## Siu Mui Tsai

## List of Publications by Year in descending order

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205 papers 10,850 citations

44069 48 h-index 96 g-index

210 all docs

210 docs citations

210 times ranked

11490 citing authors

#	Article	IF	CITATIONS
1	Comparison of the genomes of two Xanthomonas pathogens with differing host specificities. Nature, 2002, 417, 459-463.	27.8	1,074
2	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	27.8	827
3	Taxonomical and functional microbial community selection in soybean rhizosphere. ISME Journal, 2014, 8, 1577-1587.	9.8	633
4	Conversion of the Amazon rainforest to agriculture results in biotic homogenization of soil bacterial communities. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 988-993.	7.1	481
5	Comparative Genomics of Two Leptospira interrogans Serovars Reveals Novel Insights into Physiology and Pathogenesis. Journal of Bacteriology, 2004, 186, 2164-2172.	2.2	406
6	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of Xylella fastidiosa. Journal of Bacteriology, 2003, 185, 1018-1026.	2.2	307
7	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. ISME Journal, 2018, 12, 212-224.	9.8	296
8	Towards an integrated linkage map of common bean. 4. Development of a core linkage map and alignment of RFLP maps. Theoretical and Applied Genetics, 1998, 97, 847-856.	3.6	275
9	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. FEMS Microbiology Ecology, 2013, 83, 607-621.	2.7	228
10	Soil-Borne Microbiome: Linking Diversity to Function. Microbial Ecology, 2015, 70, 255-265.	2.8	227
11	Flavonoids Released Naturally from Alfalfa Promote Development of Symbiotic <i>Glomus</i> Spores In Vitro. Applied and Environmental Microbiology, 1991, 57, 1485-1488.	3.1	211
12	Amazonian Anthrosols Support Similar Microbial Communities that Differ Distinctly from Those Extant in Adjacent, Unmodified Soils of the Same Mineralogy. Microbial Ecology, 2010, 60, 192-205.	2.8	186
13	Validation of reference genes for RT-qPCR normalization in common bean during biotic and abiotic stresses. Plant Cell Reports, 2012, 31, 827-838.	5.6	183
14	Soil microbiome responses to the shortâ€ŧerm effects of Amazonian deforestation. Molecular Ecology, 2015, 24, 2433-2448.	3.9	171
15	Mixed-species plantations of Acacia mangium and Eucalyptus grandis in Brazil. Forest Ecology and Management, 2008, 255, 3918-3930.	3.2	127
16	The Genome Sequence of the Gram-Positive Sugarcane Pathogen Leifsonia xyli subsp. xyli. Molecular Plant-Microbe Interactions, 2004, 17, 827-836.	2.6	119
17	Brazilian Microbiome Project: Revealing the Unexplored Microbial Diversity—Challenges and Prospects. Microbial Ecology, 2014, 67, 237-241.	2.8	119
18	Land-use system shapes soil bacterial communities in Southeastern Amazon region. Applied Soil Ecology, 2015, 95, 151-160.	4.3	114

