

Eiko E Kuramae

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/814260/eiko-e-kuramae-publications-by-year.pdf>

Version: 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Ammonia-oxidizing bacteria and fungal denitrifier diversity are associated with N ₂ O production in tropical soils. <i>Soil Biology and Biochemistry</i> , 2022 , 166, 108563	7.5	2
144	Comparison of methane metabolism in the rhizomicrobiomes of wild and related cultivated rice accessions reveals a strong impact of crop domestication. <i>Science of the Total Environment</i> , 2022 , 803, 150131	10.2	1
143	Optimizing cover crop and fertilizer timing for high maize yield and nitrogen cycle control. <i>Geoderma</i> , 2022 , 405, 115423	6.7	4
142	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	5.7	4
141	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 , e0104721	7.6	0
140	Feasibility of early fertilization of maize with 15 N application to preceding cover crop. <i>European Journal of Agronomy</i> , 2022 , 135, 126485	5	0
139	Eucalypt species drive rhizosphere bacterial and fungal community assembly but soil phosphorus availability rearranges the microbiome.. <i>Science of the Total Environment</i> , 2022 , 155667	10.2	0
138	PhyloFunDB: A Pipeline to Create and Update Functional Gene Taxonomic Databases. <i>Microorganisms</i> , 2022 , 10, 1093	4.9	
137	Effects of probiotic consortia on plant metabolites are associated with soil indigenous microbiota and fertilization regimes. <i>Industrial Crops and Products</i> , 2022 , 185, 115138	5.9	0
136	Methods to Identify Soil Microbial Bioindicators of Sustainable Management of Bioenergy Crops. <i>Methods in Molecular Biology</i> , 2021 , 2232, 251-263	1.4	
135	: more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021 , 98, 100116	22.2	28
134	Succession of the Resident Soil Microbial Community in Response to Periodic Inoculations. <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4.8	10
133	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	7.5	12
132	Early nitrogen supply as an alternative management for a cover crop-maize sequence under a no-till system. <i>Nutrient Cycling in Agroecosystems</i> , 2021 , 121, 1-14	3.3	1
131	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	5	5
130	Self-Crossing Leads to Weak Co-Variation of the Bacterial and Fungal Communities in the Rice Rhizosphere. <i>Microorganisms</i> , 2021 , 9,	4.9	2
129	Plant-Growth Endophytic Bacteria Improve Nutrient Use Efficiency and Modulate Foliar N-Metabolites in Sugarcane Seedling. <i>Microorganisms</i> , 2021 , 9,	4.9	7

128	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	3.9	5
127	The influence of agar brands and micronutrients in the growth optimization of <i>Granulicella</i> sp. (Acidobacteriota). <i>Journal of Microbiological Methods</i> , 2021 , 181, 106148	2.8	2
126	Facilitation in the soil microbiome does not necessarily lead to niche expansion. <i>Environmental Microbiomes</i> , 2021 , 16, 4	5.6	0
125	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	5.7	8
124	Potassium phosphite enhances the antagonistic capability of <i>Bacillus amyloliquefaciens</i> to manage tomato bacterial wilt. <i>Plant Disease</i> , 2021 ,	1.5	1
123	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	5.5	7
122	Rearranging the sugarcane holobiont via plant growth-promoting bacteria and nitrogen input. <i>Science of the Total Environment</i> , 2021 , 800, 149493	10.2	0
121	Sorghum Growth Promotion by and : Putative Mechanisms Revealed by Genomics and Metagenomics. <i>Microorganisms</i> , 2020 , 8,	4.9	12
120	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	16.6	13
119	Bacterial Tomato Pathogen Invasion Modulates Rhizosphere Compounds and Facilitates the Cascade Effect of Fungal Pathogen. <i>Microorganisms</i> , 2020 , 8,	4.9	4
118	Bacterial Consortium and Microbial Metabolites Increase Grain Quality and Soybean Yield. <i>Journal of Soil Science and Plant Nutrition</i> , 2020 , 20, 1923-1934	3.2	16
117	Impact of Different Trace Elements on the Growth and Proteome of Two Strains of , Class "Acidobacteriia". <i>Frontiers in Microbiology</i> , 2020 , 11, 1227	5.7	5
116	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	6.7	29
115	Dynamics and resilience of soil mycobiome under multiple organic and inorganic pulse disturbances. <i>Science of the Total Environment</i> , 2020 , 733, 139173	10.2	6
114	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,	4.8	7
113	Microbial Functional Diversity in Vineyard Soils: Sulfur Metabolism and Links With Grapevine Plants and Wine Quality. <i>Frontiers in Environmental Science</i> , 2020 , 8,	4.8	4
112	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	11.9	17
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	7.5	4

