

# Terry C Hazen

## List of Publications by Year in descending order

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268  
papers

17,957  
citations

14655

66  
h-index

16650

123  
g-index

307  
all docs

307  
docs citations

307  
times ranked

15463  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sustained Ability of a Natural Microbial Community to Remove Nitrate from Groundwater. <i>Ground Water</i> , 2022, 60, 99-111.	1.3	6
2	Identification of Propionate-Degrading Microbial Populations in Methanogenic Processes for Waste Treatment: <i>Methanosaeta</i> and <i>Methanoculleus</i> . <i>Environmental Engineering Science</i> , 2022, 39, 202-211.	1.6	6
3	Effects of Cone Penetrometer Testing on Shallow Hydrogeology at a Contaminated Site. <i>Frontiers in Environmental Science</i> , 2022, 9, .	3.3	1
4	Genomic Features and Pervasive Negative Selection in <i>Rhodanobacter</i> Strains Isolated from Nitrate and Heavy Metal Contaminated Aquifer. <i>Microbiology Spectrum</i> , 2022, 10, e0259121.	3.0	8
5	Omics of oil biodegradation. <i>Current Opinion in Chemical Engineering</i> , 2022, 36, 100800.	7.8	9
6	Complete Genome Sequence of <i>Bacillus cereus</i> Strain CPT56D-587-MTF, Isolated from a Nitrate- and Metal-Contaminated Subsurface Environment. <i>Microbiology Resource Announcements</i> , 2022, 11, e0014522.	0.6	1
7	Large-Data Omics Approaches in Modern Remediation. <i>Journal of Environmental Engineering, ASCE</i> , 2022, 148, .	1.4	0
8	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
9	Mechanism Across Scales: A Holistic Modeling Framework Integrating Laboratory and Field Studies for Microbial Ecology. <i>Frontiers in Microbiology</i> , 2021, 12, 642422.	3.5	12
10	Evaluating the Impact of Hydraulic Fracturing on Streams using Microbial Molecular Signatures. <i>Journal of Visualized Experiments</i> , 2021, , .	0.3	0
11	Comparative study of the effects of biocides and metal oxide nanoparticles on microbial community structure in a stream impacted by hydraulic fracturing. <i>Chemosphere</i> , 2021, 284, 131255.	8.2	5
12	Coding-Complete Genome Sequence of a SARS-CoV-2 Variant Obtained from Raw Sewage at the University of Tennessee's Knoxville Campus. <i>Microbiology Resource Announcements</i> , 2021, 10, e0104921.	0.6	3
13	Microbial Communities across Global Marine Basins Show Important Compositional Similarities by Depth. <i>MBio</i> , 2020, 11, .	4.1	18
14	Performance and community structure dynamics of microbial electrolysis cells operated on multiple complex feedstocks. <i>Biotechnology for Biofuels</i> , 2020, 13, 169.	6.2	7
15	Patterns in extracellular enzyme activity and microbial diversity in deep-sea Mediterranean sediments. <i>Deep-Sea Research Part I: Oceanographic Research Papers</i> , 2020, 158, 103231.	1.4	9
16	Characterization of a Metal-Resistant <i>Bacillus</i> Strain With a High Molybdate Affinity ModA From Contaminated Sediments at the Oak Ridge Reservation. <i>Frontiers in Microbiology</i> , 2020, 11, 587127.	3.5	11
17	Draft Genome Sequence of <i>Bacillus</i> sp. Strain EB106-08-02-XG196, Isolated from High-Nitrate-Contaminated Sediment. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0
18	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. <i>Microbiome</i> , 2020, 8, 51.	11.1	205

