

# Joanne B Emerson

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

5,987  
citations

172207

29  
h-index

214527

47  
g-index

62  
all docs

62  
docs citations

62  
times ranked

7579  
citing authors

#	ARTICLE	IF	CITATIONS
1	RNA Viral Communities Are Structured by Host Plant Phylogeny in Oak and Conifer Leaves. <i>Phytobiomes Journal</i> , 2023, 7, 288-296.	1.4	2
2	Solutions in microbiome engineering: prioritizing barriers to organism establishment. <i>ISME Journal</i> , 2022, 16, 331-338.	4.4	58
3	Soil pH influences the structure of virus communities at local and global scales. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108569.	4.2	17
4	Experimental evidence for the impact of soil viruses on carbon cycling during surface plant litter decomposition. <i>ISME Communications</i> , 2022, 2, .	1.7	26
5	Predators of Soil Bacteria in Plant and Human Health. <i>Phytobiomes Journal</i> , 2022, 6, 184-200.	1.4	7
6	Diversity in the soil virosphere: to infinity and beyond?. <i>Trends in Microbiology</i> , 2022, 30, 1025-1035.	3.5	35
7	Evidence for non- <i>ε</i> -methanogenic metabolisms in globally distributed archaeal clades basal to the <i>Methanomassiliicoccales</i> . <i>Environmental Microbiology</i> , 2021, 23, 340-357.	1.8	19
8	Ecology and Global Impacts of Viruses. , 2021, , 621-626.		0
9	Viromes outperform total metagenomes in revealing the spatiotemporal patterns of agricultural soil viral communities. <i>ISME Journal</i> , 2021, 15, 1956-1970.	4.4	101
10	Functional capacities of microbial communities to carry out large scale geochemical processes are maintained during ex situ anaerobic incubation. <i>PLoS ONE</i> , 2021, 16, e0245857.	1.1	11
11	DNase Treatment Improves Viral Enrichment in Agricultural Soil Viromes. <i>MSystems</i> , 2021, 6, e0061421.	1.7	12
12	Diverse sediment microbiota shape methane emission temperature sensitivity in Arctic lakes. <i>Nature Communications</i> , 2021, 12, 5815.	5.8	15
13	Minnesota peat viromes reveal terrestrial and aquatic niche partitioning for local and global viral populations. <i>Microbiome</i> , 2021, 9, 233.	4.9	53
14	Cauliflower mosaic virus (CaMV) Biology, Management, and Relevance to GM Plant Detection for Sustainable Organic Agriculture. <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	1.8	19
15	Soil Viruses: A New Hope. <i>MSystems</i> , 2019, 4, .	1.7	71
16	Multiplex quantitative PCR for single-reaction genetically modified (GM) plant detection and identification of false-positive GM plants linked to Cauliflower mosaic virus (CaMV) infection. <i>BMC Biotechnology</i> , 2019, 19, 73.	1.7	14
17	Minimum Information about an Uncultivated Virus Genome (MIUViG). <i>Nature Biotechnology</i> , 2019, 37, 29-37.	9.4	414
18	Differential depth distribution of microbial function and putative symbionts through sediment-hosted aquifers in the deep terrestrial subsurface. <i>Nature Microbiology</i> , 2018, 3, 328-336.	5.9	227

