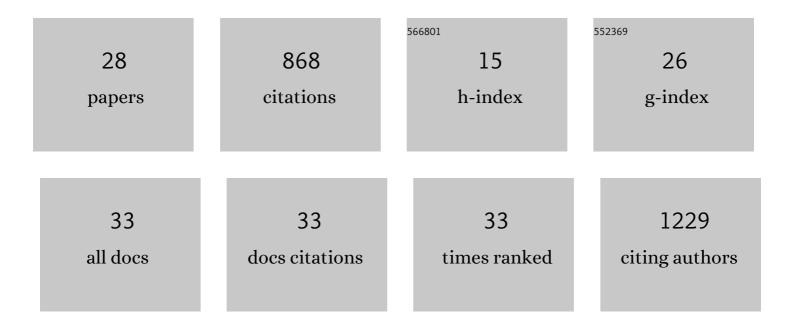
Michael R Weigand

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Widely Used Benzalkonium Chloride Disinfectants Can Promote Antibiotic Resistance. Applied and Environmental Microbiology, 2018, 84, .	1.4	134
2	<i>Bordetella pertussis</i> Strain Lacking Pertactin and Pertussis Toxin. Emerging Infectious Diseases, 2016, 22, 319-322.	2.0	62
3	Microbial Community Degradation of Widely Used Quaternary Ammonium Disinfectants. Applied and Environmental Microbiology, 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. Applied and Environmental Microbiology, 2017, 83, .	1.4	60
5	The History of Bordetella pertussis Genome Evolution Includes Structural Rearrangement. Journal of Bacteriology, 2017, 199, .	1.0	59
6	Implications of Genome-Based Discrimination between Clostridium botulinum Group I and Clostridium sporogenes Strains for Bacterial Taxonomy. Applied and Environmental Microbiology, 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. Applied and Environmental Microbiology, 2017, 83,	1.4	54
8	The microbiology of mutability. FEMS Microbiology Letters, 2007, 277, 11-20.	0.7	53
9	Genome Structural Diversity among 31 Bordetella pertussis Isolates from Two Recent U.S. Whooping Cough Statewide Epidemics. MSphere, 2016, 1, .	1.3	51
10	Genomic and Transcriptomic Insights into How Bacteria Withstand High Concentrations of Benzalkonium Chloride Biocides. Applied and Environmental Microbiology, 2018, 84, .	1.4	43
11	General and inducible hypermutation facilitate parallel adaptation in <i>Pseudomonas aeruginosa</i> despite divergent mutation spectra. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13680-13685.	3.3	33
12	Conserved Patterns of Symmetric Inversion in the Genome Evolution of <i>Bordetella</i> Respiratory Pathogens. MSystems, 2019, 4, .	1.7	30
13	Screening and Genomic Characterization of Filamentous Hemagglutinin-Deficient Bordetella pertussis. Infection and Immunity, 2018, 86, .	1.0	27
14	Genomic Survey of <i>Bordetella pertussis</i> Diversity, United States, 2000–2013. Emerging Infectious Diseases, 2018, 25, 780-783.	2.0	24
15	imGLAD: accurate detection and quantification of target organisms in metagenomes. PeerJ, 2018, 6, e5882.	0.9	24
16	Genome Sequencing Reveals the Environmental Origin of Enterococci and Potential Biomarkers for Water Quality Monitoring. Environmental Science & Technology, 2014, 48, 3707-3714.	4.6	14
17	Genomic Surveillance and Improved Molecular Typing of Bordetella pertussis Using wgMLST. Journal of Clinical Microbiology, 2021, 59, .	1.8	12
18	Long-Term Effects of Inducible Mutagenic DNA Repair on Relative Fitness and Phenotypic Diversification in Pseudomonas cichorii 302959. Genetics, 2009, 181, 199-208.	1.2	11

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