

Adina C Howe

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

2,502
citations

393982

19
h-index

214527

47
g-index

55
all docs

55
docs citations

55
times ranked

4490
citing authors

#	ARTICLE	IF	CITATIONS
1	Frontiers and Opportunities in Bioenergy Crop Microbiome Research Networks. <i>Phytobiomes Journal</i> , 2022, 6, 118-126.	1.4	1
2	Denitrifying bioreactor microbiome: Understanding pollution swapping and potential for improved performance. <i>Journal of Environmental Quality</i> , 2022, 51, 1-18.	1.0	10
3	Prairie Strips Impact on Transport of Antimicrobial Resistance Indicators in Poultry Litter. <i>Journal of Environmental Quality</i> , 2022, , .	1.0	4
4	Response of Total (DNA) and Metabolically Active (RNA) Microbial Communities in <i>Miscanthus Æ— Giganteus</i> Cultivated Soil to Different Nitrogen Fertilization Rates. <i>Microbiology Spectrum</i> , 2022, 10, e0211621.	1.2	2
5	Diversity of Antibiotic Resistance genes and Transfer Elements-Quantitative Monitoring (DARTE-QM): a method for detection of antimicrobial resistance in environmental samples. <i>Communications Biology</i> , 2022, 5, 216.	2.0	7
6	The Human Health Implications of Antibiotic Resistance in Environmental Isolates from Two Nebraska Watersheds. <i>Microbiology Spectrum</i> , 2022, 10, e0208221.	1.2	4
7	Impact of flow on woodchip properties and subsidence in denitrifying bioreactors. , 2021, 4, e20149.		14
8	Niche differentiation of bacteria and fungi in carbon and nitrogen cycling of different habitats in a temperate coniferous forest: A metaproteomic approach. <i>Soil Biology and Biochemistry</i> , 2021, 155, 108170.	4.2	28
9	Land-Use System and Forest Floor Explain Prokaryotic Metacommunity Structuring and Spatial Turnover in Amazonian Forest-to-Pasture Conversion Areas. <i>Frontiers in Microbiology</i> , 2021, 12, 657508.	1.5	4
10	Microbial linkages to soil biogeochemical processes in a poorly drained agricultural ecosystem. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108228.	4.2	22
11	Identification and Evolution of Cas9 tracrRNAs. <i>CRISPR Journal</i> , 2021, 4, 438-447.	1.4	6
12	Antibiotic resistance gene dissipation in soil microcosms amended with antibiotics and swine manure. <i>Journal of Environmental Quality</i> , 2021, 50, 911-922.	1.0	6
13	Soil net nitrogen mineralization and leaching under <i>Miscanthus</i> and <i>giganteus</i> and <i>Zea mays</i> . <i>GCB Bioenergy</i> , 2021, 13, 1545-1560.	2.5	12
14	MetaFunPrimer: an Environment-Specific, High-Throughput Primer Design Tool for Improved Quantification of Target Genes. <i>MSystems</i> , 2021, 6, e0020121.	1.7	2
15	Antimicrobial resistance in integrated agroecosystems: State of the science and future opportunities. <i>Journal of Environmental Quality</i> , 2021, 50, 1255-1265.	1.0	5
16	The Impact of Stand Age and Fertilization on the Soil Microbiome of <i>Miscanthus Æ— giganteus</i> . <i>Phytobiomes Journal</i> , 2021, 5, 51-59.	1.4	22
17	Comparison of microbial communities in replicated woodchip bioreactors. <i>Journal of Environmental Quality</i> , 2021, , .	1.0	4
18	Improved detection of <i>mcyA</i> genes and their phylogenetic origins in harmful algal blooms. <i>Water Research</i> , 2020, 176, 115730.	5.3	13

