

# 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	Deep-Sea Oil Plume Enriches Indigenous Oil-Degrading Bacteria. <i>Science</i> , 2010, 330, 204-208.	12.6	1,109
2	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
3	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
4	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
5	Metagenome, metatranscriptome and single-cell sequencing reveal microbial response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2012, 6, 1715-1727.	9.8	547
6	Environmental Genomics Reveals a Single-Species Ecosystem Deep Within Earth. <i>Science</i> , 2008, 322, 275-278.	12.6	474
7	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
8	Application of a High-Density Oligonucleotide Microarray Approach To Study Bacterial Population Dynamics during Uranium Reduction and Reoxidation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6288-6298.	3.1	404
9	Long-Term Sustainability of a High-Energy, Low-Diversity Crustal Biome. <i>Science</i> , 2006, 314, 479-482.	12.6	350
10	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
11	Metagenomic insights into evolution of a heavy metal-contaminated groundwater microbial community. <i>ISME Journal</i> , 2010, 4, 660-672.	9.8	332
12	Metagenomics reveals sediment microbial community response to Deepwater Horizon oil spill. <i>ISME Journal</i> , 2014, 8, 1464-1475.	9.8	325
13	GeoChip 3.0 as a high-throughput tool for analyzing microbial community composition, structure and functional activity. <i>ISME Journal</i> , 2010, 4, 1167-1179.	9.8	300
14	Deep-sea bacteria enriched by oil and dispersant from the Deepwater Horizon spill. <i>Environmental Microbiology</i> , 2012, 14, 2405-2416.	3.8	275
15	New Insights into the Function and Global Distribution of Polyethylene Terephthalate (PET)-Degrading Bacteria and Enzymes in Marine and Terrestrial Metagenomes. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	259
16	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
17	Microbial gene functions enriched in the Deepwater Horizon deep-sea oil plume. <i>ISME Journal</i> , 2012, 6, 451-460.	9.8	240
18	Environmental Whole-Genome Amplification To Access Microbial Populations in Contaminated Sediments. <i>Applied and Environmental Microbiology</i> , 2006, 72, 3291-3301.	3.1	213

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19	Microbial Responses to the <i>Deepwater Horizon</i> Oil Spill: From Coastal Wetlands to the Deep Sea. Annual Review of Marine Science, 2015, 7, 377-401.	11.6	205
20	Small and mighty: adaptation of superphylum Patescibacteria to groundwater environment drives their genome simplicity. Microbiome, 2020, 8, 51.	11.1	205
21	Marine Oil Biodegradation. Environmental Science & Technology, 2016, 50, 2121-2129.	10.0	183
22	Characterization of Trapped Lignin-Degrading Microbes in Tropical Forest Soil. PLoS ONE, 2011, 6, e19306.	2.5	178
23	Natural Bacterial Communities Serve as Quantitative Geochemical Biosensors. MBio, 2015, 6, e00326-15.	4.1	173
24	Assessment of the Deepwater Horizon oil spill impact on Gulf coast microbial communities. Frontiers in Microbiology, 2014, 5, 130.	3.5	172
25	Targeted Discovery of Glycoside Hydrolases from a Switchgrass-Adapted Compost Community. PLoS ONE, 2010, 5, e8812.	2.5	170
26	How sulphate-reducing microorganisms cope with stress: lessons from systems biology. Nature Reviews Microbiology, 2011, 9, 452-466.	28.6	169
27	Reoxidation of Bioreduced Uranium under Reducing Conditions. Environmental Science & Technology, 2005, 39, 6162-6169.	10.0	157
28	Salt Stress in <i>Desulfovibrio vulgaris</i> Hildenborough: an Integrated Genomics Approach. Journal of Bacteriology, 2006, 188, 4068-4078.	2.2	155
29	Comparison of bacteria from deep subsurface sediment and adjacent groundwater. Microbial Ecology, 1991, 22, 293-304.	2.8	154