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19	Differential Response of Acidobacteria Subgroups to Forest-to-Pasture Conversion and Their Biogeographic Patterns in the Western Brazilian Amazon. Frontiers in Microbiology, 2015, 6, 1443.	3.5	111
20	Soil microbial properties and temporal stability in degraded and restored lands of Northeast Brazil. Soil Biology and Biochemistry, 2013, 66, 175-181.	8.8	102
21	Breeding for soil-borne pathogen resistance impacts active rhizosphere microbiome of common bean. ISME Journal, 2018, 12, 3038-3042.	9.8	92
22	Salt-tolerant phenol-degrading microorganisms isolated from Amazonian soil samples. Archives of Microbiology, 2000, 174, 346-352.	2.2	86
23	Development, characterization, and comparative analysis of polymorphism at common bean SSR loci isolated from genic and genomic sources. Genome, 2007, 50, 266-277.	2.0	85
24	Diversity and identification of methanogenic archaea and sulphate-reducing bacteria in sediments from a pristine tropical mangrove. Antonie Van Leeuwenhoek, 2010, 97, 401-411.	1.7	80
25	Effect of phytate and storage conditions on the development of the â€~hard-to-cook' phenomenon in common beans. Journal of the Science of Food and Agriculture, 2007, 87, 1237-1243.	3.5	77
26	Endophytic bacteria in long-term in vitro cultivated "axenic―pineapple microplants revealed by PCR–DGGE. World Journal of Microbiology and Biotechnology, 2010, 26, 555-560.	3.6	77
27	Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility. Antonie Van Leeuwenhoek, 2015, 108, 741-752.	1.7	77
28	Miniprep DNA isolation from unicellular and filamentous cyanobacteria. Journal of Microbiological Methods, 2000, 39, 159-169.	1.6	74
29	Detection and Diversity Assessment of Xylella fastidiosa in Field-Collected Plant and Insect Samples by Using 16S rRNA and gyrB Sequences. Applied and Environmental Microbiology, 2003, 69, 4249-4255.	3.1	74
30	Identification of bacteria in endodontic infections by sequence analysis of 16S rDNA clone libraries. Journal of Medical Microbiology, 2006, 55, 101-107.	1.8	72
31	Extension of the core map of common bean with EST-SSR, RGA, AFLP, and putative functional markers. Molecular Breeding, 2010, 25, 25-45.	2.1	72
32	Soil microbial community dynamics and assembly under long-term land use change. FEMS Microbiology Ecology, 2017, 93, .	2.7	69
33	Long-term lime and gypsum amendment increase nitrogen fixation and decrease nitrification and denitrification gene abundances in the rhizosphere and soil in a tropical no-till intercropping system. Geoderma, 2020, 375, 114476.	5.1	69
34	Effect of a highly concentrated lipopeptide extract of Bacillus subtilis on fungal and bacterial cells. Archives of Microbiology, 2008, 190, 611-622.	2.2	66
35	A Molecular Survey of the Diversity of Microbial Communities in Different Amazonian Agricultural Model Systems. Diversity, 2010, 2, 787-809.	1.7	64
36	Land use, soil and litter chemistry drive bacterial community structures in samples of the rainforest and Cerrado (Brazilian Savannah) biomes in Southern Amazonia. European Journal of Soil Biology, 2015, 66, 32-39.	3.2	63

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37	The Influence of Different Land Uses on the Structure of Archaeal Communities in Amazonian Anthrosols Based on 16S rRNA and amoA Genes. Microbial Ecology, 2010, 59, 734-743.	2.8	61
38	Bacterial community composition of anthropogenic biochar and Amazonian anthrosols assessed by 16S rRNA gene 454 pyrosequencing. Antonie Van Leeuwenhoek, 2013, 104, 233-242.	1.7	61
39	Oxidative mitigation of aquatic methane emissions in large Amazonian rivers. Global Change Biology, 2016, 22, 1075-1085.	9.5	61
40	Forest-to-agriculture conversion in Amazon drives soil microbial communities and N-cycle. Soil Biology and Biochemistry, 2019, 137, 107567.	8.8	61
41	Acidobacteria Subgroups and Their Metabolic Potential for Carbon Degradation in Sugarcane Soil Amended With Vinasse and Nitrogen Fertilizers. Frontiers in Microbiology, 2019, 10, 1680.	3.5	61
42	Variations of Bacterial Community Structure and Composition in Mangrove Sediment at Different Depths in Southeastern Brazil. Diversity, 2014, 6, 827-843.	1.7	59
43	Gases and volatile compounds associated with micro-organisms in blown pack spoilage of Brazilian vacuum-packed beef. Letters in Applied Microbiology, 2012, 55, 467-475.	2.2	58
44	Detection of siderophores in endophytic bacteria Methylobacterium spp. associated with Xylella fastidiosa subsp. pauca. Pesquisa Agropecuaria Brasileira, 2008, 43, 521-528.	0.9	57
45	Characterization of a broad range antibacterial substance from a new Bacillus species isolated from Amazon basin. Archives of Microbiology, 2007, 188, 367-375.	2.2	56
46	Effect of drought stress on the genetic architecture of photosynthate allocation and remobilization in pods of common bean (Phaseolus vulgaris L.), a key species for food security. BMC Plant Biology, 2019, 19, 171.	3.6	55
47	Impact of Land Degradation on Soil Microbial Biomass and Activity in Northeast Brazil. Pedosphere, 2012, 22, 88-95.	4.0	53
48	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. PLoS ONE, 2015, 10, e0129765.	2.5	52
49	New Biological Insights Into How Deforestation in Amazonia Affects Soil Microbial Communities Using Metagenomics and Metagenome-Assembled Genomes. Frontiers in Microbiology, 2018, 9, 1635.	3.5	51
50	A new glance on root-to-shoot in vivo zinc transport and time-dependent physiological effects of ZnSO4 and ZnO nanoparticles on plants. Scientific Reports, 2019, 9, 10416.	3.3	51
51	Archaeal communities in the sediments of three contrasting mangroves. Journal of Soils and Sediments, 2011, 11, 1466-1476.	3.0	50
52	Characterization of nitrogen-fixing cyanobacteria in the Brazilian Amazon floodplain. Water Research, 2005, 39, 5017-5026.	11.3	49
53	Root and shoot variation in relation to potential intermittent drought adaptation of Mesoamerican wild common bean (Phaseolus vulgaris L.). Annals of Botany, 2019, 124, 917-932.	2.9	49
54	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. Current Issues in Molecular Biology, 2017, 24, 103-118.	2.4	47

