

Paula J Mouser

List of Publications by Year in descending order

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Version: 2024-02-01

51
papers

2,731
citations

201385

27
h-index

182168

51
g-index

54
all docs

54
docs citations

54
times ranked

3582
citing authors

#	ARTICLE	IF	CITATIONS
1	The fate and removal of pharmaceuticals and personal care products within wastewater treatment facilities discharging to the Great Bay Estuary. <i>Water Environment Research</i> , 2022, 94, e1680.	1.3	5
2	Toxicity of hydraulic fracturing wastewater from black shale natural-gas wells influenced by well maturity and chemical additives. <i>Environmental Sciences: Processes and Impacts</i> , 2021, 23, 621-632.	1.7	9
3	Distribution and fate of per- and polyfluoroalkyl substances (PFAS) in wastewater treatment facilities. <i>Environmental Sciences: Processes and Impacts</i> , 2021, 23, 903-913.	1.7	23
4	Comparative geochemistry of flowback chemistry from the Utica/Point Pleasant and Marcellus formations. <i>Chemical Geology</i> , 2021, 564, 120041.	1.4	11
5	Wastewater Surveillance for SARS-CoV-2 on College Campuses: Initial Efforts, Lessons Learned, and Research Needs. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 4455.	1.2	107
6	MetFish: a Metabolomics Pipeline for Studying Microbial Communities in Chemically Extreme Environments. <i>MSystems</i> , 2021, 6, e0105820.	1.7	5
7	Characterization of Antibiotic Resistance and Metal Homeostasis Genes in Midwest USA Agricultural Sediments. <i>Water (Switzerland)</i> , 2020, 12, 2476.	1.2	2
8	Seasonal changes predominant over manure application in driving dissolved organic matter shifts in agricultural runoff. <i>Journal of Great Lakes Research</i> , 2020, 46, 1570-1580.	0.8	6
9	Hydraulically Fractured Natural-Gas Well Microbial Communities Contain Genomic Halogenation and Dehalogenation Potential. <i>Environmental Science and Technology Letters</i> , 2019, 6, 585-591.	3.9	6
10	Degradation of polyethylene glycols and polypropylene glycols in microcosms simulating a spill of produced water in shallow groundwater. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 256-268.	1.7	27
11	Organic sulfur fingerprint indicates continued injection fluid signature 10 months after hydraulic fracturing. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 206-213.	1.7	4
12	Microbial lipid biomarkers detected in deep subsurface black shales. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 291-307.	1.7	2
13	In situ transformation of ethoxylate and glycol surfactants by shale-colonizing microorganisms during hydraulic fracturing. <i>ISME Journal</i> , 2019, 13, 2690-2700.	4.4	18
14	High total dissolved solids in shale gas wastewater inhibit biodegradation of alkyl and nonylphenol ethoxylate surfactants. <i>Science of the Total Environment</i> , 2019, 668, 1094-1103.	3.9	27
15	Deep-Subsurface Pressure Stimulates Metabolic Plasticity in Shale-Colonizing <i>Halanaerobium</i> spp. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	20
16	More than a decade of hydraulic fracturing and horizontal drilling research. <i>Environmental Sciences: Processes and Impacts</i> , 2019, 21, 193-194.	1.7	3
17	Genome-Resolved Metagenomics Extends the Environmental Distribution of the <i>Verrucomicrobia</i> Phylum to the Deep Terrestrial Subsurface. <i>MSphere</i> , 2019, 4, .	1.3	38
18	Viruses control dominant bacteria colonizing the terrestrial deep biosphere after hydraulic fracturing. <i>Nature Microbiology</i> , 2019, 4, 352-361.	5.9	78

