Eiko E Kuramae

List of Publications by Citations

145 papers	8,337 citations	44 h-index	90 g-index
155 ext. papers	10,960 ext. citations	5.7 avg, IF	6.31 L-index

#	Paper	IF	Citations
145	The genome sequence of the plant pathogen Xylella fastidiosa. The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing and Analysis. *Nature*, **2000**, 406, 151-9	50.4	701
144	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. *Frontiers in Microbiology*, **2016**, 7, 744	5.7	427
143	Taxonomical and functional microbial community selection in soybean rhizosphere. *ISME Journal*, **2014**, 8, 1577-87	11.9	423
142	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, 2932-41	4.8	405
141	Microbial Extracellular Polymeric Substances: Ecological Function and Impact on Soil Aggregation. *Frontiers in Microbiology*, **2018**, 9, 1636	5.7	348
140	Comparative genomics of two Leptospira interrogans serovars reveals novel insights into physiology and pathogenesis. *Journal of Bacteriology*, **2004**, 186, 2164-72	3.5	330
139	Dandruff-associated Malassezia 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, 18730-5	11.5	326
138	Comparative analyses of the complete genome sequences of Pierce's disease and citrus variegated chlorosis strains of Xylella fastidiosa. *Journal of Bacteriology*, **2003**, 185, 1018-26	3.5	276
137	Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. *Nature Communications*, **2019**, 10, 4841	17.4	267
136	Soil characteristics more strongly influence soil bacterial communities than land-use type. *FEMS Microbiology Ecology*, **2012**, 79, 12-24	4.3	254
135	Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane. *Genome Research*, **2003**, 13, 2725-35	9.7	207
134	Soil-borne microbiome: linking diversity to function. *Microbial Ecology*, **2015**, 70, 255-65	4.4	161
133	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. *FEMS Microbiology Ecology*, **2013**, 83, 607-21	4.3	155
132	Network topology reveals high connectance levels and few key microbial genera within soils. *Frontiers in Environmental Science*, **2014**, 2,	4.8	151
131	Six monophyletic lineages identified within Cryptococcus neoformans and Cryptococcus gattii by multi-locus sequence typing. *Fungal Genetics and Biology*, **2008**, 45, 400-21	3.9	150
130	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	4.3	136
129	Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. *Frontiers in Microbiology*, **2016**, 7, 2064	5.7	130

128	Functional traits dominate the diversity-related selection of bacterial communities in the rhizosphere. *ISME Journal*, **2017**, 11, 56-66	11.9	113
127	Unique hybrids between the fungal pathogens Cryptococcus neoformans and Cryptococcus gattii. *FEMS Yeast Research*, **2006**, 6, 599-607	3.1	110
126	Soil microbiome responses to the short-term effects of Amazonian deforestation. *Molecular Ecology*, **2015**, 24, 2433-48	5.7	103
125	The genome sequence of the gram-positive sugarcane pathogen Leifsonia xyli subsp. xyli. *Molecular Plant-Microbe Interactions*, **2004**, 17, 827-36	3.6	103
124	Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. *Microbiome*, **2019**, 7, 136	16.6	102
123	Effects of jasmonic acid, ethylene, and salicylic acid signaling on the rhizosphere bacterial community of Arabidopsis thaliana. *Molecular Plant-Microbe Interactions*, **2011**, 24, 395-407	3.6	94
122	Rhizobacterial community structure differences among sorghum cultivars in different growth stages and soils. *FEMS Microbiology Ecology*, **2017**, 93,	4.3	90
121	Brazilian coffee genome project: an EST-based genomic resource. *Brazilian Journal of Plant Physiology*, **2006**, 18, 95-108		90
120	Understanding and prediction of soil microbial community dynamics under global change. *Applied Soil Ecology*, **1999**, 11, 161-176	5	88
119	Sulphur-oxidizing and sulphate-reducing communities in Brazilian mangrove sediments. *Environmental Microbiology*, **2014**, 16, 845-55	5.2	82
118	AIDS patient death caused by novel Cryptococcus neoformans x C. gattii hybrid. *Emerging Infectious Diseases*, **2008**, 14, 1105-8	10.2	79
117	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. *ISME Journal*, **2019**, 13, 738-751	11.9	78
116	Non-random species loss in bacterial communities reduces antifungal volatile production. *Ecology*, **2015**, 96, 2042-8	4.6	77
115	Plant and soil fungal but not soil bacterial communities are linked in long-term fertilized grassland. *Scientific Reports*, **2016**, 6, 23680	4.9	74
114	Land-use system shapes soil bacterial communities in Southeastern Amazon region. *Applied Soil Ecology*, **2015**, 95, 151-160	5	73
113	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, 285-94	4.3	73
112	Nitrous oxide emission related to ammonia-oxidizing bacteria and mitigation options from N fertilization in a tropical soil. *Scientific Reports*, **2016**, 6, 30349	4.9	72
111	Bacterial Community Succession in Pine-Wood Decomposition. *Frontiers in Microbiology*, **2016**, 7, 231	5.7	72

