List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Long-term land use in Amazon influence the dynamic of microbial communities in soil and rhizosphere. Rhizosphere, 2022, 21, 100482.	3.0	6
2	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
3	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.	8.0	5
4	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
5	Rainforest-to-pasture conversion stimulates soil methanogenesis across the Brazilian Amazon. ISME Journal, 2021, 15, 658-672.	9.8	21
6	Amazon deforestation enriches antibiotic resistance genes. Soil Biology and Biochemistry, 2021, 153, 108110.	8.8	16
7	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
8	Molecular Markers in Bamboos: Understanding Reproductive Biology, Genetic Structure, Interspecies Diversity, and Clonal Fidelity for Conservation and Breeding. , 2021, , 33-62.		1
9	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
10	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
11	Responses of Low-Cost Input Combinations on the Microbial Structure of the Maize Rhizosphere for Greenhouse Gas Mitigation and Plant Biomass Production. Frontiers in Plant Science, 2021, 12, 683658.	3.6	3
12	Taxonomic and nitrogen-cycling microbial community functional profiles of sugarcane and adjacent forest soils in Southeast Brazil. MOJ Ecology & Environmental Sciences, 2021, 6, 119-125.	0.2	1
13	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
14	Ovarian activation delays in peripubertal ewe lambs infected with Haemonchus contortus can be avoided by supplementing protein in their diets. BMC Veterinary Research, 2021, 17, 344.	1.9	2
15	The effect of Haemonchus contortus and Trichostrongylus colubriforms infection on the ruminal microbiome of lambs. Experimental Parasitology, 2021, 231, 108175.	1.2	6
16	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. Methods in Molecular Biology, 2021, 2232, 251-263.	0.9	0
17	Combined Use of Vinasse and Nitrogen as Fertilizers Affects Nitrification, Ammonification, and Denitrification by Prokaryotes. Frontiers in Soil Science, 2021, 1,	2.2	1
18	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

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19	Belowground changes to community structure alter methane-cycling dynamics in Amazonia. Environment International, 2020, 145, 106131.	10.0	18
20	Synthesis and potential application of polygalacturonase from a Penicillium brasilianum isolate. Acta Scientiarum - Technology, 2020, 42, e48042.	0.4	0
21	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
22	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
23	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
24	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
25	Robust DNA protocols for tropical soils. Heliyon, 2020, 6, e03830.	3.2	13
26	Tannin supplementation modulates the composition and function of ruminal microbiome in lambs infected with gastrointestinal nematodes. FEMS Microbiology Ecology, 2020, 96, .	2.7	16
27	Gestational and lactational exposure to gossypol alters the testis transcriptome. BMC Genomics, 2020, 21, 59.	2.8	10
28	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
29	Forest-to-agriculture conversion in Amazon drives soil microbial communities and N-cycle. Soil Biology and Biochemistry, 2019, 137, 107567.	8.8	61
30	Does Sugarcane Straw Removal Change the Abundance of Soil Microbes?. Bioenergy Research, 2019, 12, 901-908.	3.9	13
31	Forest conversion to pasture affects soil phosphorus dynamics and nutritional status in Brazilian Amazon. Soil and Tillage Research, 2019, 194, 104330.	5.6	29
32	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
33	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
34	Resistance Breeding of Common Bean Shapes the Physiology of the Rhizosphere Microbiome. Frontiers in Microbiology, 2019, 10, 2252.	3.5	41
35	Amazon forest-to-agriculture conversion alters rhizosphere microbiome composition while functions are kept. FEMS Microbiology Ecology, 2019, 95, .	2.7	32
36	Analysis of the common bean (Phaseolus vulgaris L.) transcriptome regarding efficiency of phosphorus use. PLoS ONE, 2019, 14, e0210428.	2.5	16