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19	Characterization of subsurface media from locations up- and down-gradient of a uranium-contaminated aquifer. <i>Chemosphere</i> , 2020, 255, 126951.	8.2	18
20	In-field bioreactors demonstrate dynamic shifts in microbial communities in response to geochemical perturbations. <i>PLoS ONE</i> , 2020, 15, e0232437.	2.5	5
21	Applying Stable Isotopes for Source Fingerprinting of Dissolved Organic Nitrogen in Groundwater. , 2020, , .		0
22	Lessons from the 2010 Deepwater Horizon Accident in the Gulf of Mexico. , 2020, , 847-864.		3
23	In Situ Bioremediation via Horizontal Wells. , 2020, , 79-86.		0
24	In Situ Bioremediation via Horizontal Wells. , 2020, , 79-86.		0
25	Improved Method for Estimating Reaction Rates During Push&#x2013;Pull Tests. <i>Ground Water</i> , 2019, 57, 292-302.	1.3	8
26	Oil Biodegradation in Deep Marine Basins. , 2019, , 71-88.		1
27	High spatiotemporal variability of bacterial diversity over short time scales with unique hydrochemical associations within a shallow aquifer. <i>Water Research</i> , 2019, 164, 114917.	11.3	23
28	Unconventional Oil and Gas Energy Systems: An Unidentified Hotspot of Antimicrobial Resistance?. <i>Frontiers in Microbiology</i> , 2019, 10, 2392.	3.5	7
29	Surface Water Microbial Community Response to the Biocide 2,2-Dibromo-3-Nitrilopropionamide, Used in Unconventional Oil and Gas Extraction. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	12
30	Probing the active fraction of soil microbiomes using BONCAT-FACS. <i>Nature Communications</i> , 2019, 10, 2770.	12.8	93
31	Oil Hydrocarbon Degradation by Caspian Sea Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 995.	3.5	29
32	Large Circular Plasmids from Groundwater Plasmidomes Span Multiple Incompatibility Groups and Are Enriched in Multimetal Resistance Genes. <i>MBio</i> , 2019, 10, .	4.1	42
33	Environmental Systems Biology Approach to Bioremediation. <i>Advances in Environmental Microbiology</i> , 2019, , 103-127.	0.3	1
34	Phosphate addition increases tropical forest soil respiration primarily by deconstraining microbial population growth. <i>Soil Biology and Biochemistry</i> , 2019, 130, 43-54.	8.8	26
35	Iron&#x2013;and aluminium&#x2013;induced depletion of molybdenum in acidic environments impedes the nitrogen cycle. <i>Environmental Microbiology</i> , 2019, 21, 152-163.	3.8	22
36	TEN-YEAR INVESTIGATION OF THE SUBSURFACE MICROBIOME IN A VARIABLY SATURATED CONTAMINANT PATHWAY WITH TWO CARBON-AMENDMENTS. , 2019, , .		0

