

# Janelle R Thompson

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

4,024  
citations

218677

26  
h-index

197818

49  
g-index

62  
all docs

62  
docs citations

62  
times ranked

5553  
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 Titers in Wastewater Are Higher than Expected from Clinically Confirmed Cases. <i>MSystems</i> , 2020, 5, .	3.8	649
2	Heteroduplexes in mixed-template amplifications: formation, consequence and elimination by 'reconditioning PCR'. <i>Nucleic Acids Research</i> , 2002, 30, 2083-2088.	14.5	409
3	Genotypic Diversity Within a Natural Coastal Bacterioplankton Population. <i>Science</i> , 2005, 307, 1311-1313.	12.6	331
4	Diversity and Dynamics of a North Atlantic Coastal <i>Vibrio</i> Community. <i>Applied and Environmental Microbiology</i> , 2004, 70, 4103-4110.	3.1	310
5	Microbes in the coral holobiont: partners through evolution, development, and ecological interactions. <i>Frontiers in Cellular and Infection Microbiology</i> , 2014, 4, 176.	3.9	223
6	Next-generation sequencing (NGS) for assessment of microbial water quality: current progress, challenges, and future opportunities. <i>Frontiers in Microbiology</i> , 2015, 6, 1027.	3.5	200
7	SARS-CoV-2 RNA concentrations in wastewater foreshadow dynamics and clinical presentation of new COVID-19 cases. <i>Science of the Total Environment</i> , 2022, 805, 150121.	8.0	192
8	Minimizing errors in RT-PCR detection and quantification of SARS-CoV-2 RNA for wastewater surveillance. <i>Science of the Total Environment</i> , 2022, 805, 149877.	8.0	153
9	Making waves: Wastewater surveillance of SARS-CoV-2 for population-based health management. <i>Water Research</i> , 2020, 184, 116181.	11.3	138
10	Wastewater surveillance of SARS-CoV-2 across 40 U.S. states from February to June 2020. <i>Water Research</i> , 2021, 202, 117400.	11.3	119
11	Secondary metabolite gene expression and interplay of bacterial functions in a tropical freshwater cyanobacterial bloom. <i>ISME Journal</i> , 2014, 8, 1866-1878.	9.8	93
12	Characterization of Metagenomes in Urban Aquatic Compartments Reveals High Prevalence of Clinically Relevant Antibiotic Resistance Genes in Wastewaters. <i>Frontiers in Microbiology</i> , 2017, 8, 2200.	3.5	87
13	Quantitative SARS-CoV-2 Alpha Variant B.1.1.7 Tracking in Wastewater by Allele-Specific RT-qPCR. <i>Environmental Science and Technology Letters</i> , 2021, 8, 675-682.	8.7	68
14	Metrics to relate COVID-19 wastewater data to clinical testing dynamics. <i>Water Research</i> , 2022, 212, 118070.	11.3	68
15	Dynamics of <i>Vibrio</i> Populations and Their Role in Environmental Nutrient Cycling. , 0, , 190-203.		55
16	Bacteroidales markers for microbial source tracking in Southeast Asia. <i>Water Research</i> , 2017, 118, 239-248.	11.3	48
17	Relationship of Microbiota and Cyanobacterial Secondary Metabolites in <i>Planktothricoides</i> -Dominated Bloom. <i>Environmental Science &amp; Technology</i> , 2017, 51, 4199-4209.	10.0	45
18	Microbial Growth under Supercritical CO <sub>2</sub> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 2881-2892.	3.1	44

