

# Eiko E Kuramae

## List of Publications by Year in descending order

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152  
papers

13,019  
citations

36203

51  
h-index

25716

108  
g-index

155  
all docs

155  
docs citations

155  
times ranked

14018  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> . <i>Nature</i> , 2000, 406, 151-157.	13.7	827
2	Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. <i>Nature Communications</i> , 2019, 10, 4841.	5.8	773
3	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. <i>Frontiers in Microbiology</i> , 2016, 7, 744.	1.5	762
4	Microbial Extracellular Polymeric Substances: Ecological Function and Impact on Soil Aggregation. <i>Frontiers in Microbiology</i> , 2018, 9, 1636.	1.5	713
5	Taxonomical and functional microbial community selection in soybean rhizosphere. <i>ISME Journal</i> , 2014, 8, 1577-1587.	4.4	633
6	Study of Genetic Diversity of Eukaryotic Picoplankton in Different Oceanic Regions by Small-Subunit rRNA Gene Cloning and Sequencing. <i>Applied and Environmental Microbiology</i> , 2001, 67, 2932-2941.	1.4	470
7	Comparative Genomics of Two <i>Leptospira interrogans</i> Serovars Reveals Novel Insights into Physiology and Pathogenesis. <i>Journal of Bacteriology</i> , 2004, 186, 2164-2172.	1.0	406
8	Dandruff-associated <i>Malassezia</i> genomes reveal convergent and divergent virulence traits shared with plant and human fungal pathogens. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 18730-18735.	3.3	396
9	Soil characteristics more strongly influence soil bacterial communities than land-use type. <i>FEMS Microbiology Ecology</i> , 2012, 79, 12-24.	1.3	347
10	Comparative Analyses of the Complete Genome Sequences of Pierce's Disease and Citrus Variegated Chlorosis Strains of <i>Xylella fastidiosa</i> . <i>Journal of Bacteriology</i> , 2003, 185, 1018-1026.	1.0	307
11	Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. <i>Microbiome</i> , 2019, 7, 136.	4.9	270
12	Analysis and Functional Annotation of an Expressed Sequence Tag Collection for Tropical Crop Sugarcane. <i>Genome Research</i> , 2003, 13, 2725-2735.	2.4	254
13	Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. <i>Frontiers in Microbiology</i> , 2016, 7, 2064.	1.5	250
14	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. <i>FEMS Microbiology Ecology</i> , 2013, 83, 607-621.	1.3	228
15	Soil-Borne Microbiome: Linking Diversity to Function. <i>Microbial Ecology</i> , 2015, 70, 255-265.	1.4	227
16	Network topology reveals high connectance levels and few key microbial genera within soils. <i>Frontiers in Environmental Science</i> , 2014, 2, .	1.5	226
17	Functional traits dominate the diversity-related selection of bacterial communities in the rhizosphere. <i>ISME Journal</i> , 2017, 11, 56-66.	4.4	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. <i>FEMS Microbiology Ecology</i> , 2014, 90, 195-205.	1.3	193