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37	<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
38	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
39	Health and nutrition in sheep receiving Bacillus thuringiensis. Animal Production Science, 2019, 59, 1119.	1.3	3
40	Forest-to-pasture conversion and recovery based on assessment of microbial communities in Eastern Amazon rainforest. FEMS Microbiology Ecology, 2019, 95, .	2.7	44
41	Can alternative N-fertilization methods influence GHG emissions and biomass production in sugarcane fields?. Biomass and Bioenergy, 2019, 120, 21-27.	5.7	26
42	Rumen degradability and gas production as influenced by different strains of Bacillus thuringiensis. Canadian Journal of Animal Science, 2019, 99, 951-954.	1.5	0
43	Morphological-metric, ultrastructural and immunohistochemical effects of gossypol on cultured granulosa cells and oocytes of ewes using MOEPF. Animal Reproduction Science, 2019, 201, 22-31.	1.5	2
44	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
45	Biofilm formation and antimicrobial sensitivity of lactobacilli contaminants from sugarcane-based fuel ethanol fermentation. Antonie Van Leeuwenhoek, 2018, 111, 1631-1644.	1.7	11
46	Influence of resistance breeding in common bean on rhizosphere microbiome composition and function. ISME Journal, 2018, 12, 212-224.	9.8	296
47	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
48	Genetic Variation of Landraces of Common Bean Varying for Seed Coat Glossiness and Disease Resistance: Valuable Resources for Conservation and Breeding. , 2018, , .		0
49	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
50	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
51	Breeding for soil-borne pathogen resistance impacts active rhizosphere microbiome of common bean. ISME Journal, 2018, 12, 3038-3042.	9.8	92
52	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
53	Maintenance of N cycling gene communities with crop-livestock integration management in tropical agriculture systems. Agriculture, Ecosystems and Environment, 2018, 267, 52-62.	5.3	12
54	Molecular characterization and antibiotic resistance of Staphylococcus spp. isolated from cheese processing plants. Journal of Dairy Science, 2017, 100, 5167-5175.	3.4	23

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55	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
56	Zinc concentration affects the functional groups of microbial communities in sugarcane-cultivated soil. Agriculture, Ecosystems and Environment, 2017, 236, 187-197.	5.3	19
57	Bioinformatics for Microbiome Research: Concepts, Strategies, and Advances. , 2017, , 111-123.		3
58	Soil microbial community dynamics and assembly under long-term land use change. FEMS Microbiology Ecology, 2017, 93, .	2.7	69
59	Changes in Amino Acid Profile in Roots of Glyphosate Resistant and Susceptible Soybean (<i>Glycine) Tj ETQq1 1 65, 8823-8828.</i>	0.784314 5.2	rgBT /Over 3
60	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. Pedosphere, 2017, 27, 832-845.	4.0	8
61	Vinasse fertirrigation alters soil resistome dynamics: an analysis based on metagenomic profiles. BioData Mining, 2017, 10, 17.	4.0	13
62	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
63	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
64	Antibiotic resistance and molecular characterization of Staphylococcus species from mastitic milk. African Journal of Microbiology Research, 2017, 11, 84-91.	0.4	11
65	Fungal Community Structure as an Indicator of Soil Agricultural Management Effects in the Cerrado. Revista Brasileira De Ciencia Do Solo, 2017, 41, .	1.3	4
66	Molecular identification of bamboo genera and species based on RAPD-RFLP markers. Silva Fennica, 2017, 51, .	1.3	14
67	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. , 2017, , .		1
68	Using Metagenomics to Connect Microbial Community Biodiversity and Functions. Current Issues in Molecular Biology, 2017, 24, 103-118.	2.4	47
69	Prospecção de enzimas de interesse industrial produzidas por actinobactéria isolado de solo rizosférico da Amazônia. Scientia Plena, 2017, 13, .	0.2	1
70	5. Exploring Diversity of Soil Microorganisms: A Multidimensional Approach. , 2016, , 66-86.		0
71	Structure of Fungal Communities in Sub-Irrigated Agricultural Soil from Cerrado Floodplains. Diversity, 2016, 8, 13.	1.7	2
72	Oxidative mitigation of aquatic methane emissions in large Amazonian rivers. Global Change Biology, 2016, 22, 1075-1085.	9.5	61