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19	Distribution and abundance of human-specific <i>Bacteroides</i> and relation to traditional indicators in an urban tropical catchment. <i>Journal of Applied Microbiology</i> , 2014, 116, 1369-1383.	3.1	40
20	Extensive Variation in Intracellular Symbiont Community Composition among Members of a Single Population of the Wood-Boring Bivalve <i>Lyrodus pedicellatus</i> (Bivalvia: Teredinidae). <i>Applied and Environmental Microbiology</i> , 2006, 72, 412-417.	3.1	39
21	Sigma E Regulators Control Hemolytic Activity and Virulence in a Shrimp Pathogenic <i>Vibrio harveyi</i> . <i>PLoS ONE</i> , 2012, 7, e32523.	2.5	39
22	Engineered microbial biofuel production and recovery under supercritical carbon dioxide. <i>Nature Communications</i> , 2019, 10, 587.	12.8	39
23	Making waves: Wastewater surveillance of SARS-CoV-2 in an endemic future. <i>Water Research</i> , 2022, 219, 118535.	11.3	37
24	Microbial diversity and activity in the <i>Nematostella vectensis</i> holobiont: insights from 16S rRNA gene sequencing, isolate genomes, and a pilot-scale survey of gene expression. <i>Frontiers in Microbiology</i> , 2015, 6, 818.	3.5	33
25	Geospatial distribution of viromes in tropical freshwater ecosystems. <i>Water Research</i> , 2018, 137, 220-232.	11.3	33
26	Accurately quantifying low-abundant targets amid similar sequences by revealing hidden correlations in oligonucleotide microarray data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13629-13634.	7.1	32
27	A molecular and physiological survey of a diverse collection of hydrothermal vent <i>Thermococcus</i> and <i>Pyrococcus</i> isolates. <i>Extremophiles</i> , 2009, 13, 905-915.	2.3	32
28	Rapid displacement of SARS-CoV-2 variant Delta by Omicron revealed by allele-specific PCR in wastewater. <i>Water Research</i> , 2022, 221, 118809.	11.3	30
29	Shrimp pathogenicity, hemolysis, and the presence of hemolysin and TTSS genes in <i>Vibrio harveyi</i> isolated from Thailand. <i>Diseases of Aquatic Organisms</i> , 2009, 86, 113-122.	1.0	28
30	Gut Ruminococcaceae levels at baseline correlate with risk of antibiotic-associated diarrhea. <i>IScience</i> , 2022, 25, 103644.	4.1	28
31	Microbiota of the Major South Atlantic Reef Building Coral <i>Mussismilia</i> . <i>Microbial Ecology</i> , 2015, 69, 267-280.	2.8	26
32	Microbial potential for carbon and nutrient cycling in a geogenic supercritical carbon dioxide reservoir. <i>Environmental Microbiology</i> , 2017, 19, 2228-2245.	3.8	25
33	Diversity, Sources, and Detection of Human Bacterial Pathogens in the Marine Environment. , 2005, , 29-68.		22
34	Variably improved microbial source tracking with digital droplet PCR. <i>Water Research</i> , 2019, 159, 192-202.	11.3	22
35	<i>Vibrio campbellii</i> hmgA-mediated pyomelanization impairs quorum sensing, virulence, and cellular fitness. <i>Frontiers in Microbiology</i> , 2013, 4, 379.	3.5	21
36	Development of an efficient wastewater testing protocol for high-throughput country-wide SARS-CoV-2 monitoring. <i>Science of the Total Environment</i> , 2022, 826, 154024.	8.0	17

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37	Quantitative Detection of Active Vibrios Associated with White Plague Disease in <i>Mussismilia braziliensis</i> Corals. <i>Frontiers in Microbiology</i> , 2017, 8, 2272.	3.5	16
38	Complex Histories of Genes Encoding 3-Hydroxy-3-methylglutaryl-CoenzymeA Reductase. <i>Molecular Biology and Evolution</i> , 2006, 23, 168-178.	8.9	14
39	Coral mucus rapidly induces chemokinesis and genome-wide transcriptional shifts toward early pathogenesis in a bacterial coral pathogen. <i>ISME Journal</i> , 2021, 15, 3668-3682.	9.8	14
40	Extraction Rate and Energy Efficiency of Supercritical Carbon Dioxide Recovery of Higher Alcohols from Dilute Aqueous Solution. <i>Energy Technology</i> , 2018, 6, 683-693.	3.8	13
41	Variation of Bacterial Communities with Water Quality in an Urban Tropical Catchment. <i>Environmental Science &amp; Technology</i> , 2017, 51, 5591-5601.	10.0	11
42	Isolation, Development, and Genomic Analysis of <i>Bacillus megaterium</i> SR7 for Growth and Metabolite Production Under Supercritical Carbon Dioxide. <i>Frontiers in Microbiology</i> , 2018, 9, 2152.	3.5	9
43	Insights from the draft genome of the subsection V (Stigonematales) cyanobacterium <i>Hapalosiphon</i> sp. Strain MRB220 associated with 2-MIB production. <i>Standards in Genomic Sciences</i> , 2016, 11, 58.	1.5	8
44	Genomics insights into production of 2-methylisoborneol and a putative cyanobactin by <i>Planktothricoides</i> sp. SRO01. <i>Standards in Genomic Sciences</i> , 2017, 12, 35.	1.5	8
45	Insights on the genetic repertoire of the coral <i>Mussismilia braziliensis</i> endosymbiont <i>Symbiodinium</i> . <i>Symbiosis</i> , 2020, 80, 183-193.	2.3	7
46	Draft Genome Sequences of Supercritical CO <sub>2</sub> -Tolerant Bacteria <i>Bacillus subterraneus</i> MITOT1 and <i>Bacillus cereus</i> MIT0214. <i>Genome Announcements</i> , 2015, 3, .	0.8	4
47	Draft Genome Sequence of a Tropical Freshwater Cyanobacterium, <i>Limnothrix</i> sp. Strain P13C2. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
48	Draft Genome Sequence of <i>Cylindrospermopsis</i> sp. Strain CR12 Extracted from the Minimetagenome of a Nonaxenic Unialgal Culture from a Tropical Freshwater Lake. <i>Genome Announcements</i> , 2016, 4, .	0.8	3
49	Correction for Marcelino <i>et al.</i> , Accurately quantifying low-abundant targets amid similar sequences by revealing hidden correlations in oligonucleotide microarray data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 20045-20045.	7.1	2
50	Draft Genome Sequences of Two Benthic Cyanobacteria, <i>Oscillatoriales</i> USR 001 and <i>Nostoc</i> sp. MBR 210, Isolated from Tropical Freshwater Lakes. <i>Genome Announcements</i> , 2016, 4, .	0.8	1