110	Identification and Characterization of Colletotrichum spp. affecting Fruit after Harvest in Brazil. *Journal of Phytopathology*, **2002**, 150, 128-134	1.8	68
109	Acidobacteria strains from subdivision 1 act as plant growth-promoting bacteria. *Archives of Microbiology*, **2016**, 198, 987-993	3	65
108	Phylogenomics reveal a robust fungal tree of life. *FEMS Yeast Research*, **2006**, 6, 1213-20	3.1	57
107	Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility. *Antonie Van Leeuwenhoek*, **2015**, 108, 741-52	2.1	55
106	Microbial secondary succession in a chronosequence of chalk grasslands. *ISME Journal*, **2010**, 4, 711-5	11.9	55
105	The reach of the genome signature in prokaryotes. *BMC Evolutionary Biology*, **2006**, 6, 84	3	51
104	Exploring soil microbial 16S rRNA sequence data to increase carbon yield and nitrogen efficiency of a bioenergy crop. *GCB Bioenergy*, **2016**, 8, 867-879	5.6	50
103	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. *FEMS Microbiology Ecology*, **2013**, 84, 519-31	4.3	48
102	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, 7384-92	4.8	46
101	Characterization of novel Acidobacteria exopolysaccharides with potential industrial and ecological applications. *Scientific Reports*, **2017**, 7, 41193	4.9	44
100	Lettuce and rhizosphere microbiome responses to growth promoting Pseudomonas species under field conditions. *FEMS Microbiology Ecology*, **2016**, 92,	4.3	43
99	Resilience of the resident soil microbiome to organic and inorganic amendment disturbances and to temporary bacterial invasion. *Microbiome*, **2018**, 6, 142	16.6	42
98	Characterization of Rhizoctonia solani Associated with Soybean in Brazil. *European Journal of Plant Pathology*, **2002**, 108, 783-792	2.1	41
97	Identification of Rhizoctonia solani AG 1-IB in Lettuce, AG 4 HG-I in Tomato and Melon, and AG 4 HG-III in Broccoli and Spinach, in Brazil. *European Journal of Plant Pathology*, **2003**, 109, 391-395	2.1	40
96	Soil-borne bacterial structure and diversity does not reflect community activity in Pampa biome. *PLoS ONE*, **2013**, 8, e76465	3.7	39
95	Context dependency and saturating effects of loss of rare soil microbes on plant productivity. *Frontiers in Plant Science*, **2015**, 6, 485	6.2	35
94	Revisiting the dilution procedure used to manipulate microbial biodiversity in terrestrial systems. *Applied and Environmental Microbiology*, **2015**, 81, 4246-52	4.8	35
93	Evaluation of monocot and eudicot divergence using the sugarcane transcriptome. *Plant Physiology* , **2004**, 134, 951-9	6.6	33

