Lucas William Mendes

List of Publications by Year
in descending order

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Version: 2024-02-01

91 papers	4,037 citations	201385 27 h-index	133063 59 g-index
93 all docs	93 docs citations	93 times ranked	4367 citing authors

#	Article	IF	Citations
1	Taxonomical and functional microbial community selection in soybean rhizosphere. ISME Journal, 2014, 8, 1577-1587.	4.4	633
2	Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. Science, 2019, 366, 606-612.	6.0	621
3	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. ISME Journal, 2018, 12, 212-224.	4.4	296
4	Soil-Borne Microbiome: Linking Diversity to Function. Microbial Ecology, 2015, 70, 255-265.	1.4	227
5	Impact of long-term N, P, K, and NPK fertilization on the composition and potential functions of the bacterial community in grassland soil. FEMS Microbiology Ecology, 2014, 90, 195-205.	1.3	193
6	Soil microbiome responses to the shortâ€term effects of Amazonian deforestation. Molecular Ecology, 2015, 24, 2433-2448.	2.0	171
7	Land-use system shapes soil bacterial communities in Southeastern Amazon region. Applied Soil Ecology, 2015, 95, 151-160.	2.1	114
8	Bacterial Community Succession in Pine-Wood Decomposition. Frontiers in Microbiology, 2016, 7, 231.	1.5	106
9	The impact of tropical forest logging and oil palm agriculture on the soil microbiome. Molecular Ecology, 2016, 25, 2244-2257.	2.0	99
10	Breeding for soil-borne pathogen resistance impacts active rhizosphere microbiome of common bean. ISME Journal, 2018, 12, 3038-3042.	4.4	92
11	Multitrophic interactions in the rhizosphere microbiome of wheat: from bacteria and fungi to protists. FEMS Microbiology Ecology, 2020, 96, .	1.3	77
12	Soil microbial community dynamics and assembly under long-term land use change. FEMS Microbiology Ecology, 2017, 93, .	1.3	69
13	Forest-to-agriculture conversion in Amazon drives soil microbial communities and N-cycle. Soil Biology and Biochemistry, 2019, 137, 107567.	4.2	61
14	Variations of Bacterial Community Structure and Composition in Mangrove Sediment at Different Depths in Southeastern Brazil. Diversity, 2014, 6, 827-843.	0.7	59
15	Protist species richness and soil microbiome complexity increase towards climax vegetation in the Brazilian Cerrado. Communications Biology, 2018, 1, 135.	2.0	58
16	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. Current Issues in Molecular Biology, 2017, 24, 103-118.	1.0	47
17	Recycling organic residues in agriculture impacts soil-borne microbial community structure, function and N2O emissions. Science of the Total Environment, 2018, 631-632, 1089-1099.	3.9	45
18	Forest-to-pasture conversion and recovery based on assessment of microbial communities in Eastern Amazon rainforest. FEMS Microbiology Ecology, 2019, 95, .	1.3	44

