Eiko E Kuramae

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	The genome sequence of the plant pathogen Xylella fastidiosa. Nature, 2000, 406, 151-157.	27.8	827
2	Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. Nature Communications, 2019, 10, 4841.	12.8	773
3	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. Frontiers in Microbiology, 2016, 7, 744.	3.5	762
4	Microbial Extracellular Polymeric Substances: Ecological Function and Impact on Soil Aggregation. Frontiers in Microbiology, 2018, 9, 1636.	3.5	713
5	Taxonomical and functional microbial community selection in soybean rhizosphere. ISME Journal, 2014, 8, 1577-1587.	9.8	633
6	Study of Genetic Diversity of Eukaryotic Picoplankton in Different Oceanic Regions by Small-Subunit rRNA Gene Cloning and Sequencing. Applied and Environmental Microbiology, 2001, 67, 2932-2941.	3.1	470
7	Comparative Genomics of Two Leptospira interrogans Serovars Reveals Novel Insights into Physiology and Pathogenesis. Journal of Bacteriology, 2004, 186, 2164-2172.	2.2	406
8	Dandruff-associated <i>Malassezia</i> genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 18730-18735.	7.1	396
9	Soil characteristics more strongly influence soil bacterial communities than land-use type. FEMS Microbiology Ecology, 2012, 79, 12-24.	2.7	347
10	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
11	Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. Microbiome, 2019, 7, 136.	11.1	270
12	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. Genome Research, 2003, 13, 2725-2735.	5.5	254
13	Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. Frontiers in Microbiology, 2016, 7, 2064.	3.5	250
14	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. FEMS Microbiology Ecology, 2013, 83, 607-621.	2.7	228
15	Soil-Borne Microbiome: Linking Diversity to Function. Microbial Ecology, 2015, 70, 255-265.	2.8	227
16	Network topology reveals high connectance levels and few key microbial genera within soils. Frontiers in Environmental Science, 2014, 2, .	3.3	226
17	Functional traits dominate the diversity-related selection of bacterial communities in the rhizosphere. ISME Journal, 2017, 11, 56-66.	9.8	220
18	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.	2.7	193

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19	Soil microbiome responses to the shortâ€ŧerm effects of Amazonian deforestation. Molecular Ecology, 2015, 24, 2433-2448.	3.9	171
20	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. ISME Journal, 2019, 13, 738-751.	9.8	166
21	Six monophyletic lineages identified within Cryptococcus neoformans and Cryptococcus gattii by multi-locus sequence typing. Fungal Genetics and Biology, 2008, 45, 400-421.	2.1	163
22	Rhizobacterial community structure differences among sorghum cultivars in different growth stages and soils. FEMS Microbiology Ecology, 2017, 93, .	2.7	143
23	Acidobacteria strains from subdivision 1 act as plant growth-promoting bacteria. Archives of Microbiology, 2016, 198, 987-993.	2.2	135
24	Fusarium: more than a node or a foot-shaped basal cell. Studies in Mycology, 2021, 98, 100116.	7.2	134
25	Sulphurâ€oxidizing and sulphateâ€reducing communities in <scp>B</scp> razilian mangrove sediments. Environmental Microbiology, 2014, 16, 845-855.	3.8	126
26	Unique hybrids between the fungal pathogensCryptococcus neoformansandCryptococcus gattii. FEMS Yeast Research, 2006, 6, 599-607.	2.3	122
27	The Genome Sequence of the Gram-Positive Sugarcane Pathogen Leifsonia xyli subsp. xyli. Molecular Plant-Microbe Interactions, 2004, 17, 827-836.	2.6	119
28	Effects of Jasmonic Acid, Ethylene, and Salicylic Acid Signaling on the Rhizosphere Bacterial Community of <i>Arabidopsis thaliana</i> . Molecular Plant-Microbe Interactions, 2011, 24, 395-407.	2.6	114
29	Land-use system shapes soil bacterial communities in Southeastern Amazon region. Applied Soil Ecology, 2015, 95, 151-160.	4.3	114