110	Responses of sp. WH15 to High Carbon Revealed by Integrated Omics Analyses. <i>Microorganisms</i> , 2020 , 8,	4.9	2
109	On-Site Blackwater Treatment Fosters Microbial Groups and Functions to Efficiently and Robustly Recover Carbon and Nutrients. <i>Microorganisms</i> , 2020 , 9,	4.9	2
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	3	8
107	Effects of growth-promoting bacteria on soybean root activity, plant development, and yield. <i>Agronomy Journal</i> , 2020 , 112, 418-428	2.2	33
106	You must choose, but choose wisely: Model-based approaches for microbial community analysis. <i>Soil Biology and Biochemistry</i> , 2020 , 151, 108042	7.5	9
105	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	5	3
104	Upland rice yield enhanced by early nitrogen fertilization on previous palisade grass. <i>Nutrient Cycling in Agroecosystems</i> , 2020 , 118, 115-131	3.3	7
103	Unraveling the xylanolytic potential of Acidobacteria bacterium AB60 from Cerrado soils. <i>FEMS Microbiology Letters</i> , 2020 , 367,	2.9	5
102	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	4.9	24
101	Wood Decay Characteristics and Interspecific Interactions Control Bacterial Community Succession in (Bigtooth Aspen). <i>Frontiers in Microbiology</i> , 2019 , 10, 979	5.7	0
100	Nitrification inhibitors effectively target N O-producing Nitrosospira spp. in tropical soil. <i>Environmental Microbiology</i> , 2019 , 21, 1241-1254	5.2	17
99	Long-term farming systems modulate multi-trophic responses. <i>Science of the Total Environment</i> , 2019 , 646, 480-490	10.2	11
98	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	10.2	14
97	Peat substrate amended with chitin modulates the N-cycle, siderophore and chitinase responses in the lettuce rhizobiome. <i>Scientific Reports</i> , 2019 , 9, 9890	4.9	16
96	Assessing nickel tolerance of bacteria isolated from serpentine soils. <i>Brazilian Journal of Microbiology</i> , 2019 , 50, 705-713	2.2	5
95	Environmental filtering: A case of bacterial community assembly in soil. <i>Soil Biology and Biochemistry</i> , 2019 , 136, 107531	7.5	11
94	Fungal-bacterial diversity and microbiome complexity predict ecosystem functioning. <i>Nature Communications</i> , 2019 , 10, 4841	17.4	267
93	Root-associated microbiomes of wheat under the combined effect of plant development and nitrogen fertilization. <i>Microbiome</i> , 2019 , 7, 136	16.6	102