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37	In Situ Groundwater Bioremediation. , 2019, , 197-214.		0
38	Cometabolic Bioremediation. , 2019, , 233-247.		0
39	MODELING DYNAMIC GEOCHEMICAL PROCESSES: HOW WATER TABLE FLUCTUATIONS INFLUENCE REDOX CONDITIONS IN THE PRESENCE OF CONTAMINATION. , 2019, , .		0
40	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. MBio, 2018, 9, .	4.1	57
41	Impacts of Glutaraldehyde on Microbial Community Structure and Degradation Potential in Streams Impacted by Hydraulic Fracturing. Environmental Science & Technology, 2018, 52, 5989-5999.	10.0	35
42	Oil Biodegradation in Deep Marine Basins. , 2018, , 1-18.		0
43	Response of Aquatic Bacterial Communities to Hydraulic Fracturing in Northwestern Pennsylvania: A Five-Year Study. Scientific Reports, 2018, 8, 5683.	3.3	29
44	New Insights into the Function and Global Distribution of Polyethylene Terephthalate (PET)-Degrading Bacteria and Enzymes in Marine and Terrestrial Metagenomes. Applied and Environmental Microbiology, 2018, 84, .	3.1	259
45	Community proteogenomics reveals the systemic impact of phosphorus availability on microbial functions in tropical soil. Nature Ecology and Evolution, 2018, 2, 499-509.	7.8	116
46	Push-pull tests for estimating effective porosity: expanded analytical solution and in situ application. Hydrogeology Journal, 2018, 26, 381-393.	2.1	27
47	Microbial community and metagenome dynamics during biodegradation of dispersed oil reveals potential key-players in cold Norwegian seawater. Marine Pollution Bulletin, 2018, 129, 370-378.	5.0	91
48	Unravelling biocomplexity of electroactive biofilms for producing hydrogen from biomass. Microbial Biotechnology, 2018, 11, 84-97.	4.2	26
49	In Situ: Groundwater Bioremediation. , 2018, , 1-18.		2
50	Impact of hydrologic boundaries on microbial planktonic and biofilm communities in shallow terrestrial subsurface environments. FEMS Microbiology Ecology, 2018, 94, .	2.7	49
51	In situ decay of polyfluorinated benzoic acids under anaerobic conditions. Journal of Contaminant Hydrology, 2018, 217, 8-16.	3.3	0
52	Lessons from the 2010 Deepwater Horizon Accident in the Gulf of Mexico. , 2018, , 1-19.		3
53	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. Frontiers in Microbiology, 2018, 9, 1492.	3.5	41
54	Cometabolic Bioremediation. , 2018, , 1-15.		5

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55	Clay Flocculation Effect on Microbial Community Composition in Water and Sediment. <i>Frontiers in Environmental Science</i> , 2018, 6, .	3.3	8
56	The Effect of Hydrostatic Pressure on Enrichments of Hydrocarbon Degrading Microbes From the Gulf of Mexico Following the Deepwater Horizon Oil Spill. <i>Frontiers in Microbiology</i> , 2018, 9, 808.	3.5	40
57	Enrichment of Bacteria From Eastern Mediterranean Sea Involved in Lignin Degradation via the Phenylacetyl-CoA Pathway. <i>Frontiers in Microbiology</i> , 2018, 9, 922.	3.5	22
58	Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession. <i>Frontiers in Microbiology</i> , 2018, 9, 1234.	3.5	107
59	Bacterial Biomarkers of Marcellus Shale Activity in Pennsylvania. <i>Frontiers in Microbiology</i> , 2018, 9, 1697.	3.5	11
60	Variation in microbial community structure correlates with heavy-metal contamination in soils decades after mining ceased. <i>Soil Biology and Biochemistry</i> , 2018, 126, 57-63.	8.8	111
61	Use of in-field bioreactors demonstrate groundwater filtration influences planktonic bacterial community assembly, but not biofilm composition. <i>PLoS ONE</i> , 2018, 13, e0194663.	2.5	9
62	Bioremediation. , 2018, , 247-266.		8
63	THE ULTRAMICROBACTERIAL COMMUNITY OF THE URANIUM AND HEAVY METAL CONTAMINATED Y-12 AQUIFER. , 2018, , .		0
64	ULTRAMICROBACTERIA IN URANIUM-CONTAMINATED Y-12 GROUNDWATER. , 2018, , .		0
65	Corexit 9500 Enhances Oil Biodegradation and Changes Active Bacterial Community Structure of Oil-Enriched Microcosms. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	94
66	Temporal Dynamics of In-Field Bioreactor Populations Reflect the Groundwater System and Respond Predictably to Perturbation. <i>Environmental Science &amp; Technology</i> , 2017, 51, 2879-2889.	10.0	15
67	High-Quality Draft Genome Sequences of Four Lignocellulose-Degrading Bacteria Isolated from Puerto Rican Forest Soil: <i>Gordonia</i> sp., <i>Paenibacillus</i> sp., <i>Variovorax</i> sp., and <i>Vogesella</i> sp. <i>Genome Announcements</i> , 2017, 5, .	0.8	18
68	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. <i>Environmental Science &amp; Technology</i> , 2017, 51, 3609-3620.	10.0	22
69	Complete genome sequence of <i>Pseudomonas stutzeri</i> strain RCH2 isolated from a Hexavalent Chromium [Cr(VI)] contaminated site. <i>Standards in Genomic Sciences</i> , 2017, 12, 23.	1.5	12
70	Rapid Response of Eastern Mediterranean Deep Sea Microbial Communities to Oil. <i>Scientific Reports</i> , 2017, 7, 5762.	3.3	27
71	Environmental Selection, Dispersal, and Organism Interactions Shape Community Assembly in High-Throughput Enrichment Culturing. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	12
72	Unexpected competitiveness of <i>Methanosaeta</i> populations at elevated acetate concentrations in methanogenic treatment of animal wastewater. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1729-1738.	3.6	49