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19	Soil microbiome responses to the short-term effects of Amazonian deforestation. <i>Molecular Ecology</i> , 2015, 24, 2433-2448.	2.0	171
20	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. <i>ISME Journal</i> , 2019, 13, 738-751.	4.4	166
21	Six monophyletic lineages identified within <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> by multi-locus sequence typing. <i>Fungal Genetics and Biology</i> , 2008, 45, 400-421.	0.9	163
22	Rhizobacterial community structure differences among sorghum cultivars in different growth stages and soils. <i>FEMS Microbiology Ecology</i> , 2017, 93, .	1.3	143
23	Acidobacteria strains from subdivision 1 act as plant growth-promoting bacteria. <i>Archives of Microbiology</i> , 2016, 198, 987-993.	1.0	135
24	<i>Fusarium</i> : more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021, 98, 100116.	4.5	134
25	Sulphur-oxidizing and sulphate-reducing communities in Brazilian mangrove sediments. <i>Environmental Microbiology</i> , 2014, 16, 845-855.	1.8	126
26	Unique hybrids between the fungal pathogens <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> . <i>FEMS Yeast Research</i> , 2006, 6, 599-607.	1.1	122
27	The Genome Sequence of the Gram-Positive Sugarcane Pathogen <i>Leifsonia xyli</i> subsp. <i>xyli</i> . <i>Molecular Plant-Microbe Interactions</i> , 2004, 17, 827-836.	1.4	119
28	Effects of Jasmonic Acid, Ethylene, and Salicylic Acid Signaling on the Rhizosphere Bacterial Community of <i>Arabidopsis thaliana</i> . <i>Molecular Plant-Microbe Interactions</i> , 2011, 24, 395-407.	1.4	114
29	Land-use system shapes soil bacterial communities in Southeastern Amazon region. <i>Applied Soil Ecology</i> , 2015, 95, 151-160.	2.1	114
30	Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006, 18, 95-108.	0.5	112
31	Non-random species loss in bacterial communities reduces antifungal volatile production. <i>Ecology</i> , 2015, 96, 2042-2048.	1.5	109
32	Understanding and prediction of soil microbial community dynamics under global change. <i>Applied Soil Ecology</i> , 1999, 11, 161-176.	2.1	108
33	Bacterial Community Succession in Pine-Wood Decomposition. <i>Frontiers in Microbiology</i> , 2016, 7, 231.	1.5	106
34	Plant and soil fungal but not soil bacterial communities are linked in long-term fertilized grassland. <i>Scientific Reports</i> , 2016, 6, 23680.	1.6	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. <i>FEMS Microbiology Ecology</i> , 2011, 77, 285-294.	1.3	101
36	Nitrous oxide emission related to ammonia-oxidizing bacteria and mitigation options from N fertilization in a tropical soil. <i>Scientific Reports</i> , 2016, 6, 30349.	1.6	99

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37	AIDS Patient Death Caused by Novel <i>Cryptococcus neoformans</i> — <i>C. gattii</i> Hybrid. <i>Emerging Infectious Diseases</i> , 2008, 14, 1105-1108.	2.0	91
38	Identification and Characterization of <i>Colletotrichum</i> spp. affecting Fruit after Harvest in Brazil. <i>Journal of Phytopathology</i> , 2002, 150, 128-134.	0.5	87
39	The reach of the genome signature in prokaryotes. <i>BMC Evolutionary Biology</i> , 2006, 6, 84.	3.2	79
40	Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility. <i>Antonie Van Leeuwenhoek</i> , 2015, 108, 741-752.	0.7	77
41	Resilience of the resident soil microbiome to organic and inorganic amendment disturbances and to temporary bacterial invasion. <i>Microbiome</i> , 2018, 6, 142.	4.9	77
42	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010, 4, 711-715.	4.4	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. <i>Geoderma</i> , 2020, 375, 114476.	2.3	69
44	Lettuce and rhizosphere microbiome responses to growth promoting <i>Pseudomonas</i> species under field conditions. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw197.	1.3	68
45	Phylogenomics reveal a robust fungal tree of life. <i>FEMS Yeast Research</i> , 2006, 6, 1213-1220.	1.1	66
46	Exploring soil microbial 16S rRNA sequence data to increase carbon yield and nitrogen efficiency of a bioenergy crop. <i>GCB Bioenergy</i> , 2016, 8, 867-879.	2.5	66
47	Characterization of <i>Rhizoctonia solani</i> Associated with Soybean in Brazil. <i>European Journal of Plant Pathology</i> , 2002, 108, 783-792.	0.8	65
48	Characterization of novel <i>Acidobacteria</i> exopolysaccharides with potential industrial and ecological applications. <i>Scientific Reports</i> , 2017, 7, 41193.	1.6	61
49	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. <i>FEMS Microbiology Ecology</i> , 2013, 84, 519-531.	1.3	59
50	Effects of growth-promoting bacteria on soybean root activity, plant development, and yield. <i>Agronomy Journal</i> , 2020, 112, 418-428.	0.9	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. <i>Microbiome</i> , 2020, 8, 76.	4.9	59
52	Context dependency and saturating effects of loss of rare soil microbes on plant productivity. <i>Frontiers in Plant Science</i> , 2015, 6, 485.	1.7	56
53	Phylogenetic relationships of <i>Rhizoctonia</i> fungi within the Cantharellales. <i>Fungal Biology</i> , 2016, 120, 603-619.	1.1	56
54	Temporal variability of soil microbial communities after application of dicyandiamide-treated swine slurry and mineral fertilizers. <i>Soil Biology and Biochemistry</i> , 2016, 97, 71-82.	4.2	55

