Terrence H Bell

List of Publications by Year
in descending order

49 papers	2,211 citations	304743 22 h-index	233421 45 g-index
50 all docs	50 docs citations	50 times ranked	2928 citing authors

#	Article	IF	Citations
1	Predictable bacterial composition and hydrocarbon degradation in Arctic soils following diesel and nutrient disturbance. ISME Journal, 2013, 7, 1200-1210.	9.8	190
2	Linkage between bacterial and fungal rhizosphere communities in hydrocarbon-contaminated soils is related to plant phylogeny. ISME Journal, 2014, 8, 331-343.	9.8	190
3	The Inherent Conflicts in Developing Soil Microbial Inoculants. Trends in Biotechnology, 2019, 37, 140-151.	9.3	179
4	Culture-Dependent and -Independent Methods Capture Different Microbial Community Fractions in Hydrocarbon-Contaminated Soils. PLoS ONE, 2015, 10, e0128272.	2.5	167
5	Seasonal Responses of Extracellular Enzyme Activity and Microbial Biomass to Warming and Nitrogen Addition. Soil Science Society of America Journal, 2010, 74, 820-828.	2.2	158
6	Increasing phytoremediation efficiency and reliability using novel omics approaches. Trends in Biotechnology, 2014, 32, 271-280.	9.3	148
7	Identification of Nitrogen-Incorporating Bacteria in Petroleum-Contaminated Arctic Soils by Using [¹⁵ N]DNA-Based Stable Isotope Probing and Pyrosequencing. Applied and Environmental Microbiology, 2011, 77, 4163-4171.	3.1	120
8	Petroleum biodegradation capacity of bacteria and fungi isolated from petroleum-contaminated soil. International Biodeterioration and Biodegradation, 2017, 116, 48-57.	3.9	105
9	Transplanting Soil Microbiomes Leads to Lasting Effects on Willow Growth, but not on the Rhizosphere Microbiome. Frontiers in Microbiology, 2015, 6, 1436.	3.5	98
10	Canola Rootâ€"Associated Microbiomes in the Canadian Prairies. Frontiers in Microbiology, 2018, 9, 1188.	3.5	85
11	Soil microbiome transfer method affects microbiome composition, including dominant microorganisms, in a novel environment. FEMS Microbiology Letters, 2017, 364, .	1.8	69
12	A Diverse Soil Microbiome Degrades More Crude Oil than Specialized Bacterial Assemblages Obtained in Culture. Applied and Environmental Microbiology, 2016, 82, 5530-5541.	3.1	63
13	Early rhizosphere microbiome composition is related to the growth and <scp><scp>Zn</scp></scp> uptake of willows introduced to a former landfill. Environmental Microbiology, 2015, 17, 3025-3038.	3.8	61
14	Vineyard under-vine floor management alters soil microbial composition, while the fruit microbiome shows no corresponding shifts. Scientific Reports, 2018, 8, 11039.	3.3	58
15	Alteration of microbial community structure affects diesel biodegradation in an Arctic soil. FEMS Microbiology Ecology, 2013, 85, 51-61.	2.7	54
16	Contrasting the Community Structure of Arbuscular Mycorrhizal Fungi from Hydrocarbon-Contaminated and Uncontaminated Soils following Willow (Salix spp. L.) Planting. PLoS ONE, 2014, 9, e102838.	2.5	50
17	Fine scale variability in soil extracellular enzyme activity is insensitive to rain events and temperature in a mesic system. Pedobiologia, 2011, 54, 141-146.	1.2	45
18	Manipulating Wild and Tamed Phytobiomes: Challenges and Opportunities. Phytobiomes Journal, 2019, 3, 3-21.	2.7	38