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73	Comparison of Thaumarchaeotal populations from four deep sea basins. FEMS Microbiology Ecology, 2017, 93, .	2.7	15
74	Bacterial Community Dynamics in Dichloromethane-Contaminated Groundwater Undergoing Natural Attenuation. Frontiers in Microbiology, 2017, 8, 2300.	3.5	23
75	Construction of Viable Soil Defined Media Using Quantitative Metabolomics Analysis of Soil Metabolites. Frontiers in Microbiology, 2017, 8, 2618.	3.5	34
76	Colwellia psychrerythraea Strains from Distant Deep Sea Basins Show Adaptation to Local Conditions. Frontiers in Environmental Science, 2016, 4, .	3.3	29
77	A Novel Analysis Method for Paired-Sample Microbial Ecology Experiments. PLoS ONE, 2016, 11, e0154804.	2.5	9
78	In situ mobility of uranium in the presence of nitrate following sulfate-reducing conditions. Journal of Contaminant Hydrology, 2016, 187, 55-64.	3.3	29
79	Bacterial Interactomes: Interacting Protein Partners Share Similar Function and Are Validated in Independent Assays More Frequently Than Previously Reported. Molecular and Cellular Proteomics, 2016, 15, 1539-1555.	3.8	16
80	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. MBio, 2016, 7, e02234-15.	4.1	105
81	Metagenomic applications in environmental monitoring and bioremediation. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 1345-1354.	3.0	102
82	Near-Complete Genome Sequence of <i>Thalassospira</i> sp. Strain KO164 Isolated from a Lignin-Enriched Marine Sediment Microcosm. Genome Announcements, 2016, 4, .	0.8	1
83	Quantitative Tagless Copurification: A Method to Validate and Identify Protein-Protein Interactions. Molecular and Cellular Proteomics, 2016, 15, 2186-2202.	3.8	12
84	Rapid detection of microbial cell abundance in aquatic systems. Biosensors and Bioelectronics, 2016, 85, 915-923.	10.1	13
85	Marine Oil Biodegradation. Environmental Science & Technology, 2016, 50, 2121-2129.	10.0	183
86	Environmental Systems Microbiology of Contaminated Environments. , 2015, , 5.1.6-1-5.1.6-10.		1
87	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolomonas lignolytica</i> sp. nov.. Standards in Genomic Sciences, 2015, 10, 106.	1.5	43
88	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. Frontiers in Microbiology, 2015, 6, 1205.	3.5	77
89	The Unique Chemistry of Eastern Mediterranean Water Masses Selects for Distinct Microbial Communities by Depth. PLoS ONE, 2015, 10, e0120605.	2.5	65
90	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	4.1	173

