

Jorge L Mazza Rodrigues

List of Publications by Year in descending order

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81
papers

4,733
citations

147801

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102487

66
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86
all docs

86
docs citations

86
times ranked

6234
citing authors

#	ARTICLE	IF	CITATIONS
1	Acid stress and compost addition decouple carbon and nitrogen cycling in an agricultural soil: An incubation study. <i>Applied Soil Ecology</i> , 2022, 169, 104219.	4.3	4
2	Topographic attributes override impacts of agronomic practices on prokaryotic community structure. <i>Applied Soil Ecology</i> , 2022, 175, 104446.	4.3	2
3	Increased soil moisture intensifies the impacts of forest-to-pasture conversion on methane emissions and methane-cycling communities in the Eastern Amazon. <i>Environmental Research</i> , 2022, 212, 113139.	7.5	15
4	Maintaining grass coverage increases methane uptake in Amazonian pastures, with a reduction of methanogenic archaea in the rhizosphere. <i>Science of the Total Environment</i> , 2022, 838, 156225.	8.0	5
5	Impacts of land-use change on soil microbial communities and their function in the Amazon Rainforest. <i>Advances in Agronomy</i> , 2022, , 179-258.	5.2	3
6	Rainforest-to-pasture conversion stimulates soil methanogenesis across the Brazilian Amazon. <i>ISME Journal</i> , 2021, 15, 658-672.	9.8	21
7	Dynamics of Fungal and Bacterial Biomass Carbon in Natural Ecosystems: Site-Level Applications of the CLM-Microbe Model. <i>Journal of Advances in Modeling Earth Systems</i> , 2021, 13, e2020MS002283.	3.8	11
8	Beyond total carbon: conversion of amazon forest to pasture alters indicators of soil C cycling. <i>Biogeochemistry</i> , 2021, 152, 179-194.	3.5	12
9	Microbial Succession under Freeze-Thaw Events and Its Potential for Hydrocarbon Degradation in Nutrient-Amended Antarctic Soil. <i>Microorganisms</i> , 2021, 9, 609.	3.6	4
10	Not just a methane source: Amazonian floodplain sediments harbour a high diversity of methanotrophs with different metabolic capabilities. <i>Molecular Ecology</i> , 2021, 30, 2560-2572.	3.9	9
11	Effects of magnetic biochar-microbe composite on Cd remediation and microbial responses in paddy soil. <i>Journal of Hazardous Materials</i> , 2021, 414, 125494.	12.4	53
12	Sensitivity and variability of soil health indicators in a California cropping system. <i>Soil Science Society of America Journal</i> , 2021, 85, 1827-1842.	2.2	6
13	Influence of Recycled Waste Compost on Soil Food Webs, Nutrient Cycling and Tree Growth in a Young Almond Orchard. <i>Agronomy</i> , 2021, 11, 1745.	3.0	1
14	Species patch size at seeding affects the productivity of mixed legume-grass communities. <i>European Journal of Agronomy</i> , 2021, 129, 126342.	4.1	2
15	Habitat heterogeneity induced by pyrogenic organic matter in wildfire-perturbed soils mediates bacterial community assembly processes. <i>ISME Journal</i> , 2021, 15, 1943-1955.	9.8	23
16	Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. <i>Microbial Ecology</i> , 2020, 79, 110-122.	2.8	41
17	Introducing the Mangrove Microbiome Initiative: Identifying Microbial Research Priorities and Approaches To Better Understand, Protect, and Rehabilitate Mangrove Ecosystems. <i>MSystems</i> , 2020, 5, .	3.8	40
18	Belowground changes to community structure alter methane-cycling dynamics in Amazonia. <i>Environment International</i> , 2020, 145, 106131.	10.0	18