30	Microbial Community Analysis of a Coastal Salt Marsh Affected by the Deepwater Horizon Oil Spill. PLoS ONE, 2012, 7, e41305.	2.5	146
31	Systems biology approach to bioremediation. Current Opinion in Biotechnology, 2012, 23, 483-490.	6.6	135
32	The Electron Transfer System of Syntrophically Grown <i>Desulfovibrio vulgaris</i>. Journal of Bacteriology, 2009, 191, 5793-5801.	2.2	133
33	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
34	Distribution of hydrocarbons released during the 2010 MC252 oil spill in deep offshore waters. Environmental Pollution, 2013, 173, 224-230.	7.5	113
35	Variation in microbial community structure correlates with heavy-metal contamination in soils decades after mining ceased. Soil Biology and Biochemistry, 2018, 126, 57-63.	8.8	111
36	Microbial Interactions With Dissolved Organic Matter Drive Carbon Dynamics and Community Succession. Frontiers in Microbiology, 2018, 9, 1234.	3.5	107

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37	Global Analysis of Heat Shock Response in <i>Desulfovibrio vulgaris</i> Hildenborough. Journal of Bacteriology, 2006, 188, 1817-1828.	2.2	106
38	Lateral Gene Transfer in a Heavy Metal-Contaminated-Groundwater Microbial Community. MBio, 2016, 7, e02234-15.	4.1	105
39	Dissecting a complex chemical stress: chemogenomic profiling of plant hydrolysates. Molecular Systems Biology, 2013, 9, 674.	7.2	103
40	Enzyme activities of aerobic lignocellulolytic bacteria isolated from wet tropical forest soils. Systematic and Applied Microbiology, 2014, 37, 60-67.	2.8	103
41	Metagenomic applications in environmental monitoring and bioremediation. Journal of Industrial Microbiology and Biotechnology, 2016, 43, 1345-1354.	3.0	102
42	Strategies for Enhancing the Effectiveness of Metagenomic-based Enzyme Discovery in Lignocellulolytic Microbial Communities. Bioenergy Research, 2010, 3, 146-158.	3.9	100
43	Glycoside Hydrolase Activities of Thermophilic Bacterial Consortia Adapted to Switchgrass. Applied and Environmental Microbiology, 2011, 77, 5804-5812.	3.1	99
44	Responses of microbial community functional structures to pilot-scale uranium <i>in situ</i> bioremediation. ISME Journal, 2010, 4, 1060-1070.	9.8	98
45	GeoChip-based analysis of functional microbial communities during the reoxidation of a bioreduced uranium-contaminated aquifer. Environmental Microbiology, 2009, 11, 2611-2626.	3.8	95
46	Cell-Wide Responses to Low-Oxygen Exposure in <i>Desulfovibrio vulgaris</i> Hildenborough. Journal of Bacteriology, 2007, 189, 5996-6010.	2.2	94
47	Corexit 9500 Enhances Oil Biodegradation and Changes Active Bacterial Community Structure of Oil-Enriched Microcosms. Applied and Environmental Microbiology, 2017, 83, .	3.1	94
48	Probing the active fraction of soil microbiomes using BONCAT-FACS. Nature Communications, 2019, 10, 2770.	12.8	93
49	Energetic Consequences of Nitrite Stress in <i>Desulfovibrio vulgaris</i> Hildenborough, Inferred from Global Transcriptional Analysis. Applied and Environmental Microbiology, 2006, 72, 4370-4381.	3.1	92
50	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
51	Pathway Confirmation and Flux Analysis of Central Metabolic Pathways in <i>Desulfovibrio vulgaris</i> Hildenborough using Gas Chromatography-Mass Spectrometry and Fourier Transform-Ion Cyclotron Resonance Mass Spectrometry. Journal of Bacteriology, 2007, 189, 940-949.	2.2	90
52	Histopathology of red-sore disease ( <i>Aeromonas hydrophila</i> ) in naturally and experimentally infected largemouth bass <i>Micropterus salmoides</i> (Lacepede). Journal of Fish Diseases, 1979, 2, 263-277.	1.9	87
53	In Situ Long-Term Reductive Bioimmobilization of Cr(VI) in Groundwater Using Hydrogen Release Compound. Environmental Science & Technology, 2008, 42, 8478-8485.	10.0	86