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91	Molybdenum Availability Is Key to Nitrate Removal in Contaminated Groundwater Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4976-4983.	3.1	49
92	High-Quality Draft Genome Sequence of <i>Desulfovibrio carbinoliphilus</i> FW-101-2B, an Organic Acid-Oxidizing Sulfate-Reducing Bacterium Isolated from Uranium(VI)-Contaminated Groundwater. <i>Genome Announcements</i> , 2015, 3, .	0.8	3
93	Microbial community composition and diversity in Caspian Sea sediments. <i>FEMS Microbiology Ecology</i> , 2015, 91, 1-11.	2.7	70
94	Metals other than uranium affected microbial community composition in a historical uranium-mining site. <i>Environmental Science and Pollution Research</i> , 2015, 22, 19326-19341.	5.3	15
95	Co-extraction of DNA and PLFA from soil samples. <i>Journal of Microbiological Methods</i> , 2015, 115, 64-66.	1.6	3
96	A Slow-Release Substrate Stimulates Groundwater Microbial Communities for Long-Term in Situ Cr(VI) Reduction. <i>Environmental Science &amp; Technology</i> , 2015, 49, 12922-12931.	10.0	19
97	Rapid selective sweep of pre-existing polymorphisms and slow fixation of new mutations in experimental evolution of <i>Desulfovibrio vulgaris</i> . <i>ISME Journal</i> , 2015, 9, 2360-2372.	9.8	24
98	Genome Sequence of <i>Halomonas</i> sp. Strain KO116, an Ionic Liquid-Tolerant Marine Bacterium Isolated from a Lignin-Enriched Seawater Microcosm. <i>Genome Announcements</i> , 2015, 3, .	0.8	9
99	Microbial Responses to the Deepwater Horizon Oil Spill: From Coastal Wetlands to the Deep Sea. <i>Annual Review of Marine Science</i> , 2015, 7, 377-401.	11.6	205
100	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. <i>Frontiers in Microbiology</i> , 2014, 5, 130.	3.5	172
101	Functional Genomics with a Comprehensive Library of Transposon Mutants for the Sulfate-Reducing Bacterium <i>Desulfovibrio alaskensis</i> G20. <i>MBio</i> , 2014, 5, e01041-14.	4.1	56
102	Temperature and injection water source influence microbial community structure in four Alaskan North Slope hydrocarbon reservoirs. <i>Frontiers in Microbiology</i> , 2014, 5, 409.	3.5	37
103	Draft Genome Sequence of <i>Pseudoalteromonas</i> sp. Strain ND6B, an Oil-Degrading Isolate from Eastern Mediterranean Sea Water Collected at a Depth of 1,210 Meters. <i>Genome Announcements</i> , 2014, 2, .	0.8	3
104	Draft Genome Sequence of <i>Thalassotalea</i> sp. Strain ND16A Isolated from Eastern Mediterranean Sea Water Collected from a Depth of 1,055 Meters. <i>Genome Announcements</i> , 2014, 2, .	0.8	8
105	Complete genome sequence of the lignin-degrading bacterium <i>Klebsiella</i> sp. strain BRL6-2. <i>Standards in Genomic Sciences</i> , 2014, 9, 19.	1.5	40
106	Draft Genome Sequence of the Lignin-Degrading <i>Burkholderia</i> sp. Strain LIG30, Isolated from Wet Tropical Forest Soil. <i>Genome Announcements</i> , 2014, 2, .	0.8	26
107	Microbial Community Responses to Organophosphate Substrate Additions in Contaminated Subsurface Sediments. <i>PLoS ONE</i> , 2014, 9, e100383.	2.5	28
108	Microbial biogeography across a full-scale wastewater treatment plant transect: evidence for immigration between coupled processes. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4723-4736.	3.6	51