92	Effects of growth-promoting bacteria on soybean root activity, plant development, and yield. *Agronomy Journal*, **2020**, 112, 418-428	2.2	33
91	Amazonian dark Earth and plant species from the Amazon region contribute to shape rhizosphere bacterial communities. *Microbial Ecology*, **2015**, 69, 855-66	4.4	32
90	Temporal variability of soil microbial communities after application of dicyandiamide-treated swine slurry and mineral fertilizers. *Soil Biology and Biochemistry*, **2016**, 97, 71-82	7.5	31
89	Phylogenetic relationships of Rhizoctonia fungi within the Cantharellales. *Fungal Biology*, **2016**, 120, 603-619	2.8	30
88	sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. *Frontiers in Microbiology*, **2018**, 9, 674	5.7	30
87	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, 5735-7	9.7	30
86	Co-Variation of Bacterial and Fungal Communities in Different Sorghum Cultivars and Growth Stages is Soil Dependent. *Microbial Ecology*, **2018**, 76, 205-214	4.4	30
85	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. *Scientific Reports*, **2017**, 7, 42634	4.9	29
84	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	6.7	29
83	: more than a node or a foot-shaped basal cell. *Studies in Mycology*, **2021**, 98, 100116	22.2	28
82	Virulence profile of ten Paracoccidioides brasiliensis isolates: association with morphologic and genetic patterns. *Revista Do Instituto De Medicina Tropical De Sao Paulo*, **2005**, 47, 257-62	2.2	27
81	Native bacteria promote plant growth under drought stress condition without impacting the rhizomicrobiome. *FEMS Microbiology Ecology*, **2018**, 94,	4.3	26
80	Promiscuous mitochondria in Cryptococcus gattii. *FEMS Yeast Research*, **2009**, 9, 489-503	3.1	25
79	Conventional and organic soil management as divergent drivers of resident and active fractions of major soil food web constituents. *Scientific Reports*, **2019**, 9, 13521	4.9	24
78	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	24
77	Fungal Community Assembly in the Amazonian Dark Earth. *Microbial Ecology*, **2016**, 71, 962-73	4.4	24
76	Methanogens predominate in natural corrosion protective layers on metal sheet piles. *Scientific Reports*, **2017**, 7, 11899	4.9	24
75	Tracking fungal community responses to maize plants by DNA- and RNA-based pyrosequencing. *PLoS ONE*, **2013**, 8, e69973	3.7	24

74	Effect of and strains on sorghum growth is plant genotype dependent. *PeerJ*, **2018**, 6, e5346	3.1	22
73	Phylogenetic and metagenomic analysis of Verrucomicrobia in former agricultural grassland soil. *FEMS Microbiology Ecology*, **2010**, 71, 23-33	4.3	21
72	Recycling organic residues in agriculture impacts soil-borne microbial community structure, function and NO emissions. *Science of the Total Environment*, **2018**, 631-632, 1089-1099	10.2	20
71	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. *Frontiers in Microbiology*, **2018**, 9, 660	5.7	19
70	Cophenetic correlation analysis as a strategy to select phylogenetically informative proteins: an example from the fungal kingdom. *BMC Evolutionary Biology*, **2007**, 7, 134	3	19
69	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	2.1	19
68	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	10.2	19
67	Exploitation of new endophytic bacteria and their ability to promote sugarcane growth and nitrogen nutrition. *Antonie Van Leeuwenhoek*, **2019**, 112, 283-295	2.1	19
66	Conflicting phylogenetic position of Schizosaccharomyces pombe. *Genomics*, **2006**, 88, 387-93	4.3	18
65	Nitrification inhibitors effectively target N O-producing Nitrosospira spp. in tropical soil. *Environmental Microbiology*, **2019**, 21, 1241-1254	5.2	17
64	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	11.9	17
63	Bacterial Consortium and Microbial Metabolites Increase Grain Quality and Soybean Yield. *Journal of Soil Science and Plant Nutrition*, **2020**, 20, 1923-1934	3.2	16
62	Peat substrate amended with chitin modulates the N-cycle, siderophore and chitinase responses in the lettuce rhizobiome. *Scientific Reports*, **2019**, 9, 9890	4.9	16
61	Identification of Rhizoctonia solani associated with soybean in Brazil by rDNA-ITS sequences. *Tropical Plant Pathology*, **2003**, 28, 413-419		16
60	Organic amendment strengthens interkingdom associations in the soil and rhizosphere of barley (Hordeum vulgare). *Science of the Total Environment*, **2019**, 695, 133885	10.2	14
59	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	16.6	13
58	Sorghum Growth Promotion by and : Putative Mechanisms Revealed by Genomics and Metagenomics. *Microorganisms*, **2020**, 8,	4.9	12
57	Optimized medium culture for Acidobacteria subdivision 1 strains. *FEMS Microbiology Letters*, **2016**, 363,	2.9	12