30	Brazilian coffee genome project: an EST-based genomic resource. Brazilian Journal of Plant Physiology, 2006, 18, 95-108.	0.5	112
31	Nonâ€random species loss in bacterial communities reduces antifungal volatile production. Ecology, 2015, 96, 2042-2048.	3.2	109
32	Understanding and prediction of soil microbial community dynamics under global change. Applied Soil Ecology, 1999, 11, 161-176.	4.3	108
33	Bacterial Community Succession in Pine-Wood Decomposition. Frontiers in Microbiology, 2016, 7, 231.	3.5	106
34	Plant and soil fungal but not soil bacterial communities are linked in long-term fertilized grassland. Scientific Reports, 2016, 6, 23680.	3.3	105
35	Soil and plant factors driving the community of soil-borne microorganisms across chronosequences of secondary succession of chalk grasslands with a neutral pH. FEMS Microbiology Ecology, 2011, 77, 285-294.	2.7	101
36	Nitrous oxide emission related to ammonia-oxidizing bacteria and mitigation options from N fertilization in a tropical soil. Scientific Reports, 2016, 6, 30349.	3.3	99

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37	AIDS Patient Death Caused by NovelCryptococcus neoformans×C.gattiiHybrid. Emerging Infectious Diseases, 2008, 14, 1105-1108.	4.3	91
38	Identification and Characterization of Colletotrichum spp. affecting Fruit after Harvest in Brazil. Journal of Phytopathology, 2002, 150, 128-134.	1.0	87
39	The reach of the genome signature in prokaryotes. BMC Evolutionary Biology, 2006, 6, 84.	3.2	79
40	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
41	Resilience of the resident soil microbiome to organic and inorganic amendment disturbances and to temporary bacterial invasion. Microbiome, 2018, 6, 142.	11.1	77
42	Microbial secondary succession in a chronosequence of chalk grasslands. ISME Journal, 2010, 4, 711-715.	9.8	73
43	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
44	Lettuce and rhizosphere microbiome responses to growth promoting <i>Pseudomonas</i> species under field conditions. FEMS Microbiology Ecology, 2016, 92, fiw197.	2.7	68
45	Phylogenomics reveal a robust fungal tree of life. FEMS Yeast Research, 2006, 6, 1213-1220.	2.3	66
46	Exploring soil microbial 16S <scp>rRNA</scp> sequence data to increase carbon yield and nitrogen efficiency of a bioenergy crop. GCB Bioenergy, 2016, 8, 867-879.	5.6	66
47	Characterization of Rhizoctonia solani Associated with Soybean in Brazil. European Journal of Plant Pathology, 2002, 108, 783-792.	1.7	65
48	Characterization of novel Acidobacteria exopolysaccharides with potential industrial and ecological applications. Scientific Reports, 2017, 7, 41193.	3.3	61
49	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. FEMS Microbiology Ecology, 2013, 84, 519-531.	2.7	59
50	Effects of growthâ€promoting bacteria on soybean root activity, plant development, and yield. Agronomy Journal, 2020, 112, 418-428.	1.8	59
51	Cultivation-independent and cultivation-dependent metagenomes reveal genetic and enzymatic potential of microbial community involved in the degradation of a complex microbial polymer. Microbiome, 2020, 8, 76.	11.1	59
52	Context dependency and saturating effects of loss of rare soil microbes on plant productivity. Frontiers in Plant Science, 2015, 6, 485.	3.6	56
53	Phylogenetic relationships of Rhizoctonia fungi within the Cantharellales. Fungal Biology, 2016, 120, 603-619.	2.5	56
54	Temporal variability of soil microbial communities after application of dicyandiamide-treated swine slurry and mineral fertilizers. Soil Biology and Biochemistry, 2016, 97, 71-82.	8.8	55

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55	Native bacteria promote plant growth under drought stress condition without impacting the rhizomicrobiome. FEMS Microbiology Ecology, 2018, 94, .	2.7	54