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109	Enzyme activities of aerobic lignocellulolytic bacteria isolated from wet tropical forest soils. <i>Systematic and Applied Microbiology</i> , 2014, 37, 60-67.	2.8	103
110	Stochasticity, succession, and environmental perturbations in a fluidic ecosystem. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E836-45.	7.1	595
111	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	9.8	325
112	Metallomics of two microorganisms relevant to heavy metal bioremediation reveal fundamental differences in metal assimilation and utilization. <i>Metallomics</i> , 2014, 6, 1004.	2.4	16
113	Assessing impacts of unconventional natural gas extraction on microbial communities in headwater stream ecosystems in Northwestern Pennsylvania. <i>Frontiers in Microbiology</i> , 2014, 5, 522.	3.5	58
114	Complete Genome Sequence of the Subsurface, Mesophilic Sulfate-Reducing Bacterium <i>Desulfovibrio aespoensis</i> Aspo-2. <i>Genome Announcements</i> , 2014, 2, .	0.8	6
115	Characterization of Wastewater Treatment Plant Microbial Communities and the Effects of Carbon Sources on Diversity in Laboratory Models. <i>PLoS ONE</i> , 2014, 9, e105689.	2.5	7
116	Changes in microbial dynamics during long-term decomposition in tropical forests. <i>Soil Biology and Biochemistry</i> , 2013, 66, 60-68.	8.8	47
117	Dissecting a complex chemical stress: chemogenomic profiling of plant hydrolysates. <i>Molecular Systems Biology</i> , 2013, 9, 674.	7.2	103
118	Succession of Hydrocarbon-Degrading Bacteria in the Aftermath of the <i>Deepwater Horizon</i> Oil Spill in the Gulf of Mexico. <i>Environmental Science &amp; Technology</i> , 2013, 47, 10860-10867.	10.0	344
119	The Super Chip for microbial community structure, and function from all environments. <i>Microbial Biotechnology</i> , 2013, 6, 450-452.	4.2	3
120	Advances in monitoring environmental microbes. <i>Current Opinion in Biotechnology</i> , 2013, 24, 526-533.	6.6	69
121	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. <i>ISME Journal</i> , 2013, 7, 1790-1802.	9.8	46
122	Functional gene array-based analysis of microbial communities in heavy metals-contaminated lake sediments. <i>FEMS Microbiology Ecology</i> , 2013, 86, 200-214.	2.7	39
123	Distribution of hydrocarbons released during the 2010 MC252 oil spill in deep offshore waters. <i>Environmental Pollution</i> , 2013, 173, 224-230.	7.5	113
124	StressChip as a High-Throughput Tool for Assessing Microbial Community Responses to Environmental Stresses. <i>Environmental Science &amp; Technology</i> , 2013, 47, 9841-9849.	10.0	17
125	Draft Genome Sequence for <i>Desulfovibrio africanus</i> Strain PCS. <i>Genome Announcements</i> , 2013, 1, e0014413.	0.8	5
126	Metagenomic analysis and metabolite profiling of deep-sea sediments from the Gulf of Mexico following the Deepwater Horizon oil spill. <i>Frontiers in Microbiology</i> , 2013, 4, 50.	3.5	257



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127	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. PLoS ONE, 2013, 8, e83909.	2.5	36
128	Metagenomes of tropical soil-derived anaerobic switchgrass-adapted consortia with and without iron. Standards in Genomic Sciences, 2013, 7, 382-398.	1.5	12
129	Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e41305.	2.5	146
130	Microbial Functional Gene Diversity with a Shift of Subsurface Redox Conditions during <i>In Situ</i> Uranium Reduction. Applied and Environmental Microbiology, 2012, 78, 2966-2972.	3.1	42
131	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing <i>Pelosinus</i> spp. Applied and Environmental Microbiology, 2012, 78, 2082-2091.	3.1	42
132	Global transcriptome response to ionic liquid by a tropical rain forest soil bacterium, <i>Enterobacter lignolyticus</i> . Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2173-82.	7.1	85
133	Draft Genome Sequences for Two Metal-Reducing <i>Pelosinus fermentans</i> Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7. Journal of Bacteriology, 2012, 194, 5147-5148.	2.2	24
134	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in <i>Desulfovibrio vulgaris</i> Hildenborough. Applied and Environmental Microbiology, 2012, 78, 1168-1177.	3.1	32
135	Anaerobic Decomposition of Switchgrass by Tropical Soil-Derived Feedstock-Adapted Consortia. MBio, 2012, 3, .	4.1	19
136	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of <i>Desulfovibrio vulgaris</i> . Journal of Proteome Research, 2012, 11, 5720-5735.	3.7	22
137	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. ISME Journal, 2012, 6, 1715-1727.	9.8	547
138	Glycoside Hydrolases from a targeted Compost Metagenome, activity-screening and functional characterization. BMC Biotechnology, 2012, 12, 38.	3.3	48
139	Systems biology approach to bioremediation. Current Opinion in Biotechnology, 2012, 23, 483-490.	6.6	135
140	Environmental biotechnology. Current Opinion in Biotechnology, 2012, 23, 414.	6.6	3
141	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. ISME Journal, 2012, 6, 451-460.	9.8	240
142	Microbial Response to the MC-252 Oil and Corexit 9500 in the Gulf of Mexico. Frontiers in Microbiology, 2012, 3, 357.	3.5	86
143	Substrate perturbation alters the glycoside hydrolase activities and community composition of switchgrass-adapted bacterial consortia. Biotechnology and Bioengineering, 2012, 109, 1140-1145.	3.3	17
144	Application of phenotypic microarrays to environmental microbiology. Current Opinion in Biotechnology, 2012, 23, 41-48.	6.6	45