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19	Soil microbial communities in restored and unrestored coastal dune ecosystems in California. <i>Restoration Ecology</i> , 2020, 28, S311.	2.9	16
20	Boosting landfill gas production from lignin-containing wastes via termite hindgut microorganism. <i>Waste Management</i> , 2020, 105, 299-308.	7.4	9
21	Impacts of directed evolution and soil management legacy on the maize rhizobiome. <i>Soil Biology and Biochemistry</i> , 2020, 145, 107794.	8.8	22
22	Draft Genome Sequences of Strains TAV3 and TAV4 (<i>Verrucomicrobia</i> : <i>Opiritaceae</i>), Isolated from a Wood-Feeding Termite, and <i>In Silico</i> Analysis of Their Polysaccharide-Degrading Enzymes. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
23	Diazotrophs Show Signs of Restoration in Amazon Rain Forest Soils with Ecosystem Rehabilitation. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	11
24	Global biogeography of fungal and bacterial biomass carbon in topsoil. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108024.	8.8	70
25	Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	32
26	Deforestation impacts network co-occurrence patterns of microbial communities in Amazon soils. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	2.7	34
27	Determining landscape-level drivers of variability for over fifty soil chemical elements. <i>Science of the Total Environment</i> , 2019, 657, 279-286.	8.0	10
28	Long-term effects of grazing and topography on extra-radical hyphae of arbuscular mycorrhizal fungi in semi-arid grasslands. <i>Mycorrhiza</i> , 2018, 28, 117-127.	2.8	26
29	Iron limitation effects on nitrogen-fixing organisms with possible implications for cyanobacterial blooms. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	2.7	25
30	Draft Genome Sequence of " <i>Candidatus</i> <i>Spirobacillus cienkowskii</i> ," a Pathogen of Freshwater <i>Daphnia</i> Species, Reconstructed from Hemolymph Metagenomic Reads. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	13
31	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. <i>Frontiers in Microbiology</i> , 2018, 9, 1635.	3.5	51
32	Conversion of Amazon rainforest to agriculture alters community traits of methane cycling organisms. <i>Molecular Ecology</i> , 2017, 26, 1547-1556.	3.9	78
33	Distinct Biogeographic Patterns for Archaea, Bacteria, and Fungi along the Vegetation Gradient at the Continental Scale in Eastern China. <i>MSystems</i> , 2017, 2, .	3.8	116
34	Soil microbial community dynamics and assembly under long-term land use change. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	2.7	69
35	A Novel Multifunctional H^2 -N-Acetylhexosaminidase Revealed through Metagenomics of an Oil-Spilled Mangrove. <i>Bioengineering</i> , 2017, 4, 62.	3.5	13
36	Identification of the <i>Burkholderia pseudomallei</i> bacteriophage ST79 lysis gene cassette. <i>Journal of Applied Microbiology</i> , 2016, 121, 364-372.	3.1	6

