James B Pettengill

List of Publications by Year
in descending order

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21 papers	1,208 citations	623734 14 h-index	752698 20 g-index
22 all docs	22 docs citations	22 times ranked	1568 citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Genomic evidence of environmental and resident Salmonella Senftenberg and Montevideo contamination in the pistachio supply-chain. PLoS ONE, 2021, 16, e0259471.	2.5	11
3	Temporal Dynamics of Salmonella enterica subsp. enterica Serovar Agona Isolates From a Recurrent Multistate Outbreak. Frontiers in Microbiology, 2020, 11, 478.	3.5	14
4	Within-species contamination of bacterial whole-genome sequence data has a greater influence on clustering analyses than between-species contamination. Genome Biology, 2019, 20, 286.	8.8	16
5	Interpreting Whole-Genome Sequence Analyses of Foodborne Bacteria for Regulatory Applications and Outbreak Investigations. Frontiers in Microbiology, 2018, 9, 1482.	3.5	210
6	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 Salmonella Samples. PLoS ONE, 2016, 11, e0166162.	2.5	13
7	Mating system divergence affects the distribution of sequence diversity within and among populations of recently diverged subspecies of Clarkia xantiana (Onagraceae). American Journal of Botany, 2016, 103, 99-109.	1.7	26
8	The impact of systemic and copper pesticide applications on the phyllosphere microflora of tomatoes. Journal of the Science of Food and Agriculture, 2015, 95, 1116-1125.	3.5	40
9	Cilantro microbiome before and after nonselective pre-enrichment for Salmonella using 16S rRNA and metagenomic sequencing. BMC Microbiology, 2015, 15, 160.	3.3	53
10	Characterization and evolution of Salmonella CRISPR-Cas systems. Microbiology (United Kingdom), 2015, 161, 374-386.	1.8	98
11	The Time to Most Recent Common Ancestor Does Not (Usually) Approximate the Date of Divergence. PLoS ONE, 2015, 10, e0128407.	2.5	7
12	The evolutionary history and diagnostic utility of the CRISPR-Cas system within<i>Salmonella enterica</i>ssp.<i>enterica</i>. PeerJ, 2014, 2, e340.	2.0	31
13	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with<i>Salmonella</i>. PeerJ, 2014, 2, e620.	2.0	45
14	Phylogenetic Diversity of the Enteric Pathogen Salmonella enterica subsp. enterica Inferred from Genome-Wide Reference-Free SNP Characters. Genome Biology and Evolution, 2013, 5, 2109-2123.	2.5	139
15	Co-Enriching Microflora Associated with Culture Based Methods to Detect Salmonella from Tomato Phyllosphere. PLoS ONE, 2013, 8, e73079.	2.5	49
16	Using metagenomic analyses to estimate the consequences of enrichment bias for pathogen detection. BMC Research Notes, 2012, 5, 378.	1.4	37
17	Phylogeography of speciation: allopatric divergence and secondary contact between outcrossing and selfing <i>Clarkia</i>. Molecular Ecology, 2012, 21, 4578-4592.	3.9	43
18	TEMPO AND MODE OF MATING SYSTEM EVOLUTION BETWEEN INCIPIENT CLARKIA SPECIES. Evolution; International Journal of Organic Evolution, 2012, 66, 1210-1225.	2.3	50

#	ARTICLE	IF	CITATIONS
19	An evaluation of candidate plant DNA barcodes and assignment methods in diagnosing 29 species in the genus <i>Agalinis</i> (Orobanchaceae). American Journal of Botany, 2010, 97, 1391-1406.	1.7	52
20	Phylogenetic patterns and conservation among North American members of the genus Agalinis (Orobanchaceae). BMC Evolutionary Biology, 2008, 8, 264.	3.2	13
21	CFSAN SNP Pipeline: an automated method for constructing SNP matrices from next-generation sequence data. PeerJ Computer Science, 0, 1, e20.	4.5	254