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55	Native bacteria promote plant growth under drought stress condition without impacting the rhizomicrobiome. <i>FEMS Microbiology Ecology</i> , 2018, 94, .	1.3	54
56	Conventional and organic soil management as divergent drivers of resident and active fractions of major soil food web constituents. <i>Scientific Reports</i> , 2019, 9, 13521.	1.6	54
57	Title is missing!. <i>European Journal of Plant Pathology</i> , 2003, 109, 391-395.	0.8	53
58	Testing Potential Effects of Maize Expressing the <i>Bacillus thuringiensis</i> Cry1Ab Endotoxin (Bt Maize) on Mycorrhizal Fungal Communities via DNA- and RNA-Based Pyrosequencing and Molecular Fingerprinting. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7384-7392.	1.4	52
59	Soil-Borne Bacterial Structure and Diversity Does Not Reflect Community Activity in Pampa Biome. <i>PLoS ONE</i> , 2013, 8, e76465.	1.1	52
60	Revisiting the Dilution Procedure Used To Manipulate Microbial Biodiversity in Terrestrial Systems. <i>Applied and Environmental Microbiology</i> , 2015, 81, 4246-4252.	1.4	50
61	Peat substrate amended with chitin modulates the N-cycle, siderophore and chitinase responses in the lettuce rhizobiome. <i>Scientific Reports</i> , 2019, 9, 9890.	1.6	50
62	Co-Variation of Bacterial and Fungal Communities in Different Sorghum Cultivars and Growth Stages is Soil Dependent. <i>Microbial Ecology</i> , 2018, 76, 205-214.	1.4	46
63	Recycling organic residues in agriculture impacts soil-borne microbial community structure, function and N <sub>2</sub> O emissions. <i>Science of the Total Environment</i> , 2018, 631-632, 1089-1099.	3.9	45
64	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. <i>Scientific Reports</i> , 2017, 7, 42634.	1.6	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. <i>Resources, Conservation and Recycling</i> , 2020, 161, 104924.	5.3	42
66	Amazonian Dark Earth and Plant Species from the Amazon Region Contribute to Shape Rhizosphere Bacterial Communities. <i>Microbial Ecology</i> , 2015, 69, 855-866.	1.4	41
67	Dominance of bacterial ammonium oxidizers and fungal denitrifiers in the complex nitrogen cycle pathways related to nitrous oxide emission. <i>GCB Bioenergy</i> , 2018, 10, 645-660.	2.5	41
68	<i>Nitrosospora</i> sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. <i>Frontiers in Microbiology</i> , 2018, 9, 674.	1.5	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. <i>Soil Biology and Biochemistry</i> , 2021, 156, 108188.	4.2	41
70	Evaluation of Monocot and Eudicot Divergence Using the Sugarcane Transcriptome. <i>Plant Physiology</i> , 2004, 134, 951-959.	2.3	38
71	Methanogens predominate in natural corrosion protective layers on metal sheet piles. <i>Scientific Reports</i> , 2017, 7, 11899.	1.6	37
72	Exploitation of new endophytic bacteria and their ability to promote sugarcane growth and nitrogen nutrition. <i>Antonie Van Leeuwenhoek</i> , 2019, 112, 283-295.	0.7	37