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145	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	3.8	275
146	Lignin-baited Bio-trap Beads to Search for Novel Lignin Degrading Microbes in Tropical Forest Soil. , 2012, , .		0
147	Colloid-based multiplexed screening for plant biomass-degrading glycoside hydrolase activities in microbial communities. <i>Energy and Environmental Science</i> , 2011, 4, 2884.	30.8	29
148	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. <i>Applied and Environmental Microbiology</i> , 2011, 77, 6313-6322.	3.1	74
149	Glycoside Hydrolase Activities of Thermophilic Bacterial Consortia Adapted to Switchgrass. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5804-5812.	3.1	99
150	Hydrocarbon-Degrading Bacteria and the Bacterial Community Response in Gulf of Mexico Beach Sands Impacted by the Deepwater Horizon Oil Spill. <i>Applied and Environmental Microbiology</i> , 2011, 77, 7962-7974.	3.1	779
151	Oil Biodegradation and Bioremediation: A Tale of the Two Worst Spills in U.S. History. <i>Environmental Science &amp; Technology</i> , 2011, 45, 6709-6715.	10.0	711
152	Microfluidic fluorescence in situ hybridization and flow cytometry (¼FlowFISH). <i>Lab on A Chip</i> , 2011, 11, 2673.	6.0	58
153	Use of immunomagnetic separation for the detection of <i>Desulfovibrio vulgaris</i> from environmental samples. <i>Journal of Microbiological Methods</i> , 2011, 86, 204-209.	1.6	17
154	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. <i>Nature Reviews Microbiology</i> , 2011, 9, 452-466.	28.6	169
155	Characterization of Trapped Lignin-Degrading Microbes in Tropical Forest Soil. <i>PLoS ONE</i> , 2011, 6, e19306.	2.5	178
156	Complete genome sequence of "Enterobacter lignolyticus" SCF1. <i>Standards in Genomic Sciences</i> , 2011, 5, 69-85.	1.5	76
157	16S rRNA Gene Microarray Analysis of Microbial Communities in Ethanol-Stimulated Subsurface Sediment. <i>Microbes and Environments</i> , 2011, 26, 261-265.	1.6	2
158	Enrichment, isolation and characterization of fungi tolerant to 1-ethyl-3-methylimidazolium acetate. <i>Journal of Applied Microbiology</i> , 2011, 110, 1023-1031.	3.1	34
159	Microbial community response to addition of polylactate compounds to stimulate hexavalent chromium reduction in groundwater. <i>Chemosphere</i> , 2011, 85, 660-665.	8.2	50
160	Bioenergy feedstock-specific enrichment of microbial populations during high-solids thermophilic deconstruction. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2088-2098.	3.3	23
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