

James B Pettengill

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

1,208
citations

623734

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752698

20
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22
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22
docs citations

22
times ranked

1568
citing authors

#	ARTICLE	IF	CITATIONS
1	CFSAN SNP Pipeline: an automated method for constructing SNP matrices from next-generation sequence data. <i>PeerJ Computer Science</i> , 0, 1, e20.	4.5	254
2	Interpreting Whole-Genome Sequence Analyses of Foodborne Bacteria for Regulatory Applications and Outbreak Investigations. <i>Frontiers in Microbiology</i> , 2018, 9, 1482.	3.5	210
3	Phylogenetic Diversity of the Enteric Pathogen <i>Salmonella enterica</i> subsp. <i>enterica</i> Inferred from Genome-Wide Reference-Free SNP Characters. <i>Genome Biology and Evolution</i> , 2013, 5, 2109-2123.	2.5	139
4	Characterization and evolution of <i>Salmonella</i> CRISPR-Cas systems. <i>Microbiology (United Kingdom)</i> , 2015, 161, 374-386.	1.8	98
5	Cilantro microbiome before and after nonselective pre-enrichment for <i>Salmonella</i> using 16S rRNA and metagenomic sequencing. <i>BMC Microbiology</i> , 2015, 15, 160.	3.3	53
6	An evaluation of candidate plant DNA barcodes and assignment methods in diagnosing 29 species in the genus <i>Agalinis</i> (Orobanchaceae). <i>American Journal of Botany</i> , 2010, 97, 1391-1406.	1.7	52
7	TEMPO AND MODE OF MATING SYSTEM EVOLUTION BETWEEN INCIPIENT <i>CLARKIA</i> SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 2012, 66, 1210-1225.	2.3	50
8	Co-Enriching Microflora Associated with Culture Based Methods to Detect <i>Salmonella</i> from Tomato Phyllosphere. <i>PLoS ONE</i> , 2013, 8, e73079.	2.5	49
9	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with <i>Salmonella</i> . <i>PeerJ</i> , 2014, 2, e620.	2.0	45
10	Phylogeography of speciation: allopatric divergence and secondary contact between outcrossing and selfing <i>Clarkia</i> . <i>Molecular Ecology</i> , 2012, 21, 4578-4592.	3.9	43
11	The impact of systemic and copper pesticide applications on the phyllosphere microflora of tomatoes. <i>Journal of the Science of Food and Agriculture</i> , 2015, 95, 1116-1125.	3.5	40
12	Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. <i>BMC Research Notes</i> , 2012, 5, 378.	1.4	37
13	The evolutionary history and diagnostic utility of the CRISPR-Cas system within <i>Salmonella enterica</i> ssp. <i>enterica</i> . <i>PeerJ</i> , 2014, 2, e340.	2.0	31
14	Mating system divergence affects the distribution of sequence diversity within and among populations of recently diverged subspecies of <i>Clarkia xantiana</i> (Onagraceae). <i>American Journal of Botany</i> , 2016, 103, 99-109.	1.7	26
15	Within-species contamination of bacterial whole-genome sequence data has a greater influence on clustering analyses than between-species contamination. <i>Genome Biology</i> , 2019, 20, 286.	8.8	16
16	Temporal Dynamics of <i>Salmonella enterica</i> subsp. <i>enterica</i> Serovar <i>Agona</i> Isolates From a Recurrent Multistate Outbreak. <i>Frontiers in Microbiology</i> , 2020, 11, 478.	3.5	14
17	Phylogenetic patterns and conservation among North American members of the genus <i>Agalinis</i> (Orobanchaceae). <i>BMC Evolutionary Biology</i> , 2008, 8, 264.	3.2	13
18	Real-Time Pathogen Detection in the Era of Whole-Genome Sequencing and Big Data: Comparison of k-mer and Site-Based Methods for Inferring the Genetic Distances among Tens of Thousands of <i>Salmonella</i> Samples. <i>PLoS ONE</i> , 2016, 11, e0166162.	2.5	13

#	ARTICLE	IF	CITATIONS
19	Genomic evidence of environmental and resident Salmonella Senftenberg and Montevideo contamination in the pistachio supply-chain. PLoS ONE, 2021, 16, e0259471.	2.5	11
20	The Time to Most Recent Common Ancestor Does Not (Usually) Approximate the Date of Divergence. PLoS ONE, 2015, 10, e0128407.	2.5	7
21	Genomic analysis of Listeria monocytogenes from US food processing environments reveals a high prevalence of QAC efflux genes but limited evidence of their contribution to environmental persistence. BMC Genomics, 2022, 23, .	2.8	7