56	Conventional and organic soil management as divergent drivers of resident and active fractions of major soil food web constituents. Scientific Reports, 2019, 9, 13521.	3.3	54
57	Title is missing!. European Journal of Plant Pathology, 2003, 109, 391-395.	1.7	53
58	Testing Potential Effects of Maize Expressing the Bacillus thuringiensis Cry1Ab Endotoxin (Bt Maize) on Mycorrhizal Fungal Communities via DNA- and RNA-Based Pyrosequencing and Molecular Fingerprinting. Applied and Environmental Microbiology, 2012, 78, 7384-7392.	3.1	52
59	Soil-Borne Bacterial Structure and Diversity Does Not Reflect Community Activity in Pampa Biome. PLoS ONE, 2013, 8, e76465.	2.5	52
60	Revisiting the Dilution Procedure Used To Manipulate Microbial Biodiversity in Terrestrial Systems. Applied and Environmental Microbiology, 2015, 81, 4246-4252.	3.1	50
61	Peat substrate amended with chitin modulates the N-cycle, siderophore and chitinase responses in the lettuce rhizobiome. Scientific Reports, 2019, 9, 9890.	3.3	50
62	Co-Variation of Bacterial and Fungal Communities in Different Sorghum Cultivars and Growth Stages is Soil Dependent. Microbial Ecology, 2018, 76, 205-214.	2.8	46
63	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.	8.0	45
64	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. Scientific Reports, 2017, 7, 42634.	3.3	44
65	From toilet to agriculture: Fertilization with microalgal biomass from wastewater impacts the soil and rhizosphere active microbiomes, greenhouse gas emissions and plant growth. Resources, Conservation and Recycling, 2020, 161, 104924.	10.8	42
66	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
67	Dominance of bacterial ammonium oxidizers and fungal denitrifiers in the complex nitrogen cycle pathways related to nitrous oxide emission. GCB Bioenergy, 2018, 10, 645-660.	5.6	41
68	Nitrosospira sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. Frontiers in Microbiology, 2018, 9, 674.	3.5	41
69	Modulation of the soil microbiome by long-term Ca-based soil amendments boosts soil organic carbon and physicochemical quality in a tropical no-till crop rotation system. Soil Biology and Biochemistry, 2021, 156, 108188.	8.8	41
70	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. Plant Physiology, 2004, 134, 951-959.	4.8	38
71	Methanogens predominate in natural corrosion protective layers on metal sheet piles. Scientific Reports, 2017, 7, 11899.	3.3	37
72	Exploitation of new endophytic bacteria and their ability to promote sugarcane growth and nitrogen nutrition. Antonie Van Leeuwenhoek, 2019, 112, 283-295.	1.7	37

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73	Fungal Community Assembly in the Amazonian Dark Earth. Microbial Ecology, 2016, 71, 962-973.	2.8	35
74	Sorghum Growth Promotion by Paraburkholderia tropica and Herbaspirillum frisingense: Putative Mechanisms Revealed by Genomics and Metagenomics. Microorganisms, 2020, 8, 725.	3.6	34
75	The influence of soil chemistry on branched tetraether lipids in mid- and high latitude soils: Implications for brGDGT- based paleothermometry. Geochimica Et Cosmochimica Acta, 2021, 310, 95-112.	3.9	34
76	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. Frontiers in Microbiology, 2018, 9, 660.	3.5	33
77	Effect of <i>Burkholderia tropica</i> and <i>Herbaspirillum frisingense</i> strains on sorghum growth is plant genotype dependent. PeerJ, 2018, 6, e5346.	2.0	32
78	Comparison of the Sequences of the Internal Transcribed Spacer Regions and PbGP43 Genes of Paracoccidioides brasiliensis from Patients and Armadillos (Dasypus novemcinctus). Journal of Clinical Microbiology, 2003, 41, 5735-5737.	3.9	31
79	Nitrification inhibitors effectively target N ₂ Oâ€producing <i>Nitrosospira</i> spp. in tropical soil. Environmental Microbiology, 2019, 21, 1241-1254.	3.8	31
80	Strategies to mitigate the nitrous oxide emissions from nitrogen fertilizer applied with organic fertilizers in sugarcane. Science of the Total Environment, 2019, 650, 1476-1486.	8.0	30
