Highly Fit Clone. <i>Journal of Bacteriology</i> , 2009, 191, 2474-2484.	2.2	176
3	KlebSeq, a Diagnostic Tool for Surveillance, Detection, and Monitoring of <i>Klebsiella pneumoniae</i> . <i>Journal of Clinical Microbiology</i> , 2016, 54, 2582-2596.	3.9	50
4	Dust Devil: The Life and Times of the Fungus That Causes Valley Fever. <i>PLoS Pathogens</i> , 2015, 11, e1004762.	4.7	49
5	Comparison of TaqMan PCR Assays for Detection of the Melioidosis Agent <i>Burkholderia pseudomallei</i> in Clinical Specimens. <i>Journal of Clinical Microbiology</i> , 2012, 50, 2059-2062.	3.9	44
6	Using Whole Genome Analysis to Examine Recombination across Diverse Sequence Types of <i>Staphylococcus aureus</i> . <i>PLoS ONE</i> , 2015, 10, e0130955.	2.5	40
7	BurkDiff: A Real-Time PCR Allelic Discrimination Assay for <i>Burkholderia Pseudomallei</i> and <i>B. mallei</i> . <i>PLoS ONE</i> , 2010, 5, e15413.	2.5	38
8	Improved Subtyping of <i>Staphylococcus aureus</i> Clonal Complex 8 Strains Based on Whole-Genome Phylogenetic Analysis. <i>MSphere</i> , 2018, 3, .	2.9	32
9	Dominance of multidrug resistant CC271 clones in macrolide-resistant streptococcus pneumoniae in Arizona. <i>BMC Microbiology</i> , 2012, 12, 12.	3.3	31
10	Towards a rapid molecular diagnostic for melioidosis: Comparison of DNA extraction methods from clinical specimens. <i>Journal of Microbiological Methods</i> , 2012, 88, 179-181.	1.6	26
11	The detection of <i>Coccidioides</i> from ambient air in Phoenix, Arizona: Evidence of uneven distribution and seasonality. <i>Medical Mycology</i> , 2020, 58, 552-559.	0.7	23
12	Coyotes as Reservoirs for <i>Onchocerca lupi</i> , United States, 2015–2018. <i>Emerging Infectious Diseases</i> , 2020, 26, 2989-2993.	4.3	17
13	Genomic Analyses of Acute Flaccid Myelitis Cases among a Cluster in Arizona Provide Further Evidence of Enterovirus D68 Role. <i>MBio</i> , 2019, 10, .	4.1	15
14	Genomic investigation of a household SARS-CoV-2 disease cluster in Arizona involving a cat, dog, and pet owner. <i>One Health</i> , 2021, 13, 100333.	3.4	15
15	<i>Rhizopus microsporus</i> Infections Associated with Surgical Procedures, Argentina, 2006–2014. <i>Emerging Infectious Diseases</i> , 2020, 26, 937-944.	4.3	11
16	Suspected Locally Acquired Coccidioidomycosis in Human, Spokane, Washington, USA. <i>Emerging Infectious Diseases</i> , 2020, 26, 606-609.	4.3	10
17	Normalization of SARS-CoV-2 viral load via RT-qPCR provides higher-resolution data for comparison across time and between patients. <i>Virus Research</i> , 2021, 306, 198604.	2.2	7
18	Sequencing the pandemic: rapid and high-throughput processing and analysis of COVID-19 clinical samples for 21st century public health. <i>F1000Research</i> , 2021, 10, 48.	1.6	6

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19	Methods for sequencing the pandemic: benefits of rapid or high-throughput processing. F1000Research, 0, 10, 48.	1.6	5