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37	Hill number as a bacterial diversity measure framework with high-throughput sequence data. <i>Scientific Reports</i> , 2016, 6, 38263.	3.3	28
38	A Step Forward to Empower Global Microbiome Research Through Local Leadership. <i>Trends in Microbiology</i> , 2016, 24, 767-771.	7.7	12
39	Cloning, expression, and characterization of a peptidoglycan hydrolase from the <i>Burkholderia pseudomallei</i> phage ST79. <i>AMB Express</i> , 2016, 6, 77.	3.0	9
40	<i>Shewanella baltica</i> Ecotypes Have Wide Transcriptional Variation under the Same Growth Conditions. <i>MSphere</i> , 2016, 1, .	2.9	3
41	Land use change in the Amazon rain forest favours generalist fungi. <i>Functional Ecology</i> , 2016, 30, 1845-1853.	3.6	58
42	Land-use change drives abundance and community structure alterations of thaumarchaeal ammonia oxidizers in tropical rainforest soils in Rondônia, Brazil. <i>Applied Soil Ecology</i> , 2016, 107, 48-56.	4.3	32
43	Forest-to-pasture conversion increases the diversity of the phylum Verrucomicrobia in Amazon rainforest soils. <i>Frontiers in Microbiology</i> , 2015, 6, 779.	3.5	50
44	Differential Response of Acidobacteria Subgroups to Forest-to-Pasture Conversion and Their Biogeographic Patterns in the Western Brazilian Amazon. <i>Frontiers in Microbiology</i> , 2015, 6, 1443.	3.5	111
45	Complete Genome Sequence of the Opitutaceae Bacterium Strain TAV5, a Potential Facultative Methylophile of the Wood-Feeding Termite <i>Reticulitermes flavipes</i> . <i>Genome Announcements</i> , 2015, 3, .	0.8	22
46	THE CONTRIBUTION OF SOIL PHYSICO-CHEMICAL PROPERTIES TO THE PRESENCE AND GENETIC DIVERSITY OF <i>BURKHOLDERIA PSEUDOMALLEI</i> . <i>Southeast Asian Journal of Tropical Medicine and Public Health</i> , 2015, 46, 38-50.	1.0	16
47	Links between plant and fungal communities across a deforestation chronosequence in the Amazon rainforest. <i>ISME Journal</i> , 2014, 8, 1548-1550.	9.8	131
48	Response of Free-Living Nitrogen-Fixing Microorganisms to Land Use Change in the Amazon Rainforest. <i>Applied and Environmental Microbiology</i> , 2014, 80, 281-288.	3.1	104
49	Land use change alters functional gene diversity, composition and abundance in Amazon forest soil microbial communities. <i>Molecular Ecology</i> , 2014, 23, 2988-2999.	3.9	152
50	Stability, genotypic and phenotypic diversity of <i>Shewanella baltica</i> in the redox transition zone of the Baltic Sea. <i>Environmental Microbiology</i> , 2014, 16, 1854-1866.	3.8	26
51	The Family Opitutaceae. , 2014, , 751-756.		7
52	Development of an ecophysiological model for <i>Diplosphaera colotermitum</i> TAV2, a termite hindgut Verrucomicrobium. <i>ISME Journal</i> , 2013, 7, 1803-1813.	9.8	18
53	Tropical agricultural land management influences on soil microbial communities through its effect on soil organic carbon. <i>Soil Biology and Biochemistry</i> , 2013, 65, 33-38.	8.8	189
54	Conversion of the Amazon rainforest to agriculture results in biotic homogenization of soil bacterial communities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 988-993.	7.1	481