54	Microbial Response to the MC-252 Oil and Corexit 9500 in the Gulf of Mexico. Frontiers in Microbiology, 2012, 3, 357.	3.5	86

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55	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
56	Comparison of Aerobic and Anaerobic Biotreatment of Municipal Solid Waste. Journal of the Air and Waste Management Association, 2004, 54, 815-822.	1.9	84
57	In Situ Reduction of Chromium(VI) in Heavily Contaminated Soils through Organic Carbon Amendment. Journal of Environmental Quality, 2003, 32, 1641-1649.	2.0	81
58	Functional Gene Array-Based Analysis of Microbial Community Structure in Groundwaters with a Gradient of Contaminant Levels. Environmental Science & Technology, 2009, 43, 3529-3534.	10.0	80
59	Comparative metagenomics reveals impact of contaminants on groundwater microbiomes. Frontiers in Microbiology, 2015, 6, 1205.	3.5	77
60	Ultrastructure of Red-Sore Lesions on Largemouth Bass ( <i>Micropterus salmoides</i> ): Association of the Ciliate <i>Epistylis</i> sp. and the Bacterium <i>Aeromonas hydrophila</i> *. Journal of Protozoology, 1978, 25, 351-355.	0.8	76
61	Complete genome sequence of <i>Enterobacter lignolyticus</i> -SCF1. Standards in Genomic Sciences, 2011, 5, 69-85.	1.5	76
62	PCR Amplification-Independent Methods for Detection of Microbial Communities by the High-Density Microarray PhyloChip. Applied and Environmental Microbiology, 2011, 77, 6313-6322.	3.1	74
63	Thermal Effluent and the Epizootiology of the Ciliate <i>Epistylis</i> and the Bacterium <i>Aeromonas</i> in Association with Centrarchid Fish. Transactions of the American Microscopical Society, 1976, 95, 687.	0.3	71
64	Fecal coliforms as indicators in tropical waters: A review. Toxicity Assessment, 1988, 3, 461-477.	0.6	71
65	Chromium Diffusion and Reduction in Soil Aggregates. Environmental Science & Technology, 2001, 35, 3169-3174.	10.0	70
66	Analysis of a Ferric Uptake Regulator (Fur) Mutant of <i>Desulfovibrio vulgaris</i> Hildenborough. Applied and Environmental Microbiology, 2007, 73, 5389-5400.	3.1	70
67	Microbial community composition and diversity in Caspian Sea sediments. FEMS Microbiology Ecology, 2015, 91, 1-11.	2.7	70
68	Advances in monitoring environmental microbes. Current Opinion in Biotechnology, 2013, 24, 526-533.	6.6	69
69	Impact of elevated nitrate on sulfate-reducing bacteria: a comparative Study of <i>Desulfovibrio vulgaris</i> . ISME Journal, 2010, 4, 1386-1397.	9.8	67
70	Characterization of Coastal Urban Watershed Bacterial Communities Leads to Alternative Community-Based Indicators. PLoS ONE, 2010, 5, e11285.	2.5	66
71	Survival and activity of <i>Salmonella typhimurium</i> and <i>Escherichia coli</i> in tropical freshwater. Journal of Applied Bacteriology, 1989, 67, 61-69.	1.1	65
72	The Unique Chemistry of Eastern Mediterranean Water Masses Selects for Distinct Microbial Communities by Depth. PLoS ONE, 2015, 10, e0120605.	2.5	65

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73	Global Transcriptional, Physiological, and Metabolite Analyses of the Responses of <i>Desulfovibrio vulgaris</i> Hildenborough to Salt Adaptation. <i>Applied and Environmental Microbiology</i> , 2010, 76, 1574-1586.	3.1	64
74	Response of <i>Desulfovibrio vulgaris</i> to Alkaline Stress. <i>Journal of Bacteriology</i> , 2007, 189, 8944-8952.	2.2	62
75	Reductive Dechlorination of Trichloroethylene and Tetrachloroethylene under Aerobic Conditions in a Sediment Column. <i>Applied and Environmental Microbiology</i> , 1994, 60, 2200-2204.	3.1	62
76	Analysis of metabolic pathways and fluxes in a newly discovered thermophilic and ethanol-tolerant <i>Geobacillus</i> strain. <i>Biotechnology and Bioengineering</i> , 2009, 102, 1377-1386.	3.3	61