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19	Soil Viruses Are Underexplored Players in Ecosystem Carbon Processing. <i>MSystems</i> , 2018, 3, .	1.7	189
20	Seasonal Variability of Airborne Particulate Matter and Bacterial Concentrations in Colorado Homes. <i>Atmosphere</i> , 2018, 9, 133.	1.0	21
21	Genome-centric view of carbon processing in thawing permafrost. <i>Nature</i> , 2018, 560, 49-54.	13.7	337
22	Host-linked soil viral ecology along a permafrost thaw gradient. <i>Nature Microbiology</i> , 2018, 3, 870-880.	5.9	372
23	Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO <sub>2</sub> concentrations. <i>Environmental Microbiology</i> , 2017, 19, 459-474.	1.8	212
24	High temporal variability in airborne bacterial diversity and abundance inside single-family residences. <i>Indoor Air</i> , 2017, 27, 576-586.	2.0	24
25	Schrodinger's microbes: Tools for distinguishing the living from the dead in microbial ecosystems. <i>Microbiome</i> , 2017, 5, 86.	4.9	347
26	Putative archaeal viruses from the mesopelagic ocean. <i>PeerJ</i> , 2017, 5, e3428.	0.9	46
27	Benchmarking viromics: an <i>in silico</i> evaluation of metagenome-enabled estimates of viral community composition and diversity. <i>PeerJ</i> , 2017, 5, e3817.	0.9	235
28	Metagenomic analysis of a high carbon dioxide subsurface microbial community populated by chemolithoautotrophs and bacteria and archaea from candidate phyla. <i>Environmental Microbiology</i> , 2016, 18, 1686-1703.	1.8	78
29	<i>De Novo</i> Sequences of <i>Haloquadratum walsbyi</i> from Lake Tyrrell, Australia, Reveal a Variable Genomic Landscape. <i>Archaea</i> , 2015, 2015, 1-12.	2.3	26
30	Impacts of Flood Damage on Airborne Bacteria and Fungi in Homes after the 2013 Colorado Front Range Flood. <i>Environmental Science &amp; Technology</i> , 2015, 49, 2675-2684.	4.6	88
31	Metagenomic and lipid analyses reveal a diel cycle in a hypersaline microbial ecosystem. <i>ISME Journal</i> , 2015, 9, 2697-2711.	4.4	35
32	Biology of a widespread uncultivated archaeon that contributes to carbon fixation in the subsurface. <i>Nature Communications</i> , 2014, 5, 5497.	5.8	119
33	Seasonal fluctuations in ionic concentrations drive microbial succession in a hypersaline lake community. <i>ISME Journal</i> , 2014, 8, 979-990.	4.4	91
34	Utilizing novel diversity estimators to quantify multiple dimensions of microbial biodiversity across domains. <i>BMC Microbiology</i> , 2013, 13, 259.	1.3	9
35	Seasonal Variability in Bacterial and Fungal Diversity of the Near-Surface Atmosphere. <i>Environmental Science &amp; Technology</i> , 2013, 47, 12097-12106.	4.6	349
36	New Approaches Indicate Constant Viral Diversity despite Shifts in Assemblage Structure in an Australian Hypersaline Lake. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6755-6764.	1.4	37

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37	Characterization of eukaryotic microbial diversity in hypersaline Lake Tyrrell, Australia. <i>Frontiers in Microbiology</i> , 2013, 4, 115.	1.5	53
38	Virus-Host and CRISPR Dynamics in Archaea-Dominated Hypersaline Lake Tyrrell, Victoria, Australia. <i>Archaea</i> , 2013, 2013, 1-12.	2.3	82
39	Dynamic Viral Populations in Hypersaline Systems as Revealed by Metagenomic Assembly. <i>Applied and Environmental Microbiology</i> , 2012, 78, 6309-6320.	1.4	83
40	<i>De novo</i> metagenomic assembly reveals abundant novel major lineage of Archaea in hypersaline microbial communities. <i>ISME Journal</i> , 2012, 6, 81-93.	4.4	347
41	Bacterial diversity in the oral cavity of 10 healthy individuals. <i>ISME Journal</i> , 2010, 4, 962-974.	4.4	541
42	Gene-centric metagenomics of the fiber-adherent bovine rumen microbiome reveals forage specific glycoside hydrolases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 1948-1953.	3.3	669
43	Insights into Plant Cell Wall Degradation from the Genome Sequence of the Soil Bacterium <i>Cellvibrio japonicus</i> . <i>Journal of Bacteriology</i> , 2008, 190, 5455-5463.	1.0	159
44	Chromosome Evolution in the Thermotogales : Large-Scale Inversions and Strain Diversification of CRISPR Sequences. <i>Journal of Bacteriology</i> , 2006, 188, 2364-2374.	1.0	62
45	Secrets of Soil Survival Revealed by the Genome Sequence of <i>Arthrobacter aurescens</i> TC1. <i>PLoS Genetics</i> , 2006, 2, e214.	1.5	213