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19	Resistance Breeding of Common Bean Shapes the Physiology of the Rhizosphere Microbiome. Frontiers in Microbiology, 2019, 10, 2252.	1.5	41
20	Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. Microbial Ecology, 2020, 79, 110-122.	1.4	41
21	Shifts in phylogenetic diversity of archaeal communities in mangrove sediments at different sites and depths in southeastern Brazil. Research in Microbiology, 2012, 163, 366-377.	1.0	35
22	Responses of soil bacterial community after seventh yearly applications of composted tannery sludge. Geoderma, 2018, 318, 1-8.	2.3	35
23	Distinct taxonomic and functional composition of soil microbiomes along the gradient forest-restinga-mangrove in southeastern Brazil. Antonie Van Leeuwenhoek, 2018, 111, 101-114.	0.7	33
24	The natural recovery of soil microbial community and nitrogen functions after pasture abandonment in the Amazon region. FEMS Microbiology Ecology, 2020, 96, .	1.3	33
25	Microbiological indicators of soil quality in a riparian forest recovery gradient. Ecological Engineering, 2013, 53, 313-320.	1.6	32
26	Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. FEMS Microbiology Ecology, 2019, 95, .	1.3	32
27	Land-use systems affect Archaeal community structure and functional diversity in western Amazon soils. Revista Brasileira De Ciencia Do Solo, 2011, 35, 1527-1540.	0.5	31
28	Bacterial community associated with rhizosphere of maize and cowpea in a subsequent cultivation. Applied Soil Ecology, 2019, 143, 26-34.	2.1	31
29	Response of soil bacterial communities to the application of the herbicides imazethapyr and flumyzin. European Journal of Soil Biology, 2021, 102, 103252.	1.4	31
30	Bacillus subtilis can modulate the growth and root architecture in soybean through volatile organic compounds. Theoretical and Experimental Plant Physiology, 2020, 32, 99-108.	1.1	29
31	Molecular Characterization of the Archaeal Community in an Amazonian Wetland Soil and Culture-Dependent Isolation of Methanogenic Archaea. Diversity, 2010, 2, 1026-1047.	0.7	28
32	Metagenome assembledâ€genomes reveal similar functional profiles of <scp>CPR</scp>/Patescibacteria phyla in soils. Environmental Microbiology Reports, 2020, 12, 651-655.	1.0	27
33	Plant Compartments and Developmental Stages Modulate the Balance between Niche-Based and Neutral Processes in Soybean Microbiome. Microbial Ecology, 2021, 82, 416-428.	1.4	27
34	Liming in the sugarcane burnt system and the green harvest practice affect soil bacterial community in northeastern SÃ£o Paulo, Brazil. Antonie Van Leeuwenhoek, 2016, 109, 1643-1654.	0.7	26
35	Responses of soil microbial biomass and enzyme activity to herbicides imazethapyr and flumioxazin. Scientific Reports, 2020, 10, 7694.	1.6	26
36	Grazing exclusion regulates bacterial community in highly degraded semiarid soils from the Brazilian Caatinga biome. Land Degradation and Development, 2021, 32, 2210-2225.	1.8	23

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37	Functional diversity of bacterial genes associated with aromatic hydrocarbon degradation in anthropogenic dark earth of Amazonia. Pesquisa Agropecuaria Brasileira, 2012, 47, 654-664.	0.9	21
38	Assessment of Bacterial bph Gene in Amazonian Dark Earth and Their Adjacent Soils. PLoS ONE, 2014, 9, e99597.	1.1	21
39	Nodule microbiome from cowpea and lima bean grown in composted tannery sludge-treated soil. Applied Soil Ecology, 2020, 151, 103542.	2.1	21
40	Diversity and structure of bacterial community in rhizosphere of lima bean. Applied Soil Ecology, 2020, 150, 103490.	2.1	20
41	When the going gets tough: Emergence of a complex methane-driven interaction network during recovery from desiccation-rewetting. Soil Biology and Biochemistry, 2021, 153, 108109.	4.2	20
42	Microbial co-occurrence network and its key microorganisms in soil with permanent application of composted tannery sludge. Science of the Total Environment, 2021, 789, 147945.	3.9	20
43	Response of a methane-driven interaction network to stressor intensification. FEMS Microbiology Ecology, 2020, 96, .	1.3	19
44	Archaea diversity in vegetation gradients from the Brazilian Cerrado. Brazilian Journal of Microbiology, 2018, 49, 522-528.	0.8	16
45	Tannin supplementation modulates the composition and function of ruminal microbiome in lambs infected with gastrointestinal nematodes. FEMS Microbiology Ecology, 2020, 96, .	1.3	16
46	Amazon deforestation enriches antibiotic resistance genes. Soil Biology and Biochemistry, 2021, 153, 108110.	4.2	16
47	Land degradation affects the microbial communities in the Brazilian Caatinga biome. Catena, 2022, 211, 105961.	2.2	16
48	Dynamics of archaeal community in soil with application of composted tannery sludge. Scientific Reports, 2019, 9, 7347.	1.6	15
49	Bacillus subtilis changes the root architecture of soybean grown on nutrient-poor substrate. Rhizosphere, 2021, 18, 100348.	1.4	15
50	Long-term application of biomass and reduced use of chemicals alleviate soil compaction and improve soil quality. Soil and Tillage Research, 2012, 120, 147-153.	2.6	14
51	Recovery of Methanotrophic Activity Is Not Reflected in the Methane-Driven Interaction Network after Peat Mining. Applied and Environmental Microbiology, 2021, 87, .	1.4	14
52	Dynamics of bacterial and archaeal communities along the composting of tannery sludge. Environmental Science and Pollution Research, 2021, 28, 64295-64306.	2.7	12
53	The use of indigenous bacterial community as inoculant for plant growth promotion in soybean cultivation. Archives of Agronomy and Soil Science, 2023, 69, 135-150.	1.3	12
54	Genome-Resolved Metagenomics Is Essential for Unlocking the Microbial Black Box of the Soil. Trends in Microbiology, 2021, 29, 279-282.	3.5	11