77	Study of nitrate stress in <i>Desulfovibrio vulgaris</i> Hildenborough using iTRAQ proteomics. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2006, 5, 133-143.	3.8	60
78	Microfluidic fluorescence in situ hybridization and flow cytometry (¼FlowFISH). <i>Lab on A Chip</i> , 2011, 11, 2673.	6.0	58
79	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
80	Temporal Transcriptomic Analysis as <i>Desulfovibrio vulgaris</i> Hildenborough Transitions into Stationary Phase during Electron Donor Depletion. <i>Applied and Environmental Microbiology</i> , 2006, 72, 5578-5588.	3.1	57
81	Microbial Functional Gene Diversity Predicts Groundwater Contamination and Ecosystem Functioning. <i>MBio</i> , 2018, 9, .	4.1	57
82	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
83	Flux Analysis of Central Metabolic Pathways in <i>Geobacter metallireducens</i> during Reduction of Soluble Fe(III)-Nitrilotriacetic Acid. <i>Applied and Environmental Microbiology</i> , 2007, 73, 3859-3864.	3.1	55
84	Developments in Bioremediation of Soils and Sediments Polluted with Metals and Radionuclides: 2. Field Research on Bioremediation of Metals and Radionuclides. <i>Reviews in Environmental Science and Biotechnology</i> , 2005, 4, 157-183.	8.1	52
85	Dynamics of Microbial Community Composition and Function during In Situ Bioremediation of a Uranium-Contaminated Aquifer. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3860-3869.	3.1	51
86	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
87	Distribution and in situ survival and activity of <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> in a tropical rain forest watershed. <i>Current Microbiology</i> , 1987, 15, 213-218.	2.2	50
88	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
89	Effect of gaseous nitrogen and phosphorus injection on in situ bioremediation of a trichloroethylene-contaminated site. <i>Journal of Hazardous Materials</i> , 1995, 41, 287-298.	12.4	49
90	Molybdenum Availability Is Key to Nitrate Removal in Contaminated Groundwater Environments. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4976-4983.	3.1	49

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91	Unexpected competitiveness of Methanosaeta populations at elevated acetate concentrations in methanogenic treatment of animal wastewater. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 1729-1738.	3.6	49
92	Impact of hydrologic boundaries on microbial planktonic and biofilm communities in shallow terrestrial subsurface environments. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	49
93	Glycoside Hydrolases from a targeted Compost Metagenome, activity-screening and functional characterization. <i>BMC Biotechnology</i> , 2012, 12, 38.	3.3	48
94	Changes in microbial dynamics during long-term decomposition in tropical forests. <i>Soil Biology and Biochemistry</i> , 2013, 66, 60-68.	8.8	47
95	Hydrogen peroxide-induced oxidative stress responses in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Environmental Microbiology</i> , 2010, 12, 2645-2657.	3.8	46
96	Characterization of NaCl tolerance in <i>Desulfovibrio vulgaris</i> Hildenborough through experimental evolution. <i>ISME Journal</i> , 2013, 7, 1790-1802.	9.8	46
97	Application of phenotypic microarrays to environmental microbiology. <i>Current Opinion in Biotechnology</i> , 2012, 23, 41-48.	6.6	45
98	Geophysical Monitoring of Hydrological and Biogeochemical Transformations Associated with Cr(VI) Bioremediation. <i>Environmental Science &amp; Technology</i> , 2008, 42, 3757-3765.	10.0	44
99	Effects of nutrient dosing on subsurface methanotrophic populations and trichloroethylene degradation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 1997, 18, 204-212.	3.0	43
100	Phylogenetic and Functional Biomarkers as Indicators of Bacterial Community Responses to Mixed-Waste Contamination. <i>Environmental Science &amp; Technology</i> , 2006, 40, 2601-2607.	10.0	43