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19	Microbial Competition in Polar Soils: A Review of an Understudied but Potentially Important Control on Productivity. Biology, 2013, 2, 533-554.	2.8	34
20	100 Years Since Tolaas: Bacterial Blotch of Mushrooms in the 21stCentury. Plant Disease, 2019, 103, 2714-2732.	1.4	33
21	The hierarchy of root branching order determines bacterial composition, microbial carrying capacity and microbial filtering. Communications Biology, 2021, 4, 483.	4.4	30
22	Medicago sativa has Reduced Biomass and Nodulation When Grown with Soil Microbiomes Conditioned to High Phosphorus Inputs. Phytobiomes Journal, 2018, 2, 237-248.	2.7	25
23	Many roads to bacterial generalism. FEMS Microbiology Ecology, 2020, 97, .	2.7	21
24	Plant assemblage composition and soil P concentration differentially affect communities of AM and total fungi in a semi-arid grassland. FEMS Microbiology Ecology, 2015, 91, 1-13.	2.7	19
25	Testing sustained soil-to-soil contact as an approach for limiting the abiotic influence of source soils during experimental microbiome transfer. FEMS Microbiology Letters, 2019, 366, .	1.8	15
26	Can dispersal be leveraged to improve microbial inoculant success?. Trends in Biotechnology, 2022, 40, 12-21.	9.3	14
27	Soil salinization accelerates microbiome stabilization in iterative selections for plant performance. New Phytologist, 2022, 234, 2101-2110.	7.3	14
28	Host genomic influence on bacterial composition in the switchgrass rhizosphere. Molecular Ecology, 2022, 31, 3934-3950.	3.9	13
29	Factoring Ecological, Societal, and Economic Considerations into Inoculant Development. Trends in Biotechnology, 2019, 37, 572-573.	9.3	12
30	Comprehensive sampling of an isolated dune system demonstrates clear patterns in soil fungal communities across a successional gradient. Environmental Microbiology Reports, 2015, 7, 839-848.	2.4	11
31	Harnessing Chemical Ecology for Environment-Friendly Crop Protection. Phytopathology, 2021, 111, 1697-1710.	2.2	11
32	Treeâ€induced alterations to soil properties and rhizoplaneâ€associated bacteria following 23Âyears in a common garden. Plant and Soil, 2021, 461, 591-602.	3.7	10
33	Prospects of alleviating early plantingâ€associated cold susceptibility of soybean using microbes: New insights from microbiome analysis. Journal of Agronomy and Crop Science, 2021, 207, 171-185.	3.5	9
34	Dynamics of Physicochemical Variables and Cultivable Bacteria in Vermicompost During Steady Food Waste Addition and Upon Feed Interruption. Compost Science and Utilization, 2016, 24, 117-135.	1.2	8
35	Bark decomposition in white oak soil outperforms eastern hemlock soil, while bark type leads to consistent changes in soil microbial composition. Biogeochemistry, 2020, 150, 329-343.	3.5	8
36	Abiotic conditions outweigh microbial origin during bacterial assembly in soils. Environmental Microbiology, 2021, 23, 358-371.	3.8	8

#	Article	IF	Citations
37	Comparing Approaches for Capturing Bacterial Assemblages Associated with Symptomatic (Bacterial) Tj ETQq1 1 0.784314 rgBT /Over 90-99.	2.7	7
38	Rethinking Invasion Impacts across Multiple Field Sites Using European Swallowwort (Vincetoxicum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	E1	6
39	Hydrocarbon substrate richness impacts microbial abundance, microbiome composition, and hydrocarbon loss. Applied Soil Ecology, 2021, 165, 104015.	4.3	3
40	Relationship between soybean yield from high and low yielding field sites and selected soil characteristics. , 2020, 3, e20126.		3
41	Soybean Roots and Soil From High- and Low-Yielding Field Sites Have Different Microbiome Composition. Frontiers in Microbiology, 2021, 12, 675352.	3.5	3
42	Nitrogen services provided by interseeded cover crops in organic corn systems. Agronomy Journal, 2022, 114, 2458-2472.	1.8	3
43	Innovative Technologies Can Improve Understanding of Microbial Nitrogen Dynamics in Agricultural Soils. Agricultural and Environmental Letters, 2019, 4, 190032.	1.2	2
44	4. Merging microbial and plant profiling to understand the impact of human-generated extreme environments on natural and agricultural systems. , 2019, , 57-92.		2
45	Phylogenetic Signal, Root Morphology, Mycorrhizal Type, and Macroinvertebrate Exclusion: Exploring Wood Decomposition in Soils Conditioned by 13 Temperate Tree Species. Forests, 2022, 13, 536.	2.1	2
46	Metagenomics Potential for Bioremediation. , 2012, , 1-11.		1
47	The decay and fungal succession of apples with bitter rot across a vegetation diversity gradient. Phytobiomes Journal, 0, , .	2.7	1
48	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.6	1
49	Farm-scale differentiation of active microbial colonizers. ISME Communications, 2022, 2, .	4.2	1