

Karuna Chourey

List of Publications by Year in descending order

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35
papers

2,228
citations

279798

23
h-index

361022

35
g-index

35
all docs

35
docs citations

35
times ranked

3468
citing authors

#	ARTICLE	IF	CITATIONS
1	Respiratory Vinyl Chloride Reductive Dechlorination to Ethene in TceA-Expressing <i>Dehalococcoides mccartyi</i> . Environmental Science & Technology, 2021, 55, 4831-4841.	10.0	34
2	Targeted detection of <i>Dehalococcoides mccartyi</i> microbial protein biomarkers as indicators of reductive dechlorination activity in contaminated groundwater. Scientific Reports, 2019, 9, 10604.	3.3	8
3	Impact of Fixed Nitrogen Availability on <i>Dehalococcoides mccartyi</i> Reductive Dechlorination Activity. Environmental Science & Technology, 2019, 53, 14548-14558.	10.0	17
4	Comparing DNA, RNA and protein levels for measuring microbial dynamics in soil microcosms amended with nitrogen fertilizer. Scientific Reports, 2019, 9, 17630.	3.3	18
5	Proteogenomics Reveals Novel Reductive Dehalogenases and Methyltransferases Expressed during Anaerobic Dichloromethane Metabolism. Applied and Environmental Microbiology, 2019, 85, .	3.1	21
6	Characterization of Indole-3-acetic Acid Biosynthesis and the Effects of This Phytohormone on the Proteome of the Plant-Associated Microbe <i>Pantoea</i> sp. YR343. Journal of Proteome Research, 2018, 17, 1361-1374.	3.7	28
7	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. Frontiers in Microbiology, 2018, 9, 2917.	3.5	33
8	Utilization of a Detergent-Based Method for Direct Microbial Cellular Lysis/Proteome Extraction from Soil Samples for Metaproteomics Studies. Methods in Molecular Biology, 2018, 1841, 293-302.	0.9	5
9	The protein and neutral lipid composition of lipid droplets isolated from the fission yeast, <i>Schizosaccharomyces pombe</i> . Journal of Microbiology, 2017, 55, 112-122.	2.8	17
10	Mechanisms of subzero growth in the cryophile <i>Planococcus halocryophilus</i> determined through proteomic analysis. Environmental Microbiology, 2017, 19, 4460-4479.	3.8	25
11	Methane-Fueled Syntrophy through Extracellular Electron Transfer: Uncovering the Genomic Traits Conserved within Diverse Bacterial Partners of Anaerobic Methanotrophic Archaea. MBio, 2017, 8, .	4.1	62
12	Grape pomace compost harbors organohalide-respiring <i>Dehalogenimonas</i> species with novel reductive dehalogenase genes. ISME Journal, 2017, 11, 2767-2780.	9.8	118
13	Proteomic Stable Isotope Probing Reveals Biosynthesis Dynamics of Slow Growing Methane Based Microbial Communities. Frontiers in Microbiology, 2016, 7, 563.	3.5	34
14	Reconstructing a hydrogen-driven microbial metabolic network in Opalinus Clay rock. Nature Communications, 2016, 7, 12770.	12.8	120
15	Metabolic Regulation as a Consequence of Anaerobic 5-Methylthioadenosine Recycling in <i>Rhodospirillum rubrum</i> . MBio, 2016, 7, .	4.1	15
16	Geochemical, metagenomic and metaproteomic insights into trace metal utilization by methane-oxidizing microbial consortia in sulphidic marine sediments. Environmental Microbiology, 2014, 16, 1592-1611.	3.8	47
17	Strigolactone-Regulated Proteins Revealed by iTRAQ-Based Quantitative Proteomics in <i>Arabidopsis</i> . Journal of Proteome Research, 2014, 13, 1359-1372.	3.7	24
18	Insights into the Structure and Metabolic Function of Microbes That Shape Pelagic Iron-Rich Aggregates (Iron Snow). Applied and Environmental Microbiology, 2013, 79, 4272-4281.	3.1	60

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19	Environmental proteomics reveals early microbial community responses to biostimulation at a uranium- and nitrate- contaminated site. <i>Proteomics</i> , 2013, 13, 2921-2930.	2.2	71
20	Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. <i>ISME Journal</i> , 2013, 7, 800-816.	9.8	98
21	<i>Metaproteomics</i> : Harnessing the Power of High Performance Mass Spectrometry to Identify the Suite of Proteins That Control Metabolic Activities in Microbial Communities. <i>Analytical Chemistry</i> , 2013, 85, 4203-4214.	6.5	165
22	Systematic Comparison of Label-Free, Metabolic Labeling, and Isobaric Chemical Labeling for Quantitative Proteomics on LTQ Orbitrap Velos. <i>Journal of Proteome Research</i> , 2012, 11, 1582-1590.	3.7	301
23	Comparative <i>c</i> -type cytochrome expression analysis in <i>Shewanella oneidensis</i> strain MR-1 and <i>Anaeromyxobacter dehalogenans</i> strain 2CP-C grown with soluble and insoluble oxidized metal electron acceptors. <i>Biochemical Society Transactions</i> , 2012, 40, 1204-1210.	3.4	19
24	Microbial metaproteomics: identifying the repertoire of proteins that microorganisms use to compete and cooperate in complex environmental communities. <i>Current Opinion in Microbiology</i> , 2012, 15, 373-380.	5.1	83
25	Coupling a Detergent Lysis/Cleanup Methodology with Intact Protein Fractionation for Enhanced Proteome Characterization. <i>Journal of Proteome Research</i> , 2012, 11, 6008-6018.	3.7	76
26	Direct Cellular Lysis/Protein Extraction Protocol for Soil Metaproteomics. <i>Journal of Proteome Research</i> , 2010, 9, 6615-6622.	3.7	193
27	Proteomics reveals a core molecular response of <i>Pseudomonas putida</i> F1 to acute chromate challenge. <i>BMC Genomics</i> , 2010, 11, 311.	2.8	55
28	Comparative Temporal Proteomics of a Response Regulator (SO2426)-Deficient Strain and Wild-Type <i>Shewanella oneidensis</i> MR-1 During Chromate Transformation. <i>Journal of Proteome Research</i> , 2009, 8, 59-71.	3.7	19
29	Transcriptome analysis reveals response regulator SO2426-mediated gene expression in <i>Shewanella oneidensis</i> MR-1 under chromate challenge. <i>BMC Genomics</i> , 2008, 9, 395.	2.8	24
30	Experimental Approach for Deep Proteome Measurements from Small-Scale Microbial Biomass Samples. <i>Analytical Chemistry</i> , 2008, 80, 9517-9525.	6.5	30
31	Dosage-Dependent Proteome Response of <i>Shewanella oneidensis</i> MR-1 to Acute Chromate Challenge. <i>Journal of Proteome Research</i> , 2007, 6, 1745-1757.	3.7	60
32	Molecular Dynamics of the <i>Shewanella oneidensis</i> Response to Chromate Stress. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1054-1071.	3.8	158
33	Global Molecular and Morphological Effects of 24-Hour Chromium(VI) Exposure on <i>Shewanella oneidensis</i> MR-1. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6331-6344.	3.1	96
34	Cellular Response of <i>Shewanella oneidensis</i> to Strontium Stress. <i>Applied and Environmental Microbiology</i> , 2006, 72, 890-900.	3.1	44
35	Accumulation of LEA proteins in salt (NaCl) stressed young seedlings of rice (<i>Oryza sativa</i> L.) cultivar Bura Rata and their degradation during recovery from salinity stress. <i>Journal of Plant Physiology</i> , 2003, 160, 1165-1174.	3.5	50