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19	Changes on the intestinal bacterial community of white shrimp <i>Penaeus vannamei</i> fed with green seaweeds. <i>Journal of Applied Phycology</i> , 2020, 32, 2061-2070.	1.5	11
20	Seasonal variations in export of antibiotic resistance genes and bacteria in runoff from an agricultural watershed in Iowa. <i>Science of the Total Environment</i> , 2020, 738, 140224.	3.9	20
21	Catchment-scale export of antibiotic resistance genes and bacteria from an agricultural watershed in central Iowa. <i>PLoS ONE</i> , 2020, 15, e0227136.	1.1	9
22	Toward Antibiotic Stewardship: Route of Antibiotic Administration Impacts the Microbiota and Resistance Gene Diversity in Swine Feces. <i>Frontiers in Veterinary Science</i> , 2020, 7, 255.	0.9	26
23	An Improved Approach to Identify Bacterial Pathogens to Human in Environmental Metagenome. <i>Journal of Microbiology and Biotechnology</i> , 2020, 30, 1335-1342.	0.9	2
24	Characterizing the soil microbiome and quantifying antibiotic resistance gene dynamics in agricultural soil following swine CAFO manure application. <i>PLoS ONE</i> , 2019, 14, e0220770.	1.1	42
25	A meta-analysis of global fungal distribution reveals climate-driven patterns. <i>Nature Communications</i> , 2019, 10, 5142.	5.8	232
26	Investigating the dispersal of antibiotic resistance associated genes from manure application to soil and drainage waters in simulated agricultural farmland systems. <i>PLoS ONE</i> , 2019, 14, e0222470.	1.1	20
27	RefSoil+: a Reference Database for Genes and Traits of Soil Plasmids. <i>MSystems</i> , 2019, 4, .	1.7	16
28	Complexities in understanding antimicrobial resistance across domesticated animal, human, and environmental systems. <i>Annals of the New York Academy of Sciences</i> , 2019, 1441, 17-30.	1.8	112
29	Strategies for Building Computing Skills To Support Microbiome Analysis: a Five-Year Perspective from the EDAMAME Workshop. <i>MSystems</i> , 2019, 4, .	1.7	10
30	Practical implications of erythromycin resistance gene diversity on surveillance and monitoring of resistance. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	12
31	Narasin as a Manure Additive to Reduce Methane Production from Swine Manure. <i>Transactions of the ASABE</i> , 2018, 61, 943-953.	1.1	2
32	Temporal Dynamics of Bacterial Communities in Soil and Leachate Water After Swine Manure Application. <i>Frontiers in Microbiology</i> , 2018, 9, 3197.	1.5	30
33	Metagenomic Insights into the Degradation of Resistant Starch by Human Gut Microbiota. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	1.4	63
34	Primer set 2.0 for highly parallel qPCR array targeting antibiotic resistance genes and mobile genetic elements. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	95
35	The principles of tomorrow's university. <i>F1000Research</i> , 2018, 7, 1926.	0.8	6
36	Strategies to improve reference databases for soil microbiomes. <i>ISME Journal</i> , 2017, 11, 829-834.	4.4	106

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37	The In-Feed Antibiotic Carbadox Induces Phage Gene Transcription in the Swine Gut Microbiome. MBio, 2017, 8, .	1.8	37
38	Allelic Variation in Outer Membrane Protein A and Its Influence on Attachment of Escherichia coli to Corn Stover. Frontiers in Microbiology, 2017, 8, 708.	1.5	22
39	Imagining tomorrow's university in an era of open science. F1000Research, 2017, 6, 405.	0.8	9
40	Identification of Soil Microbes Capable of Utilizing Cellobiosan. PLoS ONE, 2016, 11, e0149336.	1.1	16
41	Identification of the Core Set of Carbon-Associated Genes in a Bioenergy Grassland Soil. PLoS ONE, 2016, 11, e0166578.	1.1	27
42	Microbial activity in forest soil reflects the changes in ecosystem properties between summer and winter. Environmental Microbiology, 2016, 18, 288-301.	1.8	321
43	Methodologies for probing the metatranscriptome of grassland soil. Journal of Microbiological Methods, 2016, 131, 122-129.	0.7	19
44	Divergent responses of viral and bacterial communities in the gut microbiome to dietary disturbances in mice. ISME Journal, 2016, 10, 1217-1227.	4.4	85
45	Challenges and opportunities in understanding microbial communities with metagenome assembly (accompanied by IPython Notebook tutorial). Frontiers in Microbiology, 2015, 6, 678.	1.5	28
46	The khmer software package: enabling efficient nucleotide sequence analysis. F1000Research, 2015, 4, 900.	0.8	362
47	Demonstrating microbial co-occurrence pattern analyses within and between ecosystems. Frontiers in Microbiology, 2014, 5, 358.	1.5	302
48	Metagenomic approaches for direct and cell culture evaluation of the virological quality of wastewater. Journal of Virological Methods, 2014, 210, 15-21.	1.0	72
49	Scaling metagenome sequence assembly with probabilistic de Bruijn graphs. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13272-13277.	3.3	219
50	Imagining tomorrow's university: open science and its impact. F1000Research, 0, 6, 405.	0.8	0