101	Genome sequence and description of the anaerobic lignin-degrading bacterium <i>Tolomonas lignolytica</i> sp. nov.. <i>Standards in Genomic Sciences</i> , 2015, 10, 106.	1.5	43
102	Microbial Functional Gene Diversity with a Shift of Subsurface Redox Conditions during <i>In Situ</i> Uranium Reduction. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2966-2972.	3.1	42
103	Microbial Community Succession during Lactate Amendment and Electron Acceptor Limitation Reveals a Predominance of Metal-Reducing <i>Pelosinus</i> spp. <i>Applied and Environmental Microbiology</i> , 2012, 78, 2082-2091.	3.1	42
104	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
105	Distribution of Chromium Contamination and Microbial Activity in Soil Aggregates. <i>Journal of Environmental Quality</i> , 2003, 32, 541-549.	2.0	41
106	Microbial Community Structure and Functional Potential Along a Hypersaline Gradient. <i>Frontiers in Microbiology</i> , 2018, 9, 1492.	3.5	41
107	ISOLATION OF <i>Aeromonas hydrophila</i> FROM THE AMERICAN ALLIGATOR, <i>Alligator mississippiensis</i> . <i>Journal of Wildlife Diseases</i> , 1979, 15, 239-243.	0.8	40
108	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

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109	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
110	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
111	Real-time molecular monitoring of chemical environment in obligate anaerobes during oxygen adaptive response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12599-12604.	7.1	38
112	Use of gene probes to assess the impact and effectiveness of aerobic in situ bioremediation of TCE. <i>Archives of Microbiology</i> , 2009, 191, 221-232.	2.2	38
113	Complete Genome Sequence of the Electricity-Producing <i>Thermincola potens</i> Strain JR. <i>Journal of Bacteriology</i> , 2010, 192, 4078-4079.	2.2	38
114	Tropical Source Water. <i>Brock/Springer Series in Contemporary Bioscience</i> , 1990, , 32-53.	0.3	38
115	Comparison of the in situ survival and activity of <i>Klebsiella pneumoniae</i> and <i>Escherichia coli</i> in tropical marine environments. <i>Microbial Ecology</i> , 1988, 15, 41-57.	2.8	37
116	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
117	Hexavalent Chromium Reduction under Fermentative Conditions with Lactate Stimulated Native Microbial Communities. <i>PLoS ONE</i> , 2013, 8, e83909.	2.5	36
118	Survival and distribution of <i>aeromonas hydrophila</i> in near-shore coastal waters of Puerto Rico receiving rum distillery effluent. <i>Water Research</i> , 1983, 17, 319-326.	11.3	35
119	Mineralogical, Chemical and Biological Characterization of an Anaerobic Biofilm Collected from a Borehole in a Deep Gold Mine in South Africa. <i>Geomicrobiology Journal</i> , 2007, 24, 491-504.	2.0	35
120	Impacts of Glutaraldehyde on Microbial Community Structure and Degradation Potential in Streams Impacted by Hydraulic Fracturing. <i>Environmental Science &amp; Technology</i> , 2018, 52, 5989-5999.	10.0	35
121	Stress and Body Condition in a Population of Largemouth Bass: Implications for Red-Sore Disease. <i>Transactions of the American Fisheries Society</i> , 1980, 109, 532-536.	1.4	34
122	Effects of Organic Carbon Supply Rates on Uranium Mobility in a Previously Bioreduced Contaminated Sediment. <i>Environmental Science &amp; Technology</i> , 2008, 42, 7573-7579.	10.0	34
123	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
124	Construction of Viable Soil Defined Media Using Quantitative Metabolomics Analysis of Soil Metabolites. <i>Frontiers in Microbiology</i> , 2017, 8, 2618.	3.5	34
125	Ecology of <i>Aeromonas hydrophila</i> in a South Carolina cooling reservoir. <i>Microbial Ecology</i> , 1979, 5, 179-195.	2.8	32