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55	Distinct taxonomic composition of soil bacterial community across a native gradient of Cerrado-Ecotone-Caatinga. Applied Soil Ecology, 2021, 161, 103874.	2.1	9
56	Cover crops shape the soil bacterial community in a tropical soil under no-till. Applied Soil Ecology, 2021, 168, 104166.	2.1	9
57	Distinct bacterial community structure and composition along different cowpea producing ecoregions in Northeastern Brazil. Scientific Reports, 2021, 11, 831.	1.6	8
58	Assessment of microbial diversity associated with CH4 emission from sugarcane vinasse storage and transportation systems. Journal of Environmental Management, 2020, 269, 110748.	3.8	7
59	Isolation and enzyme bioprospection of bacteria associated to Bruguiera cylindrica, a mangrove plant of North Sumatra, Indonesia. Biotechnology Reports (Amsterdam, Netherlands), 2021, 30, e00617.	2.1	7
60	Metabolic potential and survival strategies of microbial communities across extreme temperature gradients on Deception Island volcano, Antarctica. Environmental Microbiology, 2021, 23, 4054-4073.	1.8	7
61	Does algae Î²-glucan affect the fecal bacteriome in dairy calves?. PLoS ONE, 2021, 16, e0258069.	1.1	7
62	Forest-to-pasture conversion modifies the soil bacterial community in Brazilian dry forest Caatinga. Science of the Total Environment, 2022, 810, 151943.	3.9	7
63	Endophytic Bacteria and Fungi from Indonesian Medicinal Plants with Antibacterial, Pathogenic Antifungal and Extracellular Enzymes Activities: A Review. International Journal of Science Technology & Management, 2022, 3, 245-255.	0.1	7
64	Domestication of Lima Bean (Phaseolus lunatus) Changes the Microbial Communities in the Rhizosphere. Microbial Ecology, 2023, 85, 1423-1433.	1.4	7
65	Arbuscular mycorrhizal community in soil from different Brazilian Cerrado physiognomies. Rhizosphere, 2021, 19, 100375.	1.4	6
66	The effect of Haemonchus contortus and Trichostrongylus colubriforms infection on the ruminal microbiome of lambs. Experimental Parasitology, 2021, 231, 108175.	0.5	6
67	Long-term land use in Amazon influence the dynamic of microbial communities in soil and rhizosphere. Rhizosphere, 2022, 21, 100482.	1.4	6
68	The methane-driven interaction network in terrestrial methane hotspots. Environmental Microbiomes, 2022, 17, 15.	2.2	6
69	Enzymatic Stoichiometry in Soils from Physiognomies of Brazilian Cerrado. Journal of Soil Science and Plant Nutrition, 2022, 22, 2735-2742.	1.7	6
70	Capability of plant growth-promoting bacteria in chromium-contaminated soil after application of composted tannery sludge. Annals of Microbiology, 2019, 69, 665-671.	1.1	5
71	Aerobic Methanotrophy and Co-occurrence Networks of a Tropical Rainforest and Oil Palm Plantations in Malaysia. Microbial Ecology, 2022, 84, 1154-1165.	1.4	5
72	Genetically related genotypes of cowpea present similar bacterial community in the rhizosphere. Scientific Reports, 2022, 12, 3472.	1.6	5