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55	In vitro evaluation, in vivo quantification, and microbial diversity studies of nutritional strategies for reducing enteric methane production. Tropical Animal Health and Production, 2012, 44, 953-964.	1.4	45
56	Emission of nitrous oxide and dinitrogen by diverse earthworm families from Brazil and resolution of associated denitrifying and nitrate-dissimilating taxa. FEMS Microbiology Ecology, 2013, 83, 375-391.	2.7	45
57	Transcriptional Analysis of Drought-Induced Genes in the Roots of a Tolerant Genotype of the Common Bean (Phaseolus vulgaris L.). International Journal of Molecular Sciences, 2013, 14, 7155-7179.	4.1	45
58	Forest-to-pasture conversion and recovery based on assessment of microbial communities in Eastern Amazon rainforest. FEMS Microbiology Ecology, 2019, 95, .	2.7	44
59	Title is missing!. Euphytica, 2001, 118, 265-270.	1.2	43
60	Algicide production by the filamentous cyanobacterium Fischerella sp. CENA 19. Journal of Applied Phycology, 2004, 16, 237-243.	2.8	43
61	Properties of a sandy clay loam Haplic Ferralsol and soybean grain yield in a five-year field trial as affected by biochar amendment. Geoderma, 2017, 305, 100-112.	5.1	43
62	Amazonian Dark Earth and Plant Species from the Amazon Region Contribute to Shape Rhizosphere Bacterial Communities. Microbial Ecology, 2015, 69, 855-866.	2.8	41
63	Resistance Breeding of Common Bean Shapes the Physiology of the Rhizosphere Microbiome. Frontiers in Microbiology, 2019, 10, 2252.	3.5	41
64	Ecological Processes Shaping Bulk Soil and Rhizosphere Microbiome Assembly in a Long-Term Amazon Forest-to-Agriculture Conversion. Microbial Ecology, 2020, 79, 110-122.	2.8	41
65	Arbuscular Mycorrhizal Symbiosis Leads to Differential Regulation of Drought-Responsive Genes in Tissue-Specific Root Cells of Common Bean. Frontiers in Microbiology, 2018, 9, 1339.	3.5	40
66	Soil bacterial diversity in degraded and restored lands of Northeast Brazil. Antonie Van Leeuwenhoek, 2014, 106, 891-899.	1.7	39
67	Disentangling the influence of earthworms in sugarcane rhizosphere. Scientific Reports, 2016, 6, 38923.	3.3	38
68	Growth and siderophore production of Xylella fastidiosa under iron-limited conditions. Microbiological Research, 2005, 160, 429-436.	5.3	37
69	Spore density and root colonization by arbuscular mycorrhizal fungi in preserved or disturbed Araucaria angustifolia (Bert.) O. Ktze. ecosystems. Scientia Agricola, 2006, 63, 380-385.	1.2	36
70	Dissecting Phaseolus vulgaris Innate Immune System against Colletotrichum lindemuthianum Infection. PLoS ONE, 2012, 7, e43161.	2.5	36
71	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.	2.1	35
72	Fungal Community Assembly in the Amazonian Dark Earth. Microbial Ecology, 2016, 71, 962-973.	2.8	35