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19	Temporal dynamics of halogenated organic compounds in Marcellus Shale flowback. <i>Water Research</i> , 2018, 136, 200-206.	5.3	31
20	Members of <i>Marinobacter</i> and <i>Arcobacter</i> Influence System Biogeochemistry During Early Production of Hydraulically Fractured Natural Gas Wells in the Appalachian Basin. <i>Frontiers in Microbiology</i> , 2018, 9, 2646.	1.5	33
21	Discrete Organic Phosphorus Signatures are Evident in Pollutant Sources within a Lake Erie Tributary. <i>Environmental Science & Technology</i> , 2018, 52, 6771-6779.	4.6	43
22	Coupled laboratory and field investigations resolve microbial interactions that underpin persistence in hydraulically fractured shales. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6585-E6594.	3.3	69
23	Draft Genome Sequences of <i>Marinobacter</i> Strains Recovered from Utica Shale-Produced Fluids. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
24	Draft Genome Sequences of Two Chemosynthetic <i>Arcobacter</i> Strains Isolated from Hydraulically Fractured Wells in Marcellus and Utica Shales. <i>Genome Announcements</i> , 2018, 6, .	0.8	5
25	Halogenated Organic Compounds Identified in Hydraulic Fracturing Wastewaters Using Ultrahigh Resolution Mass Spectrometry. <i>Environmental Science & Technology</i> , 2017, 51, 5377-5385.	4.6	71
26	Natural Attenuation of Nonionic Surfactants Used in Hydraulic Fracturing Fluids: Degradation Rates, Pathways, and Mechanisms. <i>Environmental Science & Technology</i> , 2017, 51, 13985-13994.	4.6	39
27	Sulfide Generation by Dominant <i>Halanaerobium</i> Microorganisms in Hydraulically Fractured Shales. <i>MSphere</i> , 2017, 2, .	1.3	62
28	Modified Lipid Extraction Methods for Deep Subsurface Shale. <i>Frontiers in Microbiology</i> , 2017, 8, 1408.	1.5	8
29	Redox Conditions Alter Biodegradation Rates and Microbial Community Dynamics of Hydraulic Fracturing Fluid Organic Additives in Soil-Groundwater Microcosms. <i>Environmental Engineering Science</i> , 2016, 33, 827-838.	0.8	28
30	Toxic cyanobacteria and drinking water: Impacts, detection, and treatment. <i>Harmful Algae</i> , 2016, 54, 174-193.	2.2	229
31	Hydraulic fracturing offers view of microbial life in the deep terrestrial subsurface. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw166.	1.3	96
32	Microbial metabolisms in a 2.5-km-deep ecosystem created by hydraulic fracturing in shales. <i>Nature Microbiology</i> , 2016, 1, 16146.	5.9	207
33	Aerobic biodegradation of organic compounds in hydraulic fracturing fluids. <i>Biodegradation</i> , 2015, 26, 271-287.	1.5	83
34	Temporal and Thermal Changes in Density and Viscosity of Marcellus Shale Produced Waters. <i>Journal of Environmental Engineering, ASCE</i> , 2015, 141, 06015006.	0.7	4
35	Piezoceramic membrane with built-in ultrasonic defouling. <i>Journal of Membrane Science</i> , 2015, 494, 130-135.	4.1	36
36	Variations in potential CH ₄ flux and CO ₂ respiration from freshwater wetland sediments that differ by microsite location, depth and temperature. <i>Ecological Engineering</i> , 2014, 72, 84-94.	1.6	19

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37	Trends and future challenges in sampling the deep terrestrial biosphere. <i>Frontiers in Microbiology</i> , 2014, 5, 481.	1.5	35
38	Geochemical and mineralogical investigation of uranium in multi-element contaminated, organic-rich subsurface sediment. <i>Applied Geochemistry</i> , 2014, 42, 77-85.	1.4	40
39	Temporal Changes in Microbial Ecology and Geochemistry in Produced Water from Hydraulically Fractured Marcellus Shale Gas Wells. <i>Environmental Science & Technology</i> , 2014, 48, 6508-6517.	4.6	244
40	Suggested Reporting Parameters for Investigations of Wastewater from Unconventional Shale Gas Extraction. <i>Environmental Science & Technology</i> , 2013, 47, 13220-13221.	4.6	24
41	Genome-scale dynamic modeling of the competition between <i>Rhodoferax</i> and <i>Geobacter</i> in anoxic subsurface environments. <i>ISME Journal</i> , 2011, 5, 305-316.	4.4	275
42	Expression of acetate permease-like (<i>aplA</i>) genes in subsurface communities of <i>Geobacter</i> species under fluctuating acetate concentrations. <i>FEMS Microbiology Ecology</i> , 2010, 73, no-no.	1.3	20
43	Molecular analysis of phosphate limitation in <i>Geobacteraceae</i> during the bioremediation of a uranium-contaminated aquifer. <i>ISME Journal</i> , 2010, 4, 253-266.	4.4	51
44	Genome Sequence of the Deltaproteobacterial Strain NaphS2 and Analysis of Differential Gene Expression during Anaerobic Growth on Naphthalene. <i>PLoS ONE</i> , 2010, 5, e14072.	1.1	90
45	Analysis of Biostimulated Microbial Communities from Two Field Experiments Reveals Temporal and Spatial Differences in Proteome Profiles. <i>Environmental Science & Technology</i> , 2010, 44, 8897-8903.	4.6	54
46	Quantifying expression of <i>Geobacter</i> spp. oxidative stress genes in pure culture and during <i>in situ</i> uranium bioremediation. <i>ISME Journal</i> , 2009, 3, 454-465.	4.4	45
47	Influence of Heterogeneous Ammonium Availability on Bacterial Community Structure and the Expression of Nitrogen Fixation and Ammonium Transporter Genes during <i>in situ</i> Bioremediation of Uranium-Contaminated Groundwater. <i>Environmental Science & Technology</i> , 2009, 43, 4386-4392.	4.6	88
48	Proteogenomic Monitoring of <i>Geobacter</i> Physiology during Stimulated Uranium Bioremediation. <i>Applied and Environmental Microbiology</i> , 2009, 75, 6591-6599.	1.4	136
49	Comparison of Bacterial Communities in New England Sphagnum Bogs Using Terminal Restriction Fragment Length Polymorphism (T-RFLP). <i>Microbial Ecology</i> , 2006, 52, 34-44.	1.4	64
50	Hydrology and Geostatistics of a Vermont, USA Kettlehole Peatland. <i>Journal of Hydrology</i> , 2005, 301, 250-266.	2.3	25
51	A Multivariate Statistical Approach to Spatial Representation of Groundwater Contamination using Hydrochemistry and Microbial Community Profiles. <i>Environmental Science & Technology</i> , 2005, 39, 7551-7559.	4.6	65