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73	Taxonomy and Functional Diversity in the Fecal Microbiome of Beef Cattle Reared in Brazilian Traditional and Semi-Intensive Production Systems. Frontiers in Microbiology, 2021, 12, 768480.	1.5	5
74	Environmental DNA Sequencing to Monitor Restoration Practices on Soil Bacterial and Archaeal Communities in Soils Under Desertification in the Brazilian Semiarid. Microbial Ecology, 2023, 85, 1072-1076.	1.4	5
75	Maintaining grass coverage increases methane uptake in Amazonian pastures, with a reduction of methanogenic archaea in the rhizosphere. Science of the Total Environment, 2022, 838, 156225.	3.9	5
76	Rhizosphere Microbiome and Soil-Borne Diseases. Rhizosphere Biology, 2021, , 155-168.	0.4	4
77	Soil microbial C:N:P ratio across physiognomies of Brazilian Cerrado Soil microbial biomass across a gradient of preserved native Cerrado. Anais Da Academia Brasileira De Ciencias, 2019, 91, e20190049.	0.3	4
78	On-Site Blackwater Treatment Fosters Microbial Groups and Functions to Efficiently and Robustly Recover Carbon and Nutrients. Microorganisms, 2021, 9, 75.	1.6	4
79	Cowpea nodules host a similar bacterial community regardless of soil properties. Applied Soil Ecology, 2022, 172, 104354.	2.1	4
80	Characterization and Comparison of Intestinal Bacterial Microbiomes of Euschistus heros and Piezodorus guildinii Collected in Brazil and the United States. Frontiers in Microbiology, 2021, 12, 769965.	1.5	3
81	Seed size influences the promoting activity of rhizobia on plant growth, nodulation and N fixation in lima bean. Ciencia Rural, 2021, 51, .	0.3	2
82	Diversity, structure, and composition of plant growth-promoting bacteria in soil from Brazilian Cerrado. Rhizosphere, 2021, 20, 100435.	1.4	2
83	Microbial Assembly in Agroecosystems â€" From the Small Arise the Big. , 0, , .		1
84	Analysis of a bacterial community structure and the diversity of phzF gene in samples of the Amazonian Dark Earths cultivated with cowpea [Vigna unguiculata (L.) Wald]. African Journal of Agricultural Research Vol Pp, 2018, 13, 1980-1989.	0.2	1
85	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. , 2017, , .		1
86	BIOPROSPECTING FOR BACTERIAL ENDOPHYTES ASSOCIATED WITH ZINGIBERACEAE FAMILY RHIZOMES IN SIBOLANGIT FOREST, NORTH SUMATERA. International Journal of Science Technology & Management, 2020, 1, 27-36.	0.1	1
87	Ecosystem functions in different physiognomies of Cerrado through the Rapid Ecosystem Function Assessment (REFA). Anais Da Academia Brasileira De Ciencias, 2022, 94, e20200457.	0.3	1
88	5. Exploring Diversity of Soil Microorganisms: A Multidimensional Approach. , 2016, , 66-86.		0
89	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. Methods in Molecular Biology, 2021, 2232, 251-263.	0.4	0
90	Dataset for effects of the transition from dry forest to pasture on diversity and structure of bacterial communities in Northeastern Brazil. Data in Brief, 2022, 41, 107842.	0.5	0

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91	Biogeographic responses and niche occupancy of microbial communities following long-term land-use change. Antonie Van Leeuwenhoek, 0, , .	0.7	0