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73	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
74	Disentangling the influence of earthworms in sugarcane rhizosphere. Scientific Reports, 2016, 6, 38923.	3.3	38
75	Next-Generation Sequencing to Elucidate Biochar-Effected Microbial Community Dynamics. , 2016, , 109-132.		2
76	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
77	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
78	A Step Forward to Empower Global Microbiome Research Through Local Leadership. Trends in Microbiology, 2016, 24, 767-771.	7.7	12
79	Metagenome sequencing of the microbial community of two Brazilian anthropogenic Amazon dark earth sites, Brazil. Genomics Data, 2016, 10, 167-168.	1.3	1
80	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
81	Fungal Community Assembly in the Amazonian Dark Earth. Microbial Ecology, 2016, 71, 962-973.	2.8	35
82	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
83	Multi-Analytical Approach Reveals Potential Microbial Indicators in Soil for Sugarcane Model Systems. PLoS ONE, 2015, 10, e0129765.	2.5	52
84	Soil microbiome responses to the shortâ€ŧerm effects of Amazonian deforestation. Molecular Ecology, 2015, 24, 2433-2448.	3.9	171
85	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
86	Soil-Borne Microbiome: Linking Diversity to Function. Microbial Ecology, 2015, 70, 255-265.	2.8	227
87	Land-use system shapes soil bacterial communities in Southeastern Amazon region. Applied Soil Ecology, 2015, 95, 151-160.	4.3	114
88	The influence of nickel on the bioremediation of multi-component contaminated tropical soil: microcosm and batch bioreactor studies. World Journal of Microbiology and Biotechnology, 2015, 31, 1127-1135.	3.6	2
89	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
90	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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91	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
92	Assessment of Bacterial bph Gene in Amazonian Dark Earth and Their Adjacent Soils. PLoS ONE, 2014, 9, e99597.	2.5	21
93	Relationship between cyanogenesis and latex stability on tapping panel dryness in rubber trunk girth. Journal of Plant Interactions, 2014, 9, 418-424.	2.1	3
94	Capacity of Aromatic Compound Degradation by Bacteria from Amazon Dark Earth. Diversity, 2014, 6, 339-353.	1.7	20
95	Soil bacterial diversity in degraded and restored lands of Northeast Brazil. Antonie Van Leeuwenhoek, 2014, 106, 891-899.	1.7	39
96	Variations of Bacterial Community Structure and Composition in Mangrove Sediment at Different Depths in Southeastern Brazil. Diversity, 2014, 6, 827-843.	1.7	59
97	Development of microsatellite primers for Senna multijuga (Fabaceae): a pioneer species from the Brazilian Atlantic forest. Conservation Genetics Resources, 2014, 6, 569.	0.8	1
98	Brazilian Microbiome Project: Revealing the Unexplored Microbial Diversity—Challenges and Prospects. Microbial Ecology, 2014, 67, 237-241.	2.8	119
99	Taxonomical and functional microbial community selection in soybean rhizosphere. ISME Journal, 2014, 8, 1577-1587.	9.8	633
100	Concentration, characterization and application of lipases from Sporidiobolus pararoseus strain. Brazilian Journal of Microbiology, 2014, 45, 294-301.	2.0	16
101	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. FEMS Microbiology Ecology, 2013, 83, 607-621.	2.7	228
102	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.	5.2	18
103	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
104	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
105	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
106	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
107	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
108	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

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109	Microsatellite markers for <i>Plathymenia reticulata</i> (Leguminosae) ¹ . American Journal of Botany, 2012, 99, e391-3.	1.7	1
110	Emission of Methane by Eudrilus eugeniae and Other Earthworms from Brazil. Applied and Environmental Microbiology, 2012, 78, 3014-3019.	3.1	28
111	Impact of Land Degradation on Soil Microbial Biomass and Activity in Northeast Brazil. Pedosphere, 2012, 22, 88-95.	4.0	53
112	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
113	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.	5.2	27
114	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
115	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
116	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
117	Dissecting Phaseolus vulgaris Innate Immune System against Colletotrichum lindemuthianum Infection. PLoS ONE, 2012, 7, e43161.	2.5	36
118	'Synthetic lipase' production from a newly isolated Sporidiobolus pararoseus strain by submerged fermentation. Brazilian Journal of Microbiology, 2012, 43, 1490-1498.	2.0	12
119	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
120	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
121	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
122	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
123	Physiological effects of glyphosate over amino acid profile in conventional and transgenic soybean (Clycine max). Pesticide Biochemistry and Physiology, 2012, 102, 134-141.	3.6	15
124	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
125	Archaeal communities in the sediments of three contrasting mangroves. Journal of Soils and Sediments, 2011, 11, 1466-1476.	3.0	50
126	Characterization of feather-degrading bacteria from Brazilian soils. International Biodeterioration and Biodegradation, 2011, 65, 102-107.	3.9	27