92	Acidobacteria 2019 , 1-1		1
91	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	10.2	19
90	Exploitation of new endophytic bacteria and their ability to promote sugarcane growth and nitrogen nutrition. <i>Antonie Van Leeuwenhoek</i> , 2019 , 112, 283-295	2.1	19
89	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	4.4	12
88	Legacy of land use history determines reprogramming of plant physiology by soil microbiome. <i>ISME Journal</i> , 2019 , 13, 738-751	11.9	78
87	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	5.6	24
86	Recycling organic residues in agriculture impacts soil-borne microbial community structure, function and NO emissions. <i>Science of the Total Environment</i> , 2018 , 631-632, 1089-1099	10.2	20
85	Native bacteria promote plant growth under drought stress condition without impacting the rhizomicrobiome. <i>FEMS Microbiology Ecology</i> , 2018 , 94,	4.3	26
84	Comparative Genomics of Smut Pathogens: Insights From Orphans and Positively Selected Genes Into Host Specialization. <i>Frontiers in Microbiology</i> , 2018 , 9, 660	5.7	19
83	sp. Govern Nitrous Oxide Emissions in a Tropical Soil Amended With Residues of Bioenergy Crop. <i>Frontiers in Microbiology</i> , 2018 , 9, 674	5.7	30
82	Microbial Extracellular Polymeric Substances: Ecological Function and Impact on Soil Aggregation. <i>Frontiers in Microbiology</i> , 2018 , 9, 1636	5.7	348
81	Genome-resolved metagenomics of sugarcane vinasse bacteria. <i>Biotechnology for Biofuels</i> , 2018 , 11, 48	7.8	10
80	Resilience of the resident soil microbiome to organic and inorganic amendment disturbances and to temporary bacterial invasion. <i>Microbiome</i> , 2018 , 6, 142	16.6	42
79	Effect of and strains on sorghum growth is plant genotype dependent. <i>PeerJ</i> , 2018 , 6, e5346	3.1	22
78	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	4.4	30
77	Characterization of novel Acidobacteria exopolysaccharides with potential industrial and ecological applications. <i>Scientific Reports</i> , 2017 , 7, 41193	4.9	44
76	Organic nitrogen rearranges both structure and activity of the soil-borne microbial seedbank. <i>Scientific Reports</i> , 2017 , 7, 42634	4.9	29
75	Methanogens predominate in natural corrosion protective layers on metal sheet piles. <i>Scientific Reports</i> , 2017 , 7, 11899	4.9	24

74	Rhizobacterial community structure differences among sorghum cultivars in different growth stages and soils. <i>FEMS Microbiology Ecology</i> , 2017 , 93,	4.3	90
73	Amazonian Dark Earth and Its Black Carbon Particles Harbor Different Fungal Abundance and Diversity. <i>Pedosphere</i> , 2017 , 27, 832-845	5	5
72	Functional traits dominate the diversity-related selection of bacterial communities in the rhizosphere. <i>ISME Journal</i> , 2017 , 11, 56-66	11.9	113
71	Successive DNA extractions improve characterization of soil microbial communities. <i>PeerJ</i> , 2017 , 5, e29151	5.1	11
70	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	4.9	72
69	Plant and soil fungal but not soil bacterial communities are linked in long-term fertilized grassland. <i>Scientific Reports</i> , 2016 , 6, 23680	4.9	74
68	Optimized medium culture for Acidobacteria subdivision 1 strains. <i>FEMS Microbiology Letters</i> , 2016 , 363,	2.9	12
67	Acidobacteria strains from subdivision 1 act as plant growth-promoting bacteria. <i>Archives of Microbiology</i> , 2016 , 198, 987-993	3	65
66	Phylogenetic relationships of Rhizoctonia fungi within the Cantharellales. <i>Fungal Biology</i> , 2016 , 120, 603-619	2.8	30
65	Fungal Community Assembly in the Amazonian Dark Earth. <i>Microbial Ecology</i> , 2016 , 71, 962-73	4.4	24
64	Soil Microbiome Is More Heterogeneous in Organic Than in Conventional Farming System. <i>Frontiers in Microbiology</i> , 2016 , 7, 2064	5.7	130
63	Bacterial Community Succession in Pine-Wood Decomposition. <i>Frontiers in Microbiology</i> , 2016 , 7, 231	5.7	72
62	The Ecology of Acidobacteria: Moving beyond Genes and Genomes. <i>Frontiers in Microbiology</i> , 2016 , 7, 744	5.7	427
61	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	5.6	50
60	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	7.5	31
59	Lettuce and rhizosphere microbiome responses to growth promoting <i>Pseudomonas</i> species under field conditions. <i>FEMS Microbiology Ecology</i> , 2016 , 92,	4.3	43
58	Land-use system shapes soil bacterial communities in Southeastern Amazon region. <i>Applied Soil Ecology</i> , 2015 , 95, 151-160	5	73
57	Verrucomicrobial community structure and abundance as indicators for changes in chemical factors linked to soil fertility. <i>Antonie Van Leeuwenhoek</i> , 2015 , 108, 741-52	2.1	55