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73	Fungal Community Assembly in the Amazonian Dark Earth. <i>Microbial Ecology</i> , 2016, 71, 962-973.	1.4	35
74	Sorghum Growth Promotion by <i>Paraburkholderia tropica</i> and <i>Herbaspirillum frisingense</i> : Putative Mechanisms Revealed by Genomics and Metagenomics. <i>Microorganisms</i> , 2020, 8, 725.	1.6	34
75	The influence of soil chemistry on branched tetraether lipids in mid- and high latitude soils: Implications for brGDGT- based paleothermometry. <i>Geochimica Et Cosmochimica Acta</i> , 2021, 310, 95-112.	1.6	34
76	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018, 9, 660.	1.5	33
77	Effect of <i>Burkholderia tropica</i> and <i>Herbaspirillum frisingense</i> strains on sorghum growth is plant genotype dependent. <i>PeerJ</i> , 2018, 6, e5346.	0.9	32
78	Comparison of the Sequences of the Internal Transcribed Spacer Regions and PbGP43 Genes of <i>Paracoccidioides brasiliensis</i> from Patients and Armadillos ( <i>Dasypus novemcinctus</i> ). <i>Journal of Clinical Microbiology</i> , 2003, 41, 5735-5737.	1.8	31
79	Nitrification inhibitors effectively target N <sub>2</sub> -producing <i>Nitrosospora</i> spp. in tropical soil. <i>Environmental Microbiology</i> , 2019, 21, 1241-1254.	1.8	31
80	Strategies to mitigate the nitrous oxide emissions from nitrogen fertilizer applied with organic fertilizers in sugarcane. <i>Science of the Total Environment</i> , 2019, 650, 1476-1486.	3.9	30
81	You must choose, but choose wisely: Model-based approaches for microbial community analysis. <i>Soil Biology and Biochemistry</i> , 2020, 151, 108042.	4.2	30
82	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	30
83	Virulence profile of ten <i>Paracoccidioides brasiliensis</i> isolates: association with morphologic and genetic patterns. <i>Revista Do Instituto De Medicina Tropical De Sao Paulo</i> , 2005, 47, 257-262.	0.5	30
84	Bacterial Consortium and Microbial Metabolites Increase Grain Quality and Soybean Yield. <i>Journal of Soil Science and Plant Nutrition</i> , 2020, 20, 1923-1934.	1.7	29
85	The Structure of Rhizosphere Fungal Communities of Wild and Domesticated Rice: Changes in Diversity and Co-occurrence Patterns. <i>Frontiers in Microbiology</i> , 2021, 12, 610823.	1.5	29
86	Effect of strigolactones on recruitment of the rice root-associated microbiome. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	29
87	Promiscuous mitochondria in <i>Cryptococcus gattii</i> . <i>FEMS Yeast Research</i> , 2009, 9, 489-503.	1.1	28
88	Moisture Is More Important than Temperature for Assembly of Both Potentially Active and Whole Prokaryotic Communities in Subtropical Grassland. <i>Microbial Ecology</i> , 2019, 77, 460-470.	1.4	28
89	Ammonia-oxidizing bacteria and fungal denitrifier diversity are associated with N <sub>2</sub> O production in tropical soils. <i>Soil Biology and Biochemistry</i> , 2022, 166, 108563.	4.2	28
90	Organic amendment strengthens interkingdom associations in the soil and rhizosphere of barley ( <i>Hordeum vulgare</i> ). <i>Science of the Total Environment</i> , 2019, 695, 133885.	3.9	27

