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List of Publications by Year
in descending order

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47 papers	3,638 citations	159358 30 h-index	205818 48 g-index
53 all docs	53 docs citations	53 times ranked	4861 citing authors

#	Article	IF	Citations
1	Frontiers and Opportunities in Bioenergy Crop Microbiome Research Networks. Phytobiomes Journal, 2022, 6, 118-126.	1.4	1
2	Evolutionary transition to the ectomycorrhizal habit in the genomes of a hyperdiverse lineage of mushroomâ€forming fungi. New Phytologist, 2022, 233, 2294-2309.	3.5	21
3	Amantadine preferential binding and disordering of phase separated membranes. Biophysical Journal, 2022, 121, 366a-367a.	0.2	0
4	Phylogenetic diversity of 200+ isolates of the ectomycorrhizal fungus Cenococcum geophilum associated with Populus trichocarpa soils in the Pacific Northwest, USA and comparison to globally distributed representatives. PLoS ONE, 2021, 16, e0231367.	1.1	7
5	Biosynthesis and characterization of deuterated chitosan in filamentous fungus and yeast. Carbohydrate Polymers, 2021, 257, 117637.	5.1	8
6	Microevolution in the pansecondary metabolome of Aspergillus flavus and its potential macroevolutionary implications for filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
7	Towards engineering ectomycorrhization into switchgrass bioenergy crops via a lectin receptorâ€like kinase. Plant Biotechnology Journal, 2021, 19, 2454-2468.	4.1	14
8	Plantâ€“Microbe Interactions: From Genes to Ecosystems Using Populus as a Model System. Phytobiomes Journal, 2021, 5, 29-38.	1.4	31
9	Heterospecific Neighbor Plants Impact Root Microbiome Diversity and Molecular Function of Root Fungi. Frontiers in Microbiology, 2021, 12, 680267.	1.5	3
10	Insight into a highly polymorphic endophyte isolated from the roots of the halophytic seepweed Suaeda salsa: Laburnicola rhizohalophila sp. nov. (Didymosphaeriaceae, Pleosporales). Fungal Biology, 2020, 124, 327-337.	1.1	13
11	Arabidopsis Câ€terminal binding protein ANGUSTIFOLIA modulates transcriptional coâ€regulation of MYB46 and WRKY33. New Phytologist, 2020, 228, 1627-1639.	3.5	17
12	Lipo-chitooligosaccharides as regulatory signals of fungal growth and development. Nature Communications, 2020, 11, 3897.	5.8	65
13	Microbe to Microbiome: A Paradigm Shift in the Application of Microorganisms for Sustainable Agriculture. Frontiers in Microbiology, 2020, 11, 622926.	1.5	88
14	Plant Biosystems Design Research Roadmap 1.0. Biodesign Research, 2020, 2020, .	0.8	16
15	Advancing How We Learn from Biodesign to Mitigate Risks with Next-Generation Genome Engineering. Biodesign Research, 2020, 2020, .	0.8	4
16	Mediation of plantâ€“mycorrhizal interaction by a lectin receptor-like kinase. Nature Plants, 2019, 5, 676-680.	4.7	42
17	Terpene Synthase Genes Originated from Bacteria through Horizontal Gene Transfer Contribute to Terpenoid Diversity in Fungi. Scientific Reports, 2019, 9, 9223.	1.6	31
18	Microfluidics and Metabolomics Reveal Symbiotic Bacterialâ€“Fungal Interactions Between Mortierella elongata and Burkholderia Include Metabolite Exchange. Frontiers in Microbiology, 2019, 10, 2163.	1.5	37