56	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	7.5	12
55	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	4.4	12
54	Long-term farming systems modulate multi-trophic responses. *Science of the Total Environment*, **2019**, 646, 480-490	10.2	11
53	Environmental filtering: A case of bacterial community assembly in soil. *Soil Biology and Biochemistry*, **2019**, 136, 107531	7.5	11
52	Variabilidade gentica de acessos de aguap˜coletados no Estado de Sõ Paulo. *Planta Daninha*, **2002**, 20, 1-5	0.7	11
51	Successive DNA extractions improve characterization of soil microbial communities. *PeerJ*, **2017**, 5, e2915	3.1	11
50	Genome-resolved metagenomics of sugarcane vinasse bacteria. *Biotechnology for Biofuels*, **2018**, 11, 48	7.8	10
49	Morphomolecular characterization of Pleurotus ostreatus (Jacq. Fr.) kummer strains in relation to luminosity and temperature of frutification. *Scientia Agricola*, **2003**, 60, 531-535	2.5	10
48	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. *Applied and Environmental Microbiology*, **2021**, 87,	4.8	10
47	Caracterizaõ citomorfolgica, cultural, molecular e patognica de Rhizoctonia solani Kn associado ao arroz em Tocantins, Brasil. *Summa Phytopathologica*, **2007**, 33, 129-136	0.4	9
46	You must choose, but choose wisely: Model-based approaches for microbial community analysis. *Soil Biology and Biochemistry*, **2020**, 151, 108042	7.5	9
45	Binucleate Rhizoctonia sp. AG G causing root rot in yacon (Smallanthus sonchifolius) in Brazil. *Plant Pathology*, **2005**, 54, 325-330	2.8	8
44	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	3	8
43	The Structure of Rhizosphere Fungal Communities of Wild and Domesticated Rice: Changes in Diversity and Co-occurrence Patterns. *Frontiers in Microbiology*, **2021**, 12, 610823	5.7	8
42	Can Palisade and Guinea Grass Sowing Time in Intercropping Systems Affect Soybean Yield and Soil Chemical Properties?. *Frontiers in Sustainable Food Systems*, **2020**, 4,	4.8	7
41	Upland rice yield enhanced by early nitrogen fertilization on previous palisade grass. *Nutrient Cycling in Agroecosystems*, **2020**, 118, 115-131	3.3	7
40	Plant-Growth Endophytic Bacteria Improve Nutrient Use Efficiency and Modulate Foliar N-Metabolites in Sugarcane Seedling. *Microorganisms*, **2021**, 9,	4.9	7
39	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	5.5	7

38	Dynamics and resilience of soil mycobiome under multiple organic and inorganic pulse disturbances. *Science of the Total Environment*, **2020**, 733, 139173	10.2	6
37	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	2.1	6
36	Impact of Different Trace Elements on the Growth and Proteome of Two Strains of , Class "Acidobacteriia". *Frontiers in Microbiology*, **2020**, 11, 1227	5.7	5
35	Assessing nickel tolerance of bacteria isolated from serpentine soils. *Brazilian Journal of Microbiology*, **2019**, 50, 705-713	2.2	5
34	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. *Pedosphere*, **2017**, 27, 832-845	5	5
33	Soil-borne microbial functional structure across different land uses. *Scientific World Journal, The*, **2014**, 2014, 216071	2.2	5
32	Unraveling the xylanolytic potential of Acidobacteria bacterium AB60 from Cerrado soils. *FEMS Microbiology Letters*, **2020**, 367,	2.9	5
31	Beneficial microbial species and metabolites alleviate soybean oxidative damage and increase grain yield during short dry spells. *European Journal of Agronomy*, **2021**, 127, 126293	5	5
30	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	3.9	5
29	Bacterial Tomato Pathogen Invasion Modulates Rhizosphere Compounds and Facilitates the Cascade Effect of Fungal Pathogen. *Microorganisms*, **2020**, 8,	4.9	4
28	Microbial Functional Diversity in Vineyard Soils: Sulfur Metabolism and Links With Grapevine Plants and Wine Quality. *Frontiers in Environmental Science*, **2020**, 8,	4.8	4
27	Dynamics of active potential bacterial and fungal interactions in the assimilation of acidobacterial EPS in soil. *Soil Biology and Biochemistry*, **2020**, 148, 107916	7.5	4
26	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. *Geoderma*, **2022**, 405, 115423	6.7	4
25	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	5.7	4
24	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	5	3
23	Responses of sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. *Microorganisms*, **2020**, 8,	4.9	2
22	Variabilidade gentica entre formae speciales de Fusarium oxysporum e raas 1 e 2 de F. oxysporum f. sp. lycopersici atravs de RAPD e sequncias de regies ITS e rDNA. *Acta Scientiarum - Agronomy*, **2008**, 24, 1481	0.6	2
21	Characterization of Xanthomonas axonopodis pv. phaseoli isolates. *Summa Phytopathologica*, **2008**, 34, 228-231	0.4	2