126	Environmental biotechnology: A bioremediation perspective. <i>Remediation</i> , 2005, 15, 5-25.	2.4	32



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127	Functional Characterization of Crp/Fnr-Type Global Transcriptional Regulators in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1168-1177.	3.1	32
128	Survey of large protein complexes in <i>D. vulgaris</i> reveals great structural diversity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 16580-16585.	7.1	29
129	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
130	<i>Colwellia psychrerythraea</i> Strains from Distant Deep Sea Basins Show Adaptation to Local Conditions. <i>Frontiers in Environmental Science</i> , 2016, 4, .	3.3	29
131	In situ mobility of uranium in the presence of nitrate following sulfate-reducing conditions. <i>Journal of Contaminant Hydrology</i> , 2016, 187, 55-64.	3.3	29
132	Response of Aquatic Bacterial Communities to Hydraulic Fracturing in Northwestern Pennsylvania: A Five-Year Study. <i>Scientific Reports</i> , 2018, 8, 5683.	3.3	29
133	Oil Hydrocarbon Degradation by Caspian Sea Microbial Communities. <i>Frontiers in Microbiology</i> , 2019, 10, 995.	3.5	29
134	Microbial Community Responses to Organophosphate Substrate Additions in Contaminated Subsurface Sediments. <i>PLoS ONE</i> , 2014, 9, e100383.	2.5	28
135	Rapid Response of Eastern Mediterranean Deep Sea Microbial Communities to Oil. <i>Scientific Reports</i> , 2017, 7, 5762.	3.3	27
136	Push-pull tests for estimating effective porosity: expanded analytical solution and in situ application. <i>Hydrogeology Journal</i> , 2018, 26, 381-393.	2.1	27
137	Using the stress response to monitor process control: pathways to more effective bioremediation. <i>Current Opinion in Biotechnology</i> , 2006, 17, 285-290.	6.6	26
138	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
139	Unravelling biocomplexity of electroactive biofilms for producing hydrogen from biomass. <i>Microbial Biotechnology</i> , 2018, 11, 84-97.	4.2	26
140	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
141	Influences of Organic Carbon Supply Rate on Uranium Bioreduction in Initially Oxidizing, Contaminated Sediment. <i>Environmental Science &amp; Technology</i> , 2008, 42, 8901-8907.	10.0	25
142	Effects of thermal effluent on body condition of largemouth bass. <i>Nature</i> , 1978, 274, 470-471.	27.8	24
143	Draft Genome Sequences for Two Metal-Reducing <i>Pelosinus fermentans</i> Strains Isolated from a Cr(VI)-Contaminated Site and for Type Strain R7. <i>Journal of Bacteriology</i> , 2012, 194, 5147-5148.	2.2	24
144	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

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145	Bioenergy feedstock-specific enrichment of microbial populations during high-solids thermophilic deconstruction. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2088-2098.	3.3	23
146	Bacterial Community Dynamics in Dichloromethane-Contaminated Groundwater Undergoing Natural Attenuation. <i>Frontiers in Microbiology</i> , 2017, 8, 2300.	3.5	23
147	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
148	Uranium Reduction in Sediments under Diffusion-Limited Transport of Organic Carbon. <i>Environmental Science &amp; Technology</i> , 2005, 39, 7077-7083.	10.0	22
149	Expression profiling of hypothetical genes in <i>Desulfovibrio vulgaris</i> leads to improved functional annotation. <i>Nucleic Acids Research</i> , 2009, 37, 2926-2939.	14.5	22
150	High-throughput Isolation and Characterization of Untagged Membrane Protein Complexes: Outer Membrane Complexes of <i>Desulfovibrio vulgaris</i> . <i>Journal of Proteome Research</i> , 2012, 11, 5720-5735.	3.7	22
151	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
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