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73	Methanogenic food web in the gut contents of methane-emitting earthworm <i>Eudrilus eugeniae</i> from Brazil. ISME Journal, 2015, 9, 1778-1792.	9.8	34
74	Distinct taxonomic and functional composition of soil microbiomes along the gradient forest-restinga-mangrove in southeastern Brazil. Antonie Van Leeuwenhoek, 2018, 111, 101-114.	1.7	33
75	The natural recovery of soil microbial community and nitrogen functions after pasture abandonment in the Amazon region. FEMS Microbiology Ecology, 2020, 96, .	2.7	33
76	Telomere and microsatellite primers reveal diversity among Sclerotinia sclerotiorum isolates from Brazil. Tropical Plant Pathology, 2002, 27, 211-215.	0.3	33
77	Seed phytate content and phosphorus uptake and distribution in dry bean genotypes. Brazilian Journal of Plant Physiology, 2002, 14, 51-58.	0.5	32
78	Biodiversity and distribution of arbuscular mycorrhizal fungi in Araucaria angustifolia forest. Scientia Agricola, 2007, 64, 393-399.	1.2	32
79	Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. FEMS Microbiology Ecology, 2019, 95, .	2.7	32
80	Land-use systems affect Archaeal community structure and functional diversity in western Amazon soils. Revista Brasileira De Ciencia Do Solo, 2011, 35, 1527-1540.	1.3	31
81	Investigation of Endophytic Bacterial Community in Supposedly Axenic Cultures of Pineapple and Orchids with Evidence on Abundant Intracellular Bacteria. Current Microbiology, 2017, 74, 103-113.	2.2	30
82	Forest conversion to pasture affects soil phosphorus dynamics and nutritional status in Brazilian Amazon. Soil and Tillage Research, 2019, 194, 104330.	5.6	29
83	Identification of Coffee Genes Expressed During Systemic Acquired Resistance and Incompatible Interaction with <i>Hemileia vastatrix</i> ). Journal of Phytopathology, 2009, 157, 625-638.	1.0	28
84	Molecular Characterization of the Archaeal Community in an Amazonian Wetland Soil and Culture-Dependent Isolation of Methanogenic Archaea. Diversity, 2010, 2, 1026-1047.	1.7	28
85	Emission of Methane by Eudrilus eugeniae and Other Earthworms from Brazil. Applied and Environmental Microbiology, 2012, 78, 3014-3019.	3.1	28
86	In silico analysis of nonribosomal peptide synthetases of Xanthomonas axonopodis pv. citri: identification of putative siderophore and lipopeptide biosynthetic genes. Microbiological Research, 2004, 159, 425-437.	<b>5.</b> 3	27
87	Purification and partial characterization of an antimicrobial peptide produced by Bacillus sp. strain P45, a bacterium from the Amazon basin fish Piaractus mesopotamicus. Journal of General and Applied Microbiology, 2006, 52, 357-363.	0.7	27
88	Real-time Polymerase Chain Reaction Quantification of Porphyromonas gingivalis and Tannerella forsythia in Primary Endodontic Infections. Journal of Endodontics, 2009, 35, 1518-1524.	3.1	27
89	Characterization of feather-degrading bacteria from Brazilian soils. International Biodeterioration and Biodegradation, 2011, 65, 102-107.	3.9	27
90	Thermal behavior of malonylglucoside isoflavones in soybean flour analyzed by RPHPLC/DAD and eletrospray ionization mass spectrometry. LWT - Food Science and Technology, 2012, 48, 114-119.	5 <b>.</b> 2	27