81	You must choose, but choose wisely: Model-based approaches for microbial community analysis. Soil Biology and Biochemistry, 2020, 151, 108042.	8.8	30
82	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. Applied and Environmental Microbiology, 2021, 87, .	3.1	30
83	Virulence profile of ten Paracoccidioides brasiliensis isolates: association with morphologic and genetic patterns. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2005, 47, 257-262.	1.1	30
84	Bacterial Consortium and Microbial Metabolites Increase Grain Quality and Soybean Yield. Journal of Soil Science and Plant Nutrition, 2020, 20, 1923-1934.	3.4	29
85	The Structure of Rhizosphere Fungal Communities of Wild and Domesticated Rice: Changes in Diversity and Co-occurrence Patterns. Frontiers in Microbiology, 2021, 12, 610823.	3.5	29
86	Effect of strigolactones on recruitment of the rice root-associated microbiome. FEMS Microbiology Ecology, 2022, 98, .	2.7	29
87	Promiscuous mitochondria in <i>Cryptococcus gattii</i> . FEMS Yeast Research, 2009, 9, 489-503.	2.3	28
88	Moisture Is More Important than Temperature for Assembly of Both Potentially Active and Whole Prokaryotic Communities in Subtropical Grassland. Microbial Ecology, 2019, 77, 460-470.	2.8	28
89	Ammonia-oxidizing bacteria and fungal denitrifier diversity are associated with N2O production in tropical soils. Soil Biology and Biochemistry, 2022, 166, 108563.	8.8	28
90	Organic amendment strengthens interkingdom associations in the soil and rhizosphere of barley (Hordeum vulgare). Science of the Total Environment, 2019, 695, 133885.	8.0	27

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91	Identification of Rhizoctonia solani associated with soybean in Brazil by rDNA-ITS sequences. Tropical Plant Pathology, 2003, 28, 413-419.	0.3	25
92	Intraspecific Evolution of Rhizoctonia solani AG-1 IA Associated with Soybean and Rice in Brazil based on Polymorphisms at the ITS-5.8S rDNA Operon. European Journal of Plant Pathology, 2005, 113, 183-196.	1.7	25
93	Tracking Fungal Community Responses to Maize Plants by DNA- and RNA-Based Pyrosequencing. PLoS ONE, 2013, 8, e69973.	2.5	25
94	Phylogenetic and metagenomic analysis of Verrucomicrobia in former agricultural grassland soil. FEMS Microbiology Ecology, 2010, 71, 23-33.	2.7	23
95	Environmental filtering: A case of bacterial community assembly in soil. Soil Biology and Biochemistry, 2019, 136, 107531.	8.8	23
96	Conflicting phylogenetic position of Schizosaccharomyces pombe. Genomics, 2006, 88, 387-393.	2.9	22
97	Plant-Growth Endophytic Bacteria Improve Nutrient Use Efficiency and Modulate Foliar N-Metabolites in Sugarcane Seedling. Microorganisms, 2021, 9, 479.	3.6	22
98	Optimized medium culture for <i>Acidobacteria</i> subdivision 1 strains. FEMS Microbiology Letters, 2016, 363, fnw245.	1.8	21
99	Cophenetic correlation analysis as a strategy to select phylogenetically informative proteins: an example from the fungal kingdom. BMC Evolutionary Biology, 2007, 7, 134.	3.2	20
100	Genome-resolved metagenomics of sugarcane vinasse bacteria. Biotechnology for Biofuels, 2018, 11, 48.	6.2	20
101	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. Geoderma, 2022, 405, 115423.	5.1	20
102	Beneficial microbial species and metabolites alleviate soybean oxidative damage and increase grain yield during short dry spells. European Journal of Agronomy, 2021, 127, 126293.	4.1	19
103	Long-term farming systems modulate multi-trophic responses. Science of the Total Environment, 2019, 646, 480-490.	8.0	18
104	Successive DNA extractions improve characterization of soil microbial communities. PeerJ, 2017, 5, e2915.	2.0	18
105	Dynamics and resilience of soil mycobiome under multiple organic and inorganic pulse disturbances. Science of the Total Environment, 2020, 733, 139173.	8.0	17