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19	Fungal Endophytes ofPopulus trichocarpaAlter Host Phenotype, Gene Expression, and Rhizobiome Composition. Molecular Plant-Microbe Interactions, 2019, 32, 853-864.	1.4	52
20	Increasing access to microfluidics for studying fungi and other branched biological structures. Fungal Biology and Biotechnology, 2019, 6, 1.	2.5	17
21	Identification of Populus Small RNAs Responsive to Mutualistic Interactions With Mycorrhizal Fungi, Laccaria bicolor and Rhizophagus irregularis. Frontiers in Microbiology, 2019, 10, 515.	1.5	17
22	The Ectomycorrhizal Fungus Laccaria bicolor Produces Lipochitooligosaccharides and Uses the Common Symbiosis Pathway to Colonize Populus Roots. Plant Cell, 2019, 31, 2386-2410.	3.1	73
23	Bacterialâ€“fungal interactions: ecology, mechanisms and challenges. FEMS Microbiology Reviews, 2018, 42, 335-352.	3.9	468
24	Russulaceae: a new genomic dataset to study ecosystem function and evolutionary diversification of ectomycorrhizal fungi with their tree associates. New Phytologist, 2018, 218, 54-65.	3.5	71
25	Phytobiome and Transcriptional Adaptation of Populus deltoides to Acute Progressive Drought and Cyclic Drought. Phytobiomes Journal, 2018, 2, 249-260.	1.4	23
26	Bacterial biofilm formation on the hyphae of ectomycorrhizal fungi: a widespread ability under controls?. FEMS Microbiology Ecology, 2018, 94, .	1.3	43
27	Perspectives on the basic and applied aspects of crassulacean acid metabolism (CAM) research. Plant Science, 2018, 274, 394-401.	1.7	18
28	Populus trichocarpa encodes small, effector-like secreted proteins that are highly induced during mutualistic symbiosis. Scientific Reports, 2017, 7, 382.	1.6	36
29	Integrated proteomics and metabolomics suggests symbiotic metabolism and multimodal regulation in a fungalâ€endobacterial system. Environmental Microbiology, 2017, 19, 1041-1053.	1.8	38
30	Diverse Plant-Associated Pleosporalean Fungi from Saline Areas: Ecological Tolerance and Nitrogen-Status Dependent Effects on Plant Growth. Frontiers in Microbiology, 2017, 8, 158.	1.5	48
31	Down-Regulation of KORRIGAN-Like Endo-Î²-1,4-Glucanase Genes Impacts Carbon Partitioning, Mycorrhizal Colonization and Biomass Production in Populus. Frontiers in Plant Science, 2016, 7, 1455.	1.7	32
32	Genome-wide analysis of lectin receptor-like kinases in Populus. BMC Genomics, 2016, 17, 699.	1.2	72
33	Specialized Microbiome of a Halophyte and its Role in Helping Non-Host Plants to Withstand Salinity. Scientific Reports, 2016, 6, 32467.	1.6	181
34	Mitigating climate change through managing constructed-microbial communities in agriculture. Agriculture, Ecosystems and Environment, 2016, 216, 304-308.	2.5	56
35	Newly identified helper bacteria stimulate ectomycorrhizal formation in Populus. Frontiers in Plant Science, 2014, 5, 579.	1.7	68
36	A Multifactor Analysis of Fungal and Bacterial Community Structure in the Root Microbiome of Mature Populus deltoides Trees. PLoS ONE, 2013, 8, e76382.	1.1	315

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37	The obscure events contributing to the evolution of an incipient sex chromosome in Populus: a retrospective working hypothesis. Tree Genetics and Genomes, 2012, 8, 559-571.	0.6	50
38	Extensive gene flow over Europe and possible speciation over Eurasia in the ectomycorrhizal basidiomycete Laccaria amethystina complex. Molecular Ecology, 2012, 21, 281-299.	2.0	62
39	Characterization of Transposable Elements in the Ectomycorrhizal Fungus Laccaria bicolor. PLoS ONE, 2012, 7, e40197.	1.1	38
40	Highly Efficient Isolation of Populus Mesophyll Protoplasts and Its Application in Transient Expression Assays. PLoS ONE, 2012, 7, e44908.	1.1	89
41	Distribution and localization of microsatellites in the Perigord black truffle genome and identification of new molecular markers. Fungal Genetics and Biology, 2011, 48, 592-601.	0.9	67
42	Identification of quantitative trait loci affecting ectomycorrhizal symbiosis in an interspecific F1 poplar cross and differential expression of genes in ectomycorrhizas of the two parents: Populus deltoides and Populus trichocarpa. Tree Genetics and Genomes, 2011, 7, 617-627.	0.6	48
43	Survey and analysis of simple sequence repeats in the Laccaria bicolor genome, with development of microsatellite markers. Current Genetics, 2011, 57, 75-88.	0.8	38
44	Effect of poplar genotypes on mycorrhizal infection and secreted enzyme activities in mycorrhizal and non-mycorrhizal roots. Journal of Experimental Botany, 2011, 62, 249-260.	2.4	63
45	The genome of Laccaria bicolor provides insights into mycorrhizal symbiosis. Nature, 2008, 452, 88-92.	13.7	1,003
46	Gene organization of the mating type regions in the ectomycorrhizal fungus Laccaria bicolor reveals distinct evolution between the two mating type loci. New Phytologist, 2008, 180, 329-342.	3.5	59
47	A genetic linkage map for the ectomycorrhizal fungus Laccaria bicolor and its alignment to the wholeâ€genome sequence assemblies. New Phytologist, 2008, 180, 316-328.	3.5	32