

# Jen Wood

## List of Publications by Year in descending order

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Version: 2024-02-01

33  
papers

929  
citations

567281

15  
h-index

501196

28  
g-index

35  
all docs

35  
docs citations

35  
times ranked

1225  
citing authors

#	ARTICLE	IF	CITATIONS
1	Biochar reduced extractable dieldrin concentrations and promoted oligotrophic growth including microbial degraders of chlorinated pollutants. <i>Journal of Hazardous Materials</i> , 2022, 423, 127156.	12.4	5
2	Elevated atmospheric CO <sub>2</sub> alters the microbial community composition and metabolic potential to mineralize organic phosphorus in the rhizosphere of wheat. <i>Microbiome</i> , 2022, 10, 12.	11.1	24
3	The role of decomposer communities in managing surface fuels: a neglected ecosystem service. <i>International Journal of Wildland Fire</i> , 2022, 31, 350-368.	2.4	6
4	From laboratory tests to field trials: a review of cathodic protection and microbially influenced corrosion. <i>Biofouling</i> , 2022, 38, 298-320.	2.2	15
5	Highly decomposed organic carbon mediates the assembly of soil communities with traits for the biodegradation of chlorinated pollutants. <i>Journal of Hazardous Materials</i> , 2021, 404, 124077.	12.4	11
6	Metabolic flexibility allows bacterial habitat generalists to become dominant in a frequently disturbed ecosystem. <i>ISME Journal</i> , 2021, 15, 2986-3004.	9.8	89
7	Rewilding with invertebrates and microbes to restore ecosystems: Present trends and future directions. <i>Ecology and Evolution</i> , 2021, 11, 7187-7200.	1.9	27
8	High Taxonomic Diversity in Ship Bilges Presents Challenges for Monitoring Microbial Corrosion and Opportunity To Utilize Community Functional Profiling. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0089021.	3.1	1
9	Town-scale microbial sewer community and H <sub>2</sub> S emissions response to common chemical and biological dosing treatments. <i>Journal of Environmental Sciences</i> , 2020, 87, 133-148.	6.1	8
10	Exercise improves metabolic function and alters the microbiome in rats with gestational diabetes. <i>FASEB Journal</i> , 2020, 34, 1728-1744.	0.5	19
11	Microbial communities associated with distance- and density-dependent seedling mortality in a tropical rainforest. <i>Plant Ecology</i> , 2020, 221, 41-54.	1.6	5
12	A pioneer calf foetus microbiome. <i>Scientific Reports</i> , 2020, 10, 17712.	3.3	34
13	Long-term CO <sub>2</sub> enrichment alters the diversity and function of the microbial community in soils with high organic carbon. <i>Soil Biology and Biochemistry</i> , 2020, 144, 107780.	8.8	33
14	Microbial communities in top- and subsoil of repacked soil columns respond differently to amendments but their diversity is negatively correlated with plant productivity. <i>Scientific Reports</i> , 2019, 9, 8890.	3.3	27
15	An efficient, cost-effective method for determining the growth rate of sulfate-reducing bacteria using spectrophotometry. <i>MethodsX</i> , 2019, 6, 2248-2257.	1.6	18
16	Gastrointestinal dysfunction in patients and mice expressing the autism-associated R451C mutation in neurologin. <i>Autism Research</i> , 2019, 12, 1043-1056.	3.8	63
17	Delving into the dark ecology: A continent-wide assessment of patterns of composition in soil fungal communities from Australian tussock grasslands. <i>Fungal Ecology</i> , 2019, 39, 356-370.	1.6	8
18	Competitive Traits Are More Important than Stress-Tolerance Traits in a Cadmium-Contaminated Rhizosphere: A Role for Trait Theory in Microbial Ecology. <i>Frontiers in Microbiology</i> , 2018, 9, 121.	3.5	60

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19	Understanding microbiomes through trait-based ecology. <i>Microbiology Australia</i> , 2018, 39, 53.	0.4	4
20	Linking microscopic interactions with macroscopic effects. <i>Journal of Vegetation Science</i> , 2017, 28, 462-463.	2.2	3
21	Draft Genome Sequence of <i>Leifsonia</i> sp. Strain NCR5, a Rhizobacterium Isolated from Cadmium-Contaminated Soil. <i>Genome Announcements</i> , 2017, 5, .	0.8	4
22	Draft Genome Sequence of <i>Rhodococcus erythropolis</i> NSX2, an Actinobacterium Isolated from a Cadmium-Contaminated Environment. <i>Genome Announcements</i> , 2016, 4, .	0.8	1
23	Draft Genome Sequence of <i>Enterobacter ludwigii</i> NCR3, a Heavy Metal-Resistant Rhizobacterium. <i>Genome Announcements</i> , 2016, 4, .	0.8	5
24	Long-term effects of elevated CO <sub>2</sub> on carbon and nitrogen functional capacity of microbial communities in three contrasting soils. <i>Soil Biology and Biochemistry</i> , 2016, 97, 157-167.	8.8	65
25	Microbial associated plant growth and heavy metal accumulation to improve phytoextraction of contaminated soils. <i>Soil Biology and Biochemistry</i> , 2016, 103, 131-137.	8.8	94
26	Microbial community dynamics in the rhizosphere of a cadmium hyper-accumulator. <i>Scientific Reports</i> , 2016, 6, 36067.	3.3	52
27	Draft Genome Sequence of <i>Bacillus cereus</i> LCR12, a Plant Growth-Promoting Rhizobacterium Isolated from a Heavy Metal-Contaminated Environment. <i>Genome Announcements</i> , 2016, 4, .	0.8	8
28	Characteristics of metal-tolerant plant growth-promoting yeast ( <i>Cryptococcus</i> sp. NSE1) and its influence on Cd hyperaccumulator <i>Sedum plumbizincicola</i> . <i>Environmental Science and Pollution Research</i> , 2016, 23, 18621-18629.	5.3	13
29	Microorganisms in heavy metal bioremediation: strategies for applying microbial-community engineering to remediate soils. <i>AIMS Bioengineering</i> , 2016, 3, 211-229.	1.1	38
30	Innovative biological approaches for monitoring and improving water quality. <i>Frontiers in Microbiology</i> , 2015, 6, 826.	3.5	29
31	Agp2p, the Plasma Membrane Transregulator of Polyamine Uptake, Regulates the Antifungal Activities of the Plant Defensin NaD1 and Other Cationic Peptides. <i>Antimicrobial Agents and Chemotherapy</i> , 2014, 58, 2688-2698.	3.2	38
32	Identification and Mechanism of Action of the Plant Defensin NaD1 as a New Member of the Antifungal Drug Arsenal against <i>Candida albicans</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 3667-3675.	3.2	104
33	Comparing the Gut Microbiome in Autism and Preclinical Models: A Systematic Review. <i>Frontiers in Cellular and Infection Microbiology</i> , 0, 12, .	3.9	16