106	Morphomolecular characterization of Pleurotus ostreatus (Jacq. Fr.) kummer strains in relation to luminosity and temperature of frutification. Scientia Agricola, 2003, 60, 531-535.	1.2	16
107	Bacterial Tomato Pathogen Ralstonia solanacearum Invasion Modulates Rhizosphere Compounds and Facilitates the Cascade Effect of Fungal Pathogen Fusarium solani. Microorganisms, 2020, 8, 806. 	3.6	16
108	Microbial N-cycling gene abundance is affected by cover crop specie and development stage in an integrated cropping system. Archives of Microbiology, 2020, 202, 2005-2012.	2.2	16

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109	The modulation of sugarcane growth and nutritional profile under aluminum stress is dependent on beneficial endophytic bacteria and plantlet origin. Applied Soil Ecology, 2020, 156, 103715.	4.3	15
110	Impact of Different Trace Elements on the Growth and Proteome of Two Strains of Granulicella, Class "Acidobacteriia― Frontiers in Microbiology, 2020, 11, 1227.	3.5	15
111	Dynamics of active potential bacterial and fungal interactions in the assimilation of acidobacterial EPS in soil. Soil Biology and Biochemistry, 2020, 148, 107916.	8.8	15
112	rDNA-based characterization of a new binucleate Rhizoctonia spp. causing root rot on kale in Brazil. European Journal of Plant Pathology, 2007, 119, 469-475.	1.7	14
113	Forage Grasses Steer Soil Nitrogen Processes, Microbial Populations, and Microbiome Composition in A Long-term Tropical Agriculture System. Agriculture, Ecosystems and Environment, 2022, 323, 107688.	5.3	14
114	Variabilidade genética de acessos de aguapé coletados no Estado de São Paulo. Planta Daninha, 2002, 20, 1-5.	0.5	13
115	Can Palisade and Guinea Grass Sowing Time in Intercropping Systems Affect Soybean Yield and Soil Chemical Properties?. Frontiers in Sustainable Food Systems, 2020, 4, .	3.9	12
116	Caracterização citomorfológica, cultural, molecular e patogênica de Rhizoctonia solani Kühn associado ao arroz em Tocantins, Brasil. Summa Phytopathologica, 2007, 33, 129-136.	0.1	11
117	Soil-Borne Microbial Functional Structure across Different Land Uses. Scientific World Journal, The, 2014, 2014, 1-8.	2.1	11
118	Microbial inoculants modulate growth traits, nutrients acquisition and bioactive compounds accumulation of Cyclocarya paliurus (Batal.) Iljinskaja under degraded field condition. Forest Ecology and Management, 2021, 482, 118897.	3.2	11
119	Variations of Bacterial and Diazotrophic Community Assemblies throughout the Soil Profile in Distinct Paddy Soil Types and Their Contributions to Soil Functionality. MSystems, 2022, 7, e0104721.	3.8	11
120	Upland rice yield enhanced by early nitrogen fertilization on previous palisade grass. Nutrient Cycling in Agroecosystems, 2020, 118, 115-131.	2.2	10
121	Rearranging the sugarcane holobiont via plant growth-promoting bacteria and nitrogen input. Science of the Total Environment, 2021, 800, 149493.	8.0	10
122	Binucleate Rhizoctonia sp. AG G causing root rot in yacon (Smallanthus sonchifolius) in Brazil. Plant Pathology, 2005, 54, 325-330.	2.4	9
123	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. Microorganisms, 2021, 9, 175.	3.6	9
124	Rhizosphere microbiome response to host genetic variability: a trade-off between bacterial and fungal community assembly. FEMS Microbiology Ecology, 2022, 98, .	2.7	9
125	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. Pedosphere, 2017, 27, 832-845.	4.0	8
126	Wood Decay Characteristics and Interspecific Interactions Control Bacterial Community Succession in Populus grandidentata (Bigtooth Aspen). Frontiers in Microbiology, 2019, 10, 979.	3.5	8

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127	Unraveling the xylanolytic potential of Acidobacteria bacterium AB60 from Cerrado soils. FEMS Microbiology Letters, 2020, 367, .	1.8	8
128	Responses of Acidobacteria Granulicella sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. Microorganisms, 2020, 8, 244.	3.6	8