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91	Identification of <i>Rhizoctonia solani</i> associated with soybean in Brazil by rDNA-ITS sequences. <i>Tropical Plant Pathology</i> , 2003, 28, 413-419.	0.3	25
92	Intraspecific Evolution of <i>Rhizoctonia solani</i> AG-1 IA Associated with Soybean and Rice in Brazil based on Polymorphisms at the ITS-5.8S rDNA Operon. <i>European Journal of Plant Pathology</i> , 2005, 113, 183-196.	0.8	25
93	Tracking Fungal Community Responses to Maize Plants by DNA- and RNA-Based Pyrosequencing. <i>PLoS ONE</i> , 2013, 8, e69973.	1.1	25
94	Phylogenetic and metagenomic analysis of <i>Verrucomicrobia</i> in former agricultural grassland soil. <i>FEMS Microbiology Ecology</i> , 2010, 71, 23-33.	1.3	23
95	Environmental filtering: A case of bacterial community assembly in soil. <i>Soil Biology and Biochemistry</i> , 2019, 136, 107531.	4.2	23
96	Conflicting phylogenetic position of <i>Schizosaccharomyces pombe</i> . <i>Genomics</i> , 2006, 88, 387-393.	1.3	22
97	Plant-Growth Endophytic Bacteria Improve Nutrient Use Efficiency and Modulate Foliar N-Metabolites in Sugarcane Seedling. <i>Microorganisms</i> , 2021, 9, 479.	1.6	22
98	Optimized medium culture for <i>Acidobacteria</i> subdivision 1 strains. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw245.	0.7	21
99	Cophenetic correlation analysis as a strategy to select phylogenetically informative proteins: an example from the fungal kingdom. <i>BMC Evolutionary Biology</i> , 2007, 7, 134.	3.2	20
100	Genome-resolved metagenomics of sugarcane vinasse bacteria. <i>Biotechnology for Biofuels</i> , 2018, 11, 48.	6.2	20
101	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. <i>Geoderma</i> , 2022, 405, 115423.	2.3	20
102	Beneficial microbial species and metabolites alleviate soybean oxidative damage and increase grain yield during short dry spells. <i>European Journal of Agronomy</i> , 2021, 127, 126293.	1.9	19
103	Long-term farming systems modulate multi-trophic responses. <i>Science of the Total Environment</i> , 2019, 646, 480-490.	3.9	18
104	Successive DNA extractions improve characterization of soil microbial communities. <i>PeerJ</i> , 2017, 5, e2915.	0.9	18
105	Dynamics and resilience of soil mycobiome under multiple organic and inorganic pulse disturbances. <i>Science of the Total Environment</i> , 2020, 733, 139173.	3.9	17
106	Morphomolecular characterization of <i>Pleurotus ostreatus</i> (Jacq. Fr.) kummer strains in relation to luminosity and temperature of frutification. <i>Scientia Agricola</i> , 2003, 60, 531-535.	0.6	16
107	Bacterial Tomato Pathogen <i>Ralstonia solanacearum</i> Invasion Modulates Rhizosphere Compounds and Facilitates the Cascade Effect of Fungal Pathogen <i>Fusarium solani</i> . <i>Microorganisms</i> , 2020, 8, 806.	1.6	16
108	Microbial N-cycling gene abundance is affected by cover crop specie and development stage in an integrated cropping system. <i>Archives of Microbiology</i> , 2020, 202, 2005-2012.	1.0	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. <i>Applied Soil Ecology</i> , 2020, 156, 103715.	2.1	15
110	Impact of Different Trace Elements on the Growth and Proteome of Two Strains of <i>Granulicella</i> , Class "Acidobacteria". <i>Frontiers in Microbiology</i> , 2020, 11, 1227.	1.5	15
111	Dynamics of active potential bacterial and fungal interactions in the assimilation of acidobacterial EPS in soil. <i>Soil Biology and Biochemistry</i> , 2020, 148, 107916.	4.2	15
112	rDNA-based characterization of a new binucleate <i>Rhizoctonia</i> spp. causing root rot on kale in Brazil. <i>European Journal of Plant Pathology</i> , 2007, 119, 469-475.	0.8	14
113	Forage Grasses Steer Soil Nitrogen Processes, Microbial Populations, and Microbiome Composition in A Long-term Tropical Agriculture System. <i>Agriculture, Ecosystems and Environment</i> , 2022, 323, 107688.	2.5	14
114	Variabilidade genética de acessos de aguapé coletados no Estado de São Paulo. <i>Planta Daninha</i> , 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?. <i>Frontiers in Sustainable Food Systems</i> , 2020, 4, .	1.8	12
116	Caracterização citomorfológica, cultural, molecular e patogênica de <i>Rhizoctonia solani</i> associado ao arroz em Tocantins, Brasil. <i>Summa Phytopathologica</i> , 2007, 33, 129-136.	0.3	11
117	Soil-Borne Microbial Functional Structure across Different Land Uses. <i>Scientific World Journal</i> , The, 2014, 2014, 1-8.	0.8	11
118	Microbial inoculants modulate growth traits, nutrients acquisition and bioactive compounds accumulation of <i>Cyclocarya paliurus</i> (Batal.) Iljinskaja under degraded field condition. <i>Forest Ecology and Management</i> , 2021, 482, 118897.	1.4	11
119	Variations of Bacterial and Diazotrophic Community Assemblies throughout the Soil Profile in Distinct Paddy Soil Types and Their Contributions to Soil Functionality. <i>MSystems</i> , 2022, 7, e0104721.	1.7	11
120	Upland rice yield enhanced by early nitrogen fertilization on previous palisade grass. <i>Nutrient Cycling in Agroecosystems</i> , 2020, 118, 115-131.	1.1	10
121	Rearranging the sugarcane holobiont via plant growth-promoting bacteria and nitrogen input. <i>Science of the Total Environment</i> , 2021, 800, 149493.	3.9	10
122	Binucleate <i>Rhizoctonia</i> sp. AG G causing root rot in yacon ( <i>Smallanthus sonchifolius</i> ) in Brazil. <i>Plant Pathology</i> , 2005, 54, 325-330.	1.2	9
123	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. <i>Microorganisms</i> , 2021, 9, 175.	1.6	9
124	Rhizosphere microbiome response to host genetic variability: a trade-off between bacterial and fungal community assembly. <i>FEMS Microbiology Ecology</i> , 2022, 98, .	1.3	9
125	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. <i>Pedosphere</i> , 2017, 27, 832-845.	2.1	8
126	Wood Decay Characteristics and Interspecific Interactions Control Bacterial Community Succession in <i>Populus grandidentata</i> (Bigtooth Aspen). <i>Frontiers in Microbiology</i> , 2019, 10, 979.	1.5	8