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91	Metagenome assembledâ€genomes reveal similar functional profiles of <scp>CPR</scp> /Patescibacteria phyla in soils. Environmental Microbiology Reports, 2020, 12, 651-655.	2.4	27
92	Alfalfa yield and quality as function of nitrogen fertilization and symbiosis with Sinorhizobium meliloti. Scientia Agricola, 2004, 61, 433-438.	1.2	26
93	Sporulation and diversity of arbuscular mycorrhizal fungi in Brazil Pine in the field and in the greenhouse. Mycorrhiza, 2007, 17, 519-526.	2.8	26
94	Changes in spatial and temporal gene expression during incompatible interaction between common bean and anthracnose pathogen. Journal of Plant Physiology, 2012, 169, 1216-1220.	3.5	26
95	Liming in the sugarcane burnt system and the green harvest practice affect soil bacterial community in northeastern São Paulo, Brazil. Antonie Van Leeuwenhoek, 2016, 109, 1643-1654.	1.7	26
96	Interface between breast cancer cells and the tumor microenvironment using platelet-rich plasma to promote tumor angiogenesis - influence of platelets and fibrin bundles on the behavior of breast tumor cells. Oncotarget, 2017, 8, 16851-16874.	1.8	26
97	Can alternative N-fertilization methods influence GHG emissions and biomass production in sugarcane fields?. Biomass and Bioenergy, 2019, 120, 21-27.	5.7	26
98	Effects of Phaseolus vulgaris QTL in controlling host-bacteria interactions under two levels of nitrogen fertilization. Genetics and Molecular Biology, 2000, 23, 155-161.	1.3	25
99	Genome-wide characterization of the NRAMP gene family in Phaseolus vulgaris provides insights into functional implications during common bean development. Genetics and Molecular Biology, 2018, 41, 820-833.	1.3	24
100	Molecular characterization and antibiotic resistance of Staphylococcus spp. isolated from cheese processing plants. Journal of Dairy Science, 2017, 100, 5167-5175.	3.4	23
101	Detection and characterization of protease secreted by the plant pathogen Xylella fastidiosa. Microbiological Research, 2006, 161, 263-272.	5.3	22
102	Expression of essential genes for biosynthesis of antimicrobial peptides of Bacillus is modulated by inactivated cells of target microorganisms. Research in Microbiology, 2016, 167, 83-89.	2.1	22
103	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
104	Assessment of Bacterial bph Gene in Amazonian Dark Earth and Their Adjacent Soils. PLoS ONE, 2014, 9, e99597.	2.5	21
105	Rainforest-to-pasture conversion stimulates soil methanogenesis across the Brazilian Amazon. ISME Journal, 2021, 15, 658-672.	9.8	21
106	Colorimetric test for the monitoring of microcystins in cyanobacterial culture and environmental samples from southeast - Brazil. Brazilian Journal of Microbiology, 2006, 37, 192-198.	2.0	21
107	In silico characterization of microsatellites in Eucalyptus spp.: abundance, length variation and transposon associations. Genetics and Molecular Biology, 2005, 28, 582-588.	1.3	20
108	Dynamics of inositol phosphate pools (tris-, tetrakis- and pentakisphosphate) in relation to the rate of phytate synthesis during seed development in common bean (Phaseolus vulgaris). Journal of Plant Physiology, 2005, 162, 1-9.	3.5	20

