

# Jonathan W Leff

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8764843/publications.pdf>

Version: 2024-02-01

37  
papers

8,745  
citations

117625

34  
h-index

330143

37  
g-index

45  
all docs

45  
docs citations

45  
times ranked

12210  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cross-biome metagenomic analyses of soil microbial communities and their functional attributes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 21390-21395.	7.1	1,260
2	Consistent responses of soil microbial communities to elevated nutrient inputs in grasslands across the globe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10967-10972.	7.1	1,023
3	Relic DNA is abundant in soil and obscures estimates of soil microbial diversity. <i>Nature Microbiology</i> , 2017, 2, 16242.	13.3	660
4	Plant diversity predicts beta but not alpha diversity of soil microbes across grasslands worldwide. <i>Ecology Letters</i> , 2015, 18, 85-95.	6.4	612
5	Reconstructing the Microbial Diversity and Function of Pre-Agricultural Tallgrass Prairie Soils in the United States. <i>Science</i> , 2013, 342, 621-624.	12.6	480
6	Continental-scale distributions of dust-associated bacteria and fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5756-5761.	7.1	372
7	Bacterial Communities Associated with the Surfaces of Fresh Fruits and Vegetables. <i>PLoS ONE</i> , 2013, 8, e59310.	2.5	366
8	Biogeographic patterns in below-ground diversity in New York City's Central Park are similar to those observed globally. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141988.	2.6	295
9	Home Life: Factors Structuring the Bacterial Diversity Found within and between Homes. <i>PLoS ONE</i> , 2013, 8, e64133.	2.5	277
10	Changes in Bacterial and Fungal Communities across Compost Recipes, Preparation Methods, and Composting Times. <i>PLoS ONE</i> , 2013, 8, e79512.	2.5	258
11	Why are some microbes more ubiquitous than others? Predicting the habitat breadth of soil bacteria. <i>Ecology Letters</i> , 2014, 17, 794-802.	6.4	243
12	Predicting the structure of soil communities from plant community taxonomy, phylogeny, and traits. <i>ISME Journal</i> , 2018, 12, 1794-1805.	9.8	210
13	The ecology of microscopic life in household dust. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2015, 282, 20151139.	2.6	205
14	Volatile organic compound (VOC) emissions from soil and litter samples. <i>Soil Biology and Biochemistry</i> , 2008, 40, 1629-1636.	8.8	199
15	Microbes follow Humboldt: temperature drives plant and soil microbial diversity patterns from the Amazon to the Andes. <i>Ecology</i> , 2018, 99, 2455-2466.	3.2	197
16	Digging the New York City Skyline: Soil Fungal Communities in Green Roofs and City Parks. <i>PLoS ONE</i> , 2013, 8, e58020.	2.5	174
17	Diversity, distribution and sources of bacteria in residential kitchens. <i>Environmental Microbiology</i> , 2013, 15, 588-596.	3.8	170
18	A method for simultaneous measurement of soil bacterial abundances and community composition via 16S rRNA gene sequencing. <i>Soil Biology and Biochemistry</i> , 2016, 96, 145-151.	8.8	170

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19	Fungal diversity regulates plant-soil feedbacks in temperate grassland. <i>Science Advances</i> , 2018, 4, eaau4578.	10.3	161
20	Composition Diversity and Abundance of Gut Microbiome in Prediabetes and Type 2 Diabetes. <i>Journal of Diabetes and Obesity</i> , 2015, 2, 108-114.	0.2	159
21	Experimental litterfall manipulation drives large and rapid changes in soil carbon cycling in a wet tropical forest. <i>Global Change Biology</i> , 2012, 18, 2969-2979.	9.5	152
22	Do we need to understand microbial communities to predict ecosystem function? A comparison of statistical models of nitrogen cycling processes. <i>Soil Biology and Biochemistry</i> , 2014, 68, 279-282.	8.8	143
23	Nitrogen and phosphorus fertilization consistently favor pathogenic over mutualistic fungi in grassland soils. <i>Nature Communications</i> , 2021, 12, 3484.	12.8	116
24	Predicting the responsiveness of soil biodiversity to deforestation: a cross-biome study. <i>Global Change Biology</i> , 2014, 20, 2983-2994.	9.5	101
25	Spatial structuring of bacterial communities within individual <i>Acacia drepanolobium</i> trees. <i>Environmental Microbiology</i> , 2015, 17, 2352-2361.	3.8	94
26	Deconstructing the Bat Skin Microbiome: Influences of the Host and the Environment. <i>Frontiers in Microbiology</i> , 2016, 7, 1753.	3.5	81
27	Infection with a Shoot-Specific Fungal Endophyte ( <i>Epichloa</i> ) Alters Tall Fescue Soil Microbial Communities. <i>Microbial Ecology</i> , 2016, 72, 197-206.	2.8	67
28	Wild plant species growing closely connected in a subalpine meadow host distinct root-associated bacterial communities. <i>PeerJ</i> , 2015, 3, e804.	2.0	65
29	Long-lasting effects of land use history on soil fungal communities in second-growth tropical rain forests. <i>Ecological Applications</i> , 2016, 26, 1881-1895.	3.8	64
30	Response of soil microbial community composition and function to a bottomland forest restoration intensity gradient. <i>Applied Soil Ecology</i> , 2017, 119, 317-326.	4.3	62
31	Consequences of tropical forest conversion to oil palm on soil bacterial community and network structure. <i>Soil Biology and Biochemistry</i> , 2017, 112, 258-268.	8.8	60
32	The Effects of Soil Bacterial Community Structure on Decomposition in a Tropical Rain Forest. <i>Ecosystems</i> , 2012, 15, 284-298.	3.4	59
33	Fungi Identify the Geographic Origin of Dust Samples. <i>PLoS ONE</i> , 2015, 10, e0122605.	2.5	53
34	Biogeochemical drivers of microbial community convergence across actively retreating glaciers. <i>Soil Biology and Biochemistry</i> , 2016, 101, 74-84.	8.8	42
35	Following Rapoport's Rule: the geographic range and genome size of bacterial taxa decline at warmer latitudes. <i>Environmental Microbiology</i> , 2017, 19, 3152-3162.	3.8	25
36	The emerging contribution of social wasps to grape rot disease ecology. <i>PeerJ</i> , 2017, 5, e3223.	2.0	19

#	ARTICLE	IF	CITATIONS
37	High-resolution temporal profiling of the human gut microbiome reveals consistent and cascading alterations in response to dietary glycans. <i>Genome Medicine</i> , 2020, 12, 59.	8.2	18