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127	Estado nutricional e teor de glicosÃdeos cianogênicos em plantas de seringueira. Bragantia, 2011, 70, 402-408.	1.3	1
128	A Molecular Survey of the Diversity of Microbial Communities in Different Amazonian Agricultural Model Systems. Diversity, 2010, 2, 787-809.	1.7	64
129	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
130	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
131	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
132	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
133	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
134	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
135	Influence of the bacterioplankton community of a tropical eutrophic lagoon on the bacterial community of its neighbouring ocean. World Journal of Microbiology and Biotechnology, 2010, 26, 1865-1873.	3.6	2
136	Evidences of siderophores synthesis by Grapevine Xylella fastidiosa, causal agent of pierce's disease, through instrumental approaches. Journal of the Brazilian Chemical Society, 2010, 21, 635-641.	0.6	3
137	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
138	Changes in isoflavone profiles of soybean treated with gamma irradiation. International Journal of Food Sciences and Nutrition, 2009, 60, 387-394.	2.8	8
139	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
140	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
141	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
142	Arbuscular mycorrhizal fungal communities in native and in replanted Araucaria forest. Scientia Agricola, 2009, 66, 677-684.	1.2	17
143	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
144	Mixed-species plantations of Acacia mangium and Eucalyptus grandis in Brazil. Forest Ecology and Management, 2008, 255, 3918-3930.	3.2	127

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145	An alternative method for Staphylococcus aureus DNA isolation. Arquivo Brasileiro De Medicina Veterinaria E Zootecnia, 2008, 60, 299-306.	0.4	19
146	Detection of siderophores in endophytic bacteria Methylobacterium spp. associated with Xylella fastidiosa subsp. pauca. Pesquisa Agropecuaria Brasileira, 2008, 43, 521-528.	0.9	57
147	Characterization of Xanthomonas axonopodis pv. phaseoli isolates. Summa Phytopathologica, 2008, 34, 228-231.	0.1	4
148	Notas sobre Acaulospora bireticulata Rothwell & Trappe e primeiro registro de Acaulospora koskei Blask. para o Brasil. Acta Botanica Brasilica, 2008, 22, 583-587.	0.8	2
149	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
150	Biodiversity and distribution of arbuscular mycorrhizal fungi in Araucaria angustifolia forest. Scientia Agricola, 2007, 64, 393-399.	1.2	32
151	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
152	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
153	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
154	Redução dos sintomas causados pela Xylella fastidiosa subsp. pauca por meio de aplicação de benzotiadiazole e silÃcio. Pesquisa Agropecuaria Brasileira, 2007, 42, 1083-1089.	0.9	3
155	Identification of citrus expressed sequence tags (ESTs) encoding pleiotropic drug resistance (PDR)-like proteins. Genetics and Molecular Biology, 2007, 30, 857-865.	1.3	2
156	16s-23S rDNA: polymorphisms and their use for detection and identification of Xylella fastidiosa strains. Brazilian Journal of Microbiology, 2007, 38, 159-165.	2.0	3
157	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
158	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
159	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
160	Detection and characterization of protease secreted by the plant pathogen Xylella fastidiosa. Microbiological Research, 2006, 161, 263-272.	5.3	22
161	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
162	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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163	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
164	Growth and siderophore production of Xylella fastidiosa under iron-limited conditions. Microbiological Research, 2005, 160, 429-436.	5.3	37
165	Phylogenetic Relationships of Xylella fastidiosa Strains Based on 16S–23S rDNA Sequences. Current Microbiology, 2005, 50, 190-195.	2.2	9
166	Utilization of the Etest Assay for Comparative Antibiotic Susceptibility Profiles of Citrus Variegated Chlorosis and Pierce's Disease Strains of Xylella fastidiosa. Current Microbiology, 2005, 51, 262-266.	2.2	3
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