Terrence H Bell

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8906089/publications.pdf

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49 2,211 papers citations

233421 22 45 h-index g-index

50 50 all docs citations

50 times ranked 2928 citing authors

#	Article	IF	CITATIONS
1	Can dispersal be leveraged to improve microbial inoculant success?. Trends in Biotechnology, 2022, 40, 12-21.	9.3	14
2	Soil salinization accelerates microbiome stabilization in iterative selections for plant performance. New Phytologist, 2022, 234, 2101-2110.	7.3	14
3	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
4	Nitrogen services provided by interseeded cover crops in organic corn systems. Agronomy Journal, 2022, 114, 2458-2472.	1.8	3
5	Farm-scale differentiation of active microbial colonizers. ISME Communications, 2022, 2, .	4.2	1
6	Host genomic influence on bacterial composition in the switchgrass rhizosphere. Molecular Ecology, 2022, 31, 3934-3950.	3.9	13
7	Abiotic conditions outweigh microbial origin during bacterial assembly in soils. Environmental Microbiology, 2021, 23, 358-371.	3.8	8
8	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
9	Harnessing Chemical Ecology for Environment-Friendly Crop Protection. Phytopathology, 2021, 111, 1697-1710.	2.2	11
10	The hierarchy of root branching order determines bacterial composition, microbial carrying capacity and microbial filtering. Communications Biology, 2021, 4, 483.	4.4	30
11	Hydrocarbon substrate richness impacts microbial abundance, microbiome composition, and hydrocarbon loss. Applied Soil Ecology, 2021, 165, 104015.	4.3	3
12	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
13	Soybean Roots and Soil From High- and Low-Yielding Field Sites Have Different Microbiome Composition. Frontiers in Microbiology, 2021, 12, 675352.	3.5	3
14	Comparing Approaches for Capturing Bacterial Assemblages Associated with Symptomatic (Bacterial) Tj ETQq0 90-99.	0 0 rgBT / 2.7	Overlock 10 Tf 7
15	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
16	Many roads to bacterial generalism. FEMS Microbiology Ecology, 2020, 97, .	2.7	21
17	Metatranscriptomic Sequencing of a Cyanobacterial Soil-Surface Consortium with and without a Diverse Underlying Soil Microbiome. Microbiology Resource Announcements, 2020, 9, .	0.6	1
18	Relationship between soybean yield from high and low yielding field sites and selected soil characteristics., 2020, 3, e20126.		3

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19	Innovative Technologies Can Improve Understanding of Microbial Nitrogen Dynamics in Agricultural Soils. Agricultural and Environmental Letters, 2019, 4, 190032.	1.2	2
20	100 Years Since Tolaas: Bacterial Blotch of Mushrooms in the 21 st Century. Plant Disease, 2019, 103, 2714-2732.	1.4	33
21	Factoring Ecological, Societal, and Economic Considerations into Inoculant Development. Trends in Biotechnology, 2019, 37, 572-573.	9.3	12
22	Manipulating Wild and Tamed Phytobiomes: Challenges and Opportunities. Phytobiomes Journal, 2019, 3, 3-21.	2.7	38
23	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
24	4. Merging microbial and plant profiling to understand the impact of human-generated extreme environments on natural and agricultural systems., 2019,, 57-92.		2
25	The Inherent Conflicts in Developing Soil Microbial Inoculants. Trends in Biotechnology, 2019, 37, 140-151.	9.3	179
26	Rethinking Invasion Impacts across Multiple Field Sites Using European Swallowwort (Vincetoxicum) Tj ETQq0 C	0 rgBT /O	verlock 10 Tf
27	<i>Medicago sativa</i> has Reduced Biomass and Nodulation When Grown with Soil Microbiomes Conditioned to High Phosphorus Inputs. Phytobiomes Journal, 2018, 2, 237-248.	2.7	25
28	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
29	Canola Root–Associated Microbiomes in the Canadian Prairies. Frontiers in Microbiology, 2018, 9, 1188.	3.5	85
30	Soil microbiome transfer method affects microbiome composition, including dominant microorganisms, in a novel environment. FEMS Microbiology Letters, 2017, 364, .	1.8	69
31	Petroleum biodegradation capacity of bacteria and fungi isolated from petroleum-contaminated soil. International Biodeterioration and Biodegradation, 2017, 116, 48-57.	3.9	105
32	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
33	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
34	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
35	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
36	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

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37	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
38	Culture-Dependent and -Independent Methods Capture Different Microbial Community Fractions in Hydrocarbon-Contaminated Soils. PLoS ONE, 2015, 10, e0128272.	2.5	167
39	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
40	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
41	Increasing phytoremediation efficiency and reliability using novel omics approaches. Trends in Biotechnology, 2014, 32, 271-280.	9.3	148
42	Alteration of microbial community structure affects diesel biodegradation in an Arctic soil. FEMS Microbiology Ecology, 2013, 85, 51-61.	2.7	54
43	Predictable bacterial composition and hydrocarbon degradation in Arctic soils following diesel and nutrient disturbance. ISME Journal, 2013, 7, 1200-1210.	9.8	190
44	Microbial Competition in Polar Soils: A Review of an Understudied but Potentially Important Control on Productivity. Biology, 2013, 2, 533-554.	2.8	34
45	Metagenomics Potential for Bioremediation. , 2012, , 1-11.		1
46	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
47	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
48	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
49	The decay and fungal succession of apples with bitter rot across a vegetation diversity gradient. Phytobiomes Journal, 0, , .	2.7	1