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109	Capacity of Aromatic Compound Degradation by Bacteria from Amazon Dark Earth. Diversity, 2014, 6, 339-353.	1.7	20
110	Caracterização da diversidade genética em feijão por meio de marcadores RAPD. Pesquisa Agropecuaria Brasileira, 2001, 36, 381-385.	0.9	19
111	An alternative method for Staphylococcus aureus DNA isolation. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 299-306.	0.4	19
112	Occurrence of powdery mildew disease in wheat fertilized with increasing silicon doses: a chemometric analysis of antioxidant response. Acta Physiologiae Plantarum, 2016, 38, 1.	2.1	19
113	Zinc concentration affects the functional groups of microbial communities in sugarcane-cultivated soil. Agriculture, Ecosystems and Environment, 2017, 236, 187-197.	5.3	19
114	Genetic analyses of Rhizoctonia solani isolates from Phaseolus vulgaris grown in the Atlantic Rainforest Region of São Paulo, Brazil. Tropical Plant Pathology, 2002, 27, 259-267.	0.3	18
115	Nodulação em cultivares de feijão dos conjuntos gênicos andino e meso-americano. Pesquisa Agropecuaria Brasileira, 2002, 37, 1145-1150.	0.9	18
116	Assessment of the Effect of Silicon on Antioxidant Enzymes in Cotton Plants by Multivariate Analysis. Journal of Agricultural and Food Chemistry, 2013, 61, 11243-11249.	<b>5.</b> 2	18
117	Belowground changes to community structure alter methane-cycling dynamics in Amazonia. Environment International, 2020, 145, 106131.	10.0	18
118	Purification and characterization of an antimicrobial peptide produced by Pseudomonas sp. strain 4B. World Journal of Microbiology and Biotechnology, 2009, 25, 205-213.	3.6	17
119	<i>DREB</i> Genes from Common Bean ( <i>Phaseolus vulgaris</i> L.) Show Broad to Specific Abiotic Stress Responses and Distinct Levels of Nucleotide Diversity. International Journal of Genomics, 2019, 2019, 1-28.	1.6	17
120	Arbuscular mycorrhizal fungal communities in native and in replanted Araucaria forest. Scientia Agricola, 2009, 66, 677-684.	1.2	17
121	Disponibilidade de nutrientes no solo, qualidade de grãos e produtividade da soja em solo adubado com lodo de esgoto. Pesquisa Agropecuaria Brasileira, 2005, 40, 919-926.	0.9	16
122	Intrapopulational genetic diversity of Araucaria angustifolia (Bertol.) Kuntze is different when assessed on the basis of chloroplast or nuclear markers. Plant Systematics and Evolution, 2010, 284, 111-122.	0.9	16
123	Concentration, characterization and application of lipases from Sporidiobolus pararoseus strain. Brazilian Journal of Microbiology, 2014, 45, 294-301.	2.0	16
124	Analysis of the common bean (Phaseolus vulgaris L.) transcriptome regarding efficiency of phosphorus use. PLoS ONE, 2019, 14, e0210428.	2.5	16
125	Tannin supplementation modulates the composition and function of ruminal microbiome in lambs infected with gastrointestinal nematodes. FEMS Microbiology Ecology, 2020, 96, .	2.7	16
126	Sorption-desorption and biodegradation of sulfometuron-methyl and its effects on the bacterial communities in Amazonian soils amended with aged biochar. Ecotoxicology and Environmental Safety, 2021, 207, 111222.	6.0	16

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127	Amazon deforestation enriches antibiotic resistance genes. Soil Biology and Biochemistry, 2021, 153, 108110.	8.8	16
128	Physiological effects of glyphosate over amino acid profile in conventional and transgenic soybean (Glycine max). Pesticide Biochemistry and Physiology, 2012, 102, 134-141.	3.6	15
129	Increased soil moisture intensifies the impacts of forest-to-pasture conversion on methane emissions and methane-cycling communities in the Eastern Amazon. Environmental Research, 2022, 212, 113139.	7.5	15
130	SYBR $<$ sup $>$ Â $^{\odot}<$ /sup $>$ Green I Used to Evaluate the Nuclei Number of Fungal Mycelia. BioTechniques, 2001, 31, 42-46.	1.8	14
131	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.	5.6	14
132	Araucaria angustifolia Aboveground Roots Presented High Arbuscular Mycorrhizal Fungal Colonization and Diversity in the Brazilian Atlantic Forest. Pedosphere, 2016, 26, 561-566.	4.0	14
133	Exploration of the Yield Potential of Mesoamerican Wild Common Beans From Contrasting Eco-Geographic Regions by Nested Recombinant Inbred Populations. Frontiers in Plant Science, 2020, 11, 346.	3.6	14
134	Molecular identification of bamboo genera and species based on RAPD-RFLP markers. Silva Fennica, 2017, 51, .	1.3	14
135	Vinasse fertirrigation alters soil resistome dynamics: an analysis based on metagenomic profiles. BioData Mining, 2017, 10, 17.	4.0	13
136	Does Sugarcane Straw Removal Change the Abundance of Soil Microbes?. Bioenergy Research, 2019, 12, 901-908.	3.9	13
137	Robust DNA protocols for tropical soils. Heliyon, 2020, 6, e03830.	3.2	13
138	'Synthetic lipase' production from a newly isolated Sporidiobolus pararoseus strain by submerged fermentation. Brazilian Journal of Microbiology, 2012, 43, 1490-1498.	2.0	12
139	Preliminary Characterization of Novel Extra-cellular Lipase from Penicillium crustosum Under Solid-State Fermentation and its Potential Application for Triglycerides Hydrolysis. Food and Bioprocess Technology, 2012, 5, 1592-1600.	4.7	12
140	A Step Forward to Empower Global Microbiome Research Through Local Leadership. Trends in Microbiology, 2016, 24, 767-771.	7.7	12
141	Maintenance of N cycling gene communities with crop-livestock integration management in tropical agriculture systems. Agriculture, Ecosystems and Environment, 2018, 267, 52-62.	<b>5.</b> 3	12
142	Rhizobial Inoculation and Molybdenum Fertilization in Peanut Crops Grown in a No Tillage System After 20 Years of Pasture. Revista Brasileira De Ciencia Do Solo, 0, 43, .	1.3	12
143	Effects of burned and unburned sugarcane harvesting systems on soil CO2 emission and soil physical, chemical, and microbiological attributes. Catena, 2021, 196, 104903.	5.0	12
144	Antibiotic resistance and molecular characterization of Staphylococcus species from mastitic milk. African Journal of Microbiology Research, 2017, 11, 84-91.	0.4	11