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55	High-Quality Draft Genome Sequence of the Opitutaceae Bacterium Strain TAV1, a Symbiont of the Wood-Feeding Termite <i>Reticulitermes flavipes</i> . <i>Journal of Bacteriology</i> , 2012, 194, 2744-2745.	2.2	24
56	Development of a Direct Isolation Procedure for Free-Living Diazotrophs under Controlled Hypoxic Conditions. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5542-5549.	3.1	52
57	Genomic and Physiological Characterization of the Verrucomicrobia Isolate <i>Diplosphaera colitermitum</i> gen. nov., sp. nov., Reveals Microaerophily and Nitrogen Fixation Genes. <i>Applied and Environmental Microbiology</i> , 2012, 78, 1544-1555.	3.1	115
58	A composite bacteriophage alters colonization by an intestinal commensal bacterium. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17621-17626.	7.1	198
59	Fnr (EtrA) acts as a fine-tuning regulator of anaerobic metabolism in <i>Shewanella oneidensis</i> MR-1. <i>BMC Microbiology</i> , 2011, 11, 64.	3.3	30
60	Large-Scale Comparative Phenotypic and Genomic Analyses Reveal Ecological Preferences of <i>Shewanella</i> Species and Identify Metabolic Pathways Conserved at the Genus Level. <i>Applied and Environmental Microbiology</i> , 2011, 77, 5352-5360.	3.1	21
61	Bacterial Communities in the Rhizosphere of Biofuel Crops Grown on Marginal Lands as Evaluated by 16S rRNA Gene Pyrosequences. <i>Bioenergy Research</i> , 2010, 3, 20-27.	3.9	40
62	Phylogenetic and metagenomic analysis of Verrucomicrobia in former agricultural grassland soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 23-33.	2.7	23
63	Characterization of a bacterial community from a Northeast Siberian seacoast permafrost sample. <i>FEMS Microbiology Ecology</i> , 2010, 74, 103-113.	2.7	31
64	DNA-Stable Isotope Probing Integrated with Metagenomics for Retrieval of Biphenyl Dioxygenase Genes from Polychlorinated Biphenyl-Contaminated River Sediment. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5501-5506.	3.1	96
65	Comparative systems biology across an evolutionary gradient within the <i>Shewanella</i> genus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15909-15914.	7.1	96
66	Towards environmental systems biology of <i>Shewanella</i> . <i>Nature Reviews Microbiology</i> , 2008, 6, 592-603.	28.6	829
67	Phylogenetic Characterization and Prevalence of <i>Spirobacillus cienkowskii</i> , a Red-Pigmented, Spiral-Shaped Bacterial Pathogen of Freshwater <i>Daphnia</i> Species. <i>Applied and Environmental Microbiology</i> , 2008, 74, 1575-1582.	3.1	24
68	Biphenyl-utilizing bacteria and their functional genes in a pine root zone contaminated with polychlorinated biphenyls (PCBs). <i>ISME Journal</i> , 2007, 1, 134-148.	9.8	198
69	Genetic and Genomic Insights into the Role of Benzoate-Catabolic Pathway Redundancy in <i>Burkholderia xenovorans</i> LB400. <i>Applied and Environmental Microbiology</i> , 2006, 72, 585-595.	3.1	99
70	In situ probing of <i>Xylella fastidiosa</i> in honeydew of a xylem sap-feeding insect using 16S rRNA-targeted fluorescent oligonucleotides. <i>Environmental Microbiology</i> , 2006, 8, 747-754.	3.8	6
71	Detection and characterization of protease secreted by the plant pathogen <i>Xylella fastidiosa</i> . <i>Microbiological Research</i> , 2006, 161, 263-272.	5.3	22
72	Degradation of Aroclor 1242 Dechlorination Products in Sediments by <i>Burkholderia xenovorans</i> LB400(ohb) and <i>Rhodococcus</i> sp. Strain RHA1(fcb). <i>Applied and Environmental Microbiology</i> , 2006, 72, 2476-2482.	3.1	78

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73	Identification of bacteria in endodontic infections by sequence analysis of 16S rDNA clone libraries. <i>Journal of Medical Microbiology</i> , 2006, 55, 101-107.	1.8	72
74	Growth and siderophore production of <i>Xylella fastidiosa</i> under iron-limited conditions. <i>Microbiological Research</i> , 2005, 160, 429-436.	5.3	37
75	Characterization of nitrogen-fixing cyanobacteria in the Brazilian Amazon floodplain. <i>Water Research</i> , 2005, 39, 5017-5026.	11.3	49
76	Validation of a more sensitive method for using spotted oligonucleotide DNA microarrays for functional genomics studies on bacterial communities. <i>Environmental Microbiology</i> , 2003, 5, 933-943.	3.8	87
77	Detection and Diversity Assessment of <i>Xylella fastidiosa</i> in Field-Collected Plant and Insect Samples by Using 16S rRNA and <i>gyrB</i> Sequences. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4249-4255.	3.1	74
78	Use of both 16S rRNA and engineered functional genes with real-time PCR to quantify an engineered, PCB-degrading <i>Rhodococcus</i> in soil. <i>Journal of Microbiological Methods</i> , 2002, 51, 181-189.	1.6	26
79	Development of a <i>Rhodococcus</i> Recombinant Strain for Degradation of Products from Anaerobic Dechlorination of PCBs. <i>Environmental Science & Technology</i> , 2001, 35, 663-668.	10.0	42
80	Fotossíntese, remobilização de reservas e crescimento de grãos em dois híbridos de milho sob deficiência hídrica na fase de enchimento dos grãos. <i>Bragantia</i> , 1992, 51, 151-159.	1.3	9
81	Biogeographic responses and niche occupancy of microbial communities following long-term land-use change. <i>Antonie Van Leeuwenhoek</i> , 0, , .	1.7	0