Cresten B Mansfeldt

List of Publications by Year in descending order

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623188 794141 14 19 530 19 citations g-index h-index papers 21 21 21 704 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Passive sampling to scale wastewater surveillance of infectious disease: Lessons learned from COVID-19. Science of the Total Environment, 2022, 835, 155347.	3.9	31
2	Standardizing data reporting in the research community to enhance the utility of open data for SARS-CoV-2 wastewater surveillance. Environmental Science: Water Research and Technology, 2021, 7, 1545-1551.	1.2	34
3	High-resolution within-sewer SARS-CoV-2 surveillance facilitates informed intervention. Water Research, 2021, 204, 117613.	5.3	38
4	Relating Metatranscriptomic Profiles to the Micropollutant Biotransformation Potential of Complex Microbial Communities. Environmental Science & Environmental Science & 2020, 54, 235-244.	4.6	29
5	Microbial community shifts in streams receiving treated wastewater effluent. Science of the Total Environment, 2020, 709, 135727.	3.9	52
6	Detection of Organohalide-Respiring Enzyme Biomarkers at a Bioaugmented TCE-Contaminated Field Site. Frontiers in Microbiology, 2019, 10, 1433.	1.5	10
7	Microbial residence time is a controlling parameter of the taxonomic composition and functional profile of microbial communities. ISME Journal, 2019, 13, 1589-1601.	4.4	24
8	Biotransformation of Sulfonamide Antibiotics in Activated Sludge: The Formation of Pterin-Conjugates Leads to Sustained Risk. Environmental Science & Enp; Technology, 2018, 52, 6265-6274.	4.6	101
9	Trends in Micropollutant Biotransformation along a Solids Retention Time Gradient. Environmental Science & Environmental Scien	4.6	22
10	Altered Microbiome Leads to Significant Phenotypic and Transcriptomic Differences in a Lipid Accumulating Chlorophyte. Environmental Science & Environ	4.6	18
11	Biomarkers' Responses to Reductive Dechlorination Rates and Oxygen Stress in Bioaugmentation Culture KB-1TM. Microorganisms, 2018, 6, 13.	1.6	26
12	Inferring Gene Networks for Strains of Dehalococcoides Highlights Conserved Relationships between Genes Encoding Core Catabolic and Cell-Wall Structural Proteins. PLoS ONE, 2016, 11, e0166234.	1.1	4
13	Use of De Novo Transcriptome Libraries to Characterize a Novel Oleaginous Marine Chlorella Species during the Accumulation of Triacylglycerols. PLoS ONE, 2016, 11, e0147527.	1.1	16
14	SPINE: SParse elgengene NEtwork Linking Gene Expression Clusters in Dehalococcoides mccartyi to Perturbations in Experimental Conditions. PLoS ONE, 2015, 10, e0118404.	1.1	3
15	Relating mRNA and protein biomarker levels in a Dehalococcoides and Methanospirillum-containing community. Applied Microbiology and Biotechnology, 2015, 99, 2313-2327.	1.7	16
16	Meta-Analyses of Dehalococcoides mccartyi Strain 195 Transcriptomic Profiles Identify a Respiration Rate-Related Gene Expression Transition Point and Interoperon Recruitment of a Key Oxidoreductase Subunit. Applied and Environmental Microbiology, 2014, 80, 6062-6072.	1.4	32
17	Molecular Biomarker-Based Biokinetic Modeling of a PCE-Dechlorinating and Methanogenic Mixed Culture. Environmental Science &	4.6	19
18	<i>Methanospirillum</i> Respiratory mRNA Biomarkers Correlate with Hydrogenotrophic Methanogenesis Rate during Growth and Competition for Hydrogen in an Organochlorine-Respiring Mixed Culture. Environmental Science & Envir	4.6	8

#	Article	IF	CITATIONS
19	Relating Chloroethene Respiration Rates in <i>Dehalococcoides</i> to Protein and mRNA Biomarkers. Environmental Science & Envi	4.6	41