56	Amazonian dark Earth and plant species from the Amazon region contribute to shape rhizosphere bacterial communities. <i>Microbial Ecology</i> , 2015 , 69, 855-66	4.4	32
55	Context dependency and saturating effects of loss of rare soil microbes on plant productivity. <i>Frontiers in Plant Science</i> , 2015 , 6, 485	6.2	35
54	Soil microbiome responses to the short-term effects of Amazonian deforestation. <i>Molecular Ecology</i> , 2015 , 24, 2433-48	5.7	103
53	Revisiting the dilution procedure used to manipulate microbial biodiversity in terrestrial systems. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 4246-52	4.8	35
52	Non-random species loss in bacterial communities reduces antifungal volatile production. <i>Ecology</i> , 2015 , 96, 2042-8	4.6	77
51	Soil-borne microbiome: linking diversity to function. <i>Microbial Ecology</i> , 2015 , 70, 255-65	4.4	161
50	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	4.3	136
49	Taxonomical and functional microbial community selection in soybean rhizosphere. <i>ISME Journal</i> , 2014 , 8, 1577-87	11.9	423
48	Soil-borne microbial functional structure across different land uses. <i>Scientific World Journal, The</i> , 2014 , 2014, 216071	2.2	5
47	Network topology reveals high connectance levels and few key microbial genera within soils. <i>Frontiers in Environmental Science</i> , 2014 , 2,	4.8	151
46	Sulphur-oxidizing and sulphate-reducing communities in Brazilian mangrove sediments. <i>Environmental Microbiology</i> , 2014 , 16, 845-55	5.2	82
45	Acidobacterial community responses to agricultural management of soybean in Amazon forest soils. <i>FEMS Microbiology Ecology</i> , 2013 , 83, 607-21	4.3	155
44	Structural and functional variation in soil fungal communities associated with litter bags containing maize leaf. <i>FEMS Microbiology Ecology</i> , 2013 , 84, 519-31	4.3	48
43	Soil-borne bacterial structure and diversity does not reflect community activity in Pampa biome. <i>PLoS ONE</i> , 2013 , 8, e76465	3.7	39
42	Tracking fungal community responses to maize plants by DNA- and RNA-based pyrosequencing. <i>PLoS ONE</i> , 2013 , 8, e69973	3.7	24
41	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, 7384-92	4.8	46
40	Soil characteristics more strongly influence soil bacterial communities than land-use type. <i>FEMS Microbiology Ecology</i> , 2012 , 79, 12-24	4.3	254
39	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	3.6	94

38	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	4.3	73
37	Phylogenetic and metagenomic analysis of Verrucomicrobia in former agricultural grassland soil. <i>FEMS Microbiology Ecology</i> , 2010 , 71, 23-33	4.3	21
36	Microbial secondary succession in a chronosequence of chalk grasslands. <i>ISME Journal</i> , 2010 , 4, 711-5	11.9	55
35	Promiscuous mitochondria in <i>Cryptococcus gattii</i> . <i>FEMS Yeast Research</i> , 2009 , 9, 489-503	3.1	25
34	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, 400-21	3.9	150
33	AIDS patient death caused by novel <i>Cryptococcus neoformans</i> x <i>C. gattii</i> hybrid. <i>Emerging Infectious Diseases</i> , 2008 , 14, 1105-8	10.2	79
32	Variabilidade genética entre formaes speciales de <i>Fusarium oxysporum</i> e raças 1 e 2 de <i>F. oxysporum</i> f. sp. <i>lycopersici</i> através de RAPD e sequências de regiões ITS e rDNA. <i>Acta Scientiarum - Agronomy</i> , 2008 , 24, 1481	0.6	2
31	Characterization of <i>Xanthomonas axonopodis</i> pv. <i>phaseoli</i> isolates. <i>Summa Phytopathologica</i> , 2008 , 34, 228-231	0.4	2
30	Caracterização citomorfológica, cultural, molecular e patogênica de <i>Rhizoctonia solani</i> Kühn associado ao arroz em Tocantins, Brasil. <i>Summa Phytopathologica</i> , 2007 , 33, 129-136	0.4	9
29	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	19
28	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	2.1	6
27	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, 18730-5	11.5	326
26	The reach of the genome signature in prokaryotes. <i>BMC Evolutionary Biology</i> , 2006 , 6, 84	3	51
25	Conflicting phylogenetic position of <i>Schizosaccharomyces pombe</i> . <i>Genomics</i> , 2006 , 88, 387-93	4.3	18
24	Brazilian coffee genome project: an EST-based genomic resource. <i>Brazilian Journal of Plant Physiology</i> , 2006 , 18, 95-108		90
23	Unique hybrids between the fungal pathogens <i>Cryptococcus neoformans</i> and <i>Cryptococcus gattii</i> . <i>FEMS Yeast Research</i> , 2006 , 6, 599-607	3.1	110
22	Phylogenomics reveal a robust fungal tree of life. <i>FEMS Yeast Research</i> , 2006 , 6, 1213-20	3.1	57
21	Yeast Genome 10th Anniversary, Académie Royale des Sciences, des Letters et des Beaux-Arts de Belgique in Brussels (Belgium), 78 September 2006. <i>FEMS Yeast Research</i> , 2006 , 6, 1103-1104	3.1	

