

# Michael R Weigand

## List of Publications by Year in descending order

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28  
papers

868  
citations

566801

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552369

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docs citations

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times ranked

1229  
citing authors

#	ARTICLE	IF	CITATIONS
1	Widely Used Benzalkonium Chloride Disinfectants Can Promote Antibiotic Resistance. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	134
2	<i>Bordetella pertussis</i> Strain Lacking Pertactin and Pertussis Toxin. <i>Emerging Infectious Diseases</i> , 2016, 22, 319-322.	2.0	62
3	Microbial Community Degradation of Widely Used Quaternary Ammonium Disinfectants. <i>Applied and Environmental Microbiology</i> , 2014, 80, 5892-5900.	1.4	60
4	Quantifying the Importance of the Rare Biosphere for Microbial Community Response to Organic Pollutants in a Freshwater Ecosystem. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	60
5	The History of <i>Bordetella pertussis</i> Genome Evolution Includes Structural Rearrangement. <i>Journal of Bacteriology</i> , 2017, 199, .	1.0	59
6	Implications of Genome-Based Discrimination between <i>Clostridium botulinum</i> Group I and <i>Clostridium sporogenes</i> Strains for Bacterial Taxonomy. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5420-5429.	1.4	57
7	Metagenomics of Two Severe Foodborne Outbreaks Provides Diagnostic Signatures and Signs of Coinfection Not Attainable by Traditional Methods. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	54
8	The microbiology of mutability. <i>FEMS Microbiology Letters</i> , 2007, 277, 11-20.	0.7	53
9	Genome Structural Diversity among 31 <i>Bordetella pertussis</i> Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. <i>MSphere</i> , 2016, 1, .	1.3	51
10	Genomic and Transcriptomic Insights into How Bacteria Withstand High Concentrations of Benzalkonium Chloride Biocides. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	43
11	General and inducible hypermutation facilitate parallel adaptation in <i>Pseudomonas aeruginosa</i> despite divergent mutation spectra. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13680-13685.	3.3	33
12	Conserved Patterns of Symmetric Inversion in the Genome Evolution of <i>Bordetella</i> Respiratory Pathogens. <i>MSystems</i> , 2019, 4, .	1.7	30
13	Screening and Genomic Characterization of Filamentous Hemagglutinin-Deficient <i>Bordetella pertussis</i> . <i>Infection and Immunity</i> , 2018, 86, .	1.0	27
14	Genomic Survey of <i>Bordetella pertussis</i> Diversity, United States, 2000–2013. <i>Emerging Infectious Diseases</i> , 2018, 25, 780-783.	2.0	24
15	imGLAD: accurate detection and quantification of target organisms in metagenomes. <i>PeerJ</i> , 2018, 6, e5882.	0.9	24
16	Genome Sequencing Reveals the Environmental Origin of Enterococci and Potential Biomarkers for Water Quality Monitoring. <i>Environmental Science &amp; Technology</i> , 2014, 48, 3707-3714.	4.6	14
17	Genomic Surveillance and Improved Molecular Typing of <i>Bordetella pertussis</i> Using wgMLST. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	12
18	Long-Term Effects of Inducible Mutagenic DNA Repair on Relative Fitness and Phenotypic Diversification in <i>Pseudomonas cichorii</i> 302959. <i>Genetics</i> , 2009, 181, 199-208.	1.2	11

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19	Complete Genome Sequences of Four <i>Bordetella pertussis</i> Vaccine Reference Strains from Serum Institute of India. <i>Genome Announcements</i> , 2016, 4, .	0.8	10
20	Complete Genome Sequences of <i>Bordetella pertussis</i> Isolates with Novel Pertactin-Deficient Deletions. <i>Genome Announcements</i> , 2017, 5, .	0.8	10
21	Draft Genome Sequence of <i>Catellibacterium marimammalium</i> , a Novel Species Commonly Found in Gull Feces. <i>Genome Announcements</i> , 2013, 1, .	0.8	9
22	Genomic epidemiology of nontoxigenic <i>Corynebacterium diphtheriae</i> from King County, Washington State, USA between July 2018 and May 2019. <i>Microbial Genomics</i> , 2020, 6, .	1.0	9
23	Complete Genome Sequences of Four Different <i>Bordetella</i> sp. Isolates Causing Human Respiratory Infections. <i>Genome Announcements</i> , 2016, 4, .	0.8	7
24	Complete Genome Sequences of Two <i>Bordetella hinzii</i> Strains Isolated from Humans. <i>Genome Announcements</i> , 2015, 3, .	0.8	5
25	Complete Genome Sequences of <i>Bordetella pertussis</i> Vaccine Reference Strains 134 and 10536. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
26	Temporal patterns of <i>Bordetella pertussis</i> genome sequence and structural evolution. , 2018, , 144-165.		2
27	Growth Parameter Components of Adaptive Specificity during Experimental Evolution of the UVR-Inducible Mutator <i>Pseudomonas cichorii</i> 302959. <i>PLoS ONE</i> , 2011, 6, e15975.	1.1	1
28	Towards comprehensive understanding of bacterial genetic diversity: large-scale amplifications in <i>Bordetella pertussis</i> and <i>Mycobacterium tuberculosis</i> . <i>Microbial Genomics</i> , 2022, 8, .	1.0	0