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145	Biofilm formation and antimicrobial sensitivity of lactobacilli contaminants from sugarcane-based fuel ethanol fermentation. Antonie Van Leeuwenhoek, 2018, 111, 1631-1644.	1.7	11
146	Gestational and lactational exposure to gossypol alters the testis transcriptome. BMC Genomics, 2020, 21, 59.	2.8	10
147	Phylogenetic Relationships of Xylella fastidiosa Strains Based on 16S–23S rDNA Sequences. Current Microbiology, 2005, 50, 190-195.	2.2	9
148	Genetic Characterization of Brazilian Annual Arachis Species from Sections Arachis and Heteranthae using RAPD Markers. Genetic Resources and Crop Evolution, 2005, 52, 1079-1086.	1.6	9
149	Not just a methane source: Amazonian floodplain sediments harbour a high diversity of methanotrophs with different metabolic capabilities. Molecular Ecology, 2021, 30, 2560-2572.	3.9	9
150	Changes in isoflavone profiles of soybean treated with gamma irradiation. International Journal of Food Sciences and Nutrition, 2009, 60, 387-394.	2.8	8
151	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. Pedosphere, 2017, 27, 832-845.	4.0	8
152	Assessment of microbial diversity associated with CH4 emission from sugarcane vinasse storage and transportation systems. Journal of Environmental Management, 2020, 269, 110748.	7.8	7
153	Active methane processing microbes and the disproportionate role of NC10 phylum in methane mitigation in Amazonian floodplains. Biogeochemistry, 2021, 156, 293-317.	3.5	7
154	Nodulação e fixação simbiótica de nitrogênio em feijoeiro com estirpes nativas de rizóbio, em solo tratado com lodo de esgoto. Pesquisa Agropecuaria Brasileira, 2005, 40, 1047-1050.	0.9	7
155	In situ probing of Xylella fastidiosa in honeydew of a xylem sap-feeding insect using 16S rRNA-targeted fluorescent oligonucleotides. Environmental Microbiology, 2006, 8, 747-754.	3.8	6
156	Influence of pH and temperature on the expression of sboA and ituD genes in Bacillus sp. P11. Antonie Van Leeuwenhoek, 2013, 104, 149-154.	1.7	6
157	Functional Genomics of Biotic and Abiotic Stresses in Phaseolus vulgaris. , 0, , .		6
158	Soil CO2 emission and soil attributes associated with the microbiota of a sugarcane area in southern Brazil. Scientific Reports, 2021, 11, 8325.	3.3	6
159	The induction of differentially expressed proteins of Xylella fastidiosa with citrus extract. Brazilian Journal of Microbiology, 2004, 35, 235-242.	2.0	6
160	The effect of Haemonchus contortus and Trichostrongylus colubriforms infection on the ruminal microbiome of lambs. Experimental Parasitology, 2021, 231, 108175.	1.2	6
161	Long-term land use in Amazon influence the dynamic of microbial communities in soil and rhizosphere. Rhizosphere, 2022, 21, 100482.	3.0	6
162	Eficiência simbiótica de estirpes Hup+, Hup hr e Hup- de Bradyrhizobium japonicum e Bradyrhizobium elkanii em cultivares de caupi. Pesquisa Agropecuaria Brasileira, 1999, 34, 1925-1931.	0.9	5

#	Article	IF	CITATIONS
163	Specific amplification of iron receptor genes in Xylella fastidiosa strains from different hosts. Genetics and Molecular Biology, 2006, 29, 137-141.	1.3	5
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