20	Binucleate Rhizoctonia sp. AG G causing root rot in yacon (<i>Smallanthus sonchifolius</i>) in Brazil. <i>Plant Pathology</i> , 2005 , 54, 325-330	2.8	8
19	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	2.1	19
18	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, 257-62	2.2	27
17	Comparative genomics of two <i>Leptospira interrogans</i> serovars reveals novel insights into physiology and pathogenesis. <i>Journal of Bacteriology</i> , 2004 , 186, 2164-72	3.5	330
16	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, 827-36	3.6	103
15	Evaluation of monocot and eudicot divergence using the sugarcane transcriptome. <i>Plant Physiology</i> , 2004 , 134, 951-9	6.6	33
14	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, 1018-26	3.5	276
13	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	2.5	10
12	Identification of <i>Rhizoctonia solani</i> associated with soybean in Brazil by rDNA-ITS sequences. <i>Tropical Plant Pathology</i> , 2003 , 28, 413-419		16
11	Identification of <i>Rhizoctonia solani</i> AG 1-IB in Lettuce, AG 4 HG-I in Tomato and Melon, and AG 4 HG-III in Broccoli and Spinach, in Brazil. <i>European Journal of Plant Pathology</i> , 2003 , 109, 391-395	2.1	40
10	Analysis and functional annotation of an expressed sequence tag collection for tropical crop sugarcane. <i>Genome Research</i> , 2003 , 13, 2725-35	9.7	207
9	Comparison of the sequences of the internal transcribed spacer regions and <i>PbGP43</i> genes of <i>Paracoccidioides brasiliensis</i> from patients and armadillos (<i>Dasypus novemcinctus</i>). <i>Journal of Clinical Microbiology</i> , 2003 , 41, 5735-7	9.7	30
8	Variabilidade genética de acessos de aguapão coletados no Estado de São Paulo. <i>Planta Daninha</i> , 2002 , 20, 1-5	0.7	11
7	Identification and Characterization of <i>Colletotrichum</i> spp. affecting Fruit after Harvest in Brazil. <i>Journal of Phytopathology</i> , 2002 , 150, 128-134	1.8	68
6	Characterization of <i>Rhizoctonia solani</i> Associated with Soybean in Brazil. <i>European Journal of Plant Pathology</i> , 2002 , 108, 783-792	2.1	41
5	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, 2932-41	4.8	405
4	Identification of 14-3-3-like protein in sugarcane (<i>Saccharum officinarum</i>). <i>Genetics and Molecular Biology</i> , 2001 , 24, 43-48	2	1
3	The genome sequence of the plant pathogen <i>Xylella fastidiosa</i> . The <i>Xylella fastidiosa</i> Consortium of the Organization for Nucleotide Sequencing and Analysis. <i>Nature</i> , 2000 , 406, 151-9	50.4	701

2	Understanding and prediction of soil microbial community dynamics under global change. <i>Applied Soil Ecology</i> , 1999 , 11, 161-176	5	88
1	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> , 1	6.1	0