20	Ammonia-oxidizing bacteria and fungal denitrifier diversity are associated with N2O production in tropical soils. *Soil Biology and Biochemistry*, **2022**, 166, 108563	7.5	2
19	On-Site Blackwater Treatment Fosters Microbial Groups and Functions to Efficiently and Robustly Recover Carbon and Nutrients. *Microorganisms*, **2020**, 9,	4.9	2
18	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. *Microorganisms*, **2021**, 9,	4.9	2
17	The influence of agar brands and micronutrients in the growth optimization of Granulicella sp. (Acidobacteriota). *Journal of Microbiological Methods*, **2021**, 181, 106148	2.8	2
16	Identification of 14-3-3-like protein in sugarcane (Saccharum officinarum). *Genetics and Molecular Biology*, **2001**, 24, 43-48	2	1
15	Acidobacteria **2019**, 1-1		1
14	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	3.3	1
13	Potassium phosphite enhances the antagonistic capability of Bacillus amyloliquefaciens to manage tomato bacterial wilt. *Plant Disease*, **2021**,	1.5	1
12	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	10.2	1
11	Wood Decay Characteristics and Interspecific Interactions Control Bacterial Community Succession in (Bigtooth Aspen). *Frontiers in Microbiology*, **2019**, 10, 979	5.7	0
10	Facilitation in the soil microbiome does not necessarily lead to niche expansion. *Environmental Microbiomes*, **2021**, 16, 4	5.6	0
9	Rearranging the sugarcane holobiont via plant growth-promoting bacteria and nitrogen input. *Science of the Total Environment*, **2021**, 800, 149493	10.2	0
8	Variations of Bacterial and Diazotrophic Community Assemblies throughout the Soil Profile in Distinct Paddy Soil Types and Their Contributions to Soil Functionality.. *MSystems*, **2022**, e0104721	7.6	0
7	Feasibility of early fertilization of maize with 15ˊN application to preceding cover crop. *European Journal of Agronomy*, **2022**, 135, 126485	5	0
6	Potassium phosphite enhanced the suppressive capacity of the soil microbiome against the tomato pathogen Ralstonia solanacearum. *Biology and Fertility of Soils*,1	6.1	0
5	Eucalypt species drive rhizosphere bacterial and fungal community assembly but soil phosphorus availability rearranges the microbiome.. *Science of the Total Environment*, **2022**, 155667	10.2	0
4	Effects of probiotic consortia on plant metabolites are associated with soil indigenous microbiota and fertilization regimes. *Industrial Crops and Products*, **2022**, 185, 115138	5.9	0
3	Yeast Genome 10th Anniversary, Acadmie Royale des Sciences, des Letters et des Beaux-Arts de Belgique in Brussels (Belgium), 7B September 2006. *FEMS Yeast Research*, **2006**, 6, 1103-1104	3.1	

2	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. *Methods in Molecular Biology*, **2021**, 2232, 251-263	1.4
1	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. *Microorganisms*, **2022**, 10, 1093	4.9