129	Comparison of methane metabolism in the rhizomicrobiomes of wild and related cultivated rice accessions reveals a strong impact of crop domestication. Science of the Total Environment, 2022, 803, 150131.	8.0	8
130	Microbial Functional Diversity in Vineyard Soils: Sulfur Metabolism and Links With Grapevine Plants and Wine Quality. Frontiers in Environmental Science, 2020, 8, .	3.3	7
131	Eucalypt species drive rhizosphere bacterial and fungal community assembly but soil phosphorus availability rearranges the microbiome. Science of the Total Environment, 2022, 836, 155667.	8.0	7
132	Assessing nickel tolerance of bacteria isolated from serpentine soils. Brazilian Journal of Microbiology, 2019, 50, 705-713.	2.0	6
133	Effects of probiotic consortia on plant metabolites are associated with soil indigenous microbiota and fertilization regimes. Industrial Crops and Products, 2022, 185, 115138.	5.2	6
134	Variabilidade genética entre formae speciales de Fusarium oxysporum e raças 1 e 2 de F. oxysporum f. sp. lycopersici através de RAPD e sequências de regiÁµes ITS e rDNA. Acta Scientiarum - Agronomy, 0, 24, 1481.	0.6	5
135	Bacterial community composition and diversity of two different forms of an organic residue of bioenergy crop. PeerJ, 2019, 7, e6768.	2.0	5
136	Sugarcane pre-sprouted seedlings produced with beneficial bacteria and arbuscular mycorrhizal fungi. Bragantia, 0, 80, .	1.3	5
137	Facilitation in the soil microbiome does not necessarily lead to niche expansion. Environmental Microbiomes, 2021, 16, 4.	5.0	5
138	A review on the impact of domestication of the rhizosphere of grain crops and a perspective on the potential role of the rhizosphere microbial community for sustainable rice crop production. Science of the Total Environment, 2022, 842, 156706.	8.0	5
139	Characterization of Xanthomonas axonopodis pv. phaseoli isolates. Summa Phytopathologica, 2008, 34, 228-231.	0.1	4
140	On-Site Blackwater Treatment Fosters Microbial Groups and Functions to Efficiently and Robustly Recover Carbon and Nutrients. Microorganisms, 2021, 9, 75.	3.6	4
141	Stem traits, compartments and tree species affect fungal communities on decaying wood. Environmental Microbiology, 2022, 24, 3625-3639.	3.8	4
142	Feasibility of early fertilization of maize with 15ÂN application to preceding cover crop. European Journal of Agronomy, 2022, 135, 126485.	4.1	4
143	The influence of agar brands and micronutrients in the growth optimization of Granulicella sp. (Acidobacteriota). Journal of Microbiological Methods, 2021, 181, 106148.	1.6	3
144	Early nitrogen supply as an alternative management for a cover crop-maize sequence under a no-till system. Nutrient Cycling in Agroecosystems, 2021, 121, 1-14.	2.2	3

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145	Potassium phosphite enhanced the suppressive capacity of the soil microbiome against the tomato pathogen Ralstonia solanacearum. Biology and Fertility of Soils, 0, , 1.	4.3	3
146	Potassium phosphite enhances the antagonistic capability of Bacillus amyloliquefaciens to manage tomato bacterial wilt. Plant Disease, 2021, , .	1.4	2
147	Acidobacteria. , 2019, , 1-1.		2
148	Identification of 14-3-3-like protein in sugarcane (Saccharum officinarum). Genetics and Molecular Biology, 2001, 24, 43-48.	1.3	1
149	Combined Use of Vinasse and Nitrogen as Fertilizers Affects Nitrification, Ammonification, and Denitrification by Prokaryotes. Frontiers in Soil Science, 2021, 1, .	2.2	1
150	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. Microorganisms, 2022, 10, 1093.	3.6	1
151	Yeast Genome 10th Anniversary, Académie Royale des Sciences, des Letters et des Beaux-Arts de Belgique in Brussels (Belgium), 7–8 September 2006. FEMS Yeast Research, 2006, 6, 1103-1104.	2.3	0
152	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. Methods in Molecular Biology, 2021, 2232, 251-263.	0.9	0