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127	Unraveling the xylanolytic potential of Acidobacteria bacterium AB60 from Cerrado soils. FEMS Microbiology Letters, 2020, 367, .	0.7	8
128	Responses of Acidobacteria Granulicella sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. Microorganisms, 2020, 8, 244.	1.6	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.	3.9	8
130	Microbial Functional Diversity in Vineyard Soils: Sulfur Metabolism and Links With Grapevine Plants and Wine Quality. Frontiers in Environmental Science, 2020, 8, .	1.5	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.	3.9	7
132	Assessing nickel tolerance of bacteria isolated from serpentine soils. Brazilian Journal of Microbiology, 2019, 50, 705-713.	0.8	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.	2.5	6
134	Variabilidade genÃ©tica entre <em>formae speciales</em> de <em>Fusarium oxysporum</em> e raÃ§as 1 e 2 de <em>F. oxysporum</em> f. sp. <em>lycopersici</em> atravÃ©s de RAPD e sequÃªncias de regiÃ¶es 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.	0.9	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.	2.2	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.	3.9	5
139	Characterization of Xanthomonas axonopodis pv. phaseoli isolates. Summa Phytopathologica, 2008, 34, 228-231.	0.3	4
140	On-Site Blackwater Treatment Fosters Microbial Groups and Functions to Efficiently and Robustly Recover Carbon and Nutrients. Microorganisms, 2021, 9, 75.	1.6	4
141	Stem traits, compartments and tree species affect fungal communities on decaying wood. Environmental Microbiology, 2022, 24, 3625-3639.	1.8	4
142	Feasibility of early fertilization of maize with 15Â application to preceding cover crop. European Journal of Agronomy, 2022, 135, 126485.	1.9	4
143	The influence of agar brands and micronutrients in the growth optimization of Granulicella sp. (Acidobacteriota). Journal of Microbiological Methods, 2021, 181, 106148.	0.7	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.	1.1	3

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145	Potassium phosphite enhanced the suppressive capacity of the soil microbiome against the tomato pathogen <i>Ralstonia solanacearum</i> . <i>Biology and Fertility of Soils</i> , 0, , 1.	2.3	3
146	Potassium phosphite enhances the antagonistic capability of <i>Bacillus amyloliquefaciens</i> to manage tomato bacterial wilt. <i>Plant Disease</i> , 2021, , .	0.7	2
147	<i>Acidobacteria</i> . , 2019, , 1-1.		2
148	Identification of 14-3-3-like protein in sugarcane ( <i>Saccharum officinarum</i> ). <i>Genetics and Molecular Biology</i> , 2001, 24, 43-48.	0.6	1
149	Combined Use of Vinasse and Nitrogen as Fertilizers Affects Nitrification, Ammonification, and Denitrification by Prokaryotes. <i>Frontiers in Soil Science</i> , 2021, 1, .	0.8	1
150	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. <i>Microorganisms</i> , 2022, 10, 1093.	1.6	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. <i>FEMS Yeast Research</i> , 2006, 6, 1103-1104.	1.1	0
152	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. <i>Methods in Molecular Biology</i> , 2021, 2232, 251-263.	0.4	0