

Sara Mayer Branco

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7128864/publications.pdf>

Version: 2024-02-01

30
papers

5,541
citations

361045

20
h-index

500791

28
g-index

31
all docs

31
docs citations

31
times ranked

6932
citing authors

#	ARTICLE	IF	CITATIONS
1	Fungal Community Shift Along Steep Environmental Gradients from Geothermal Soils in Yellowstone National Park. <i>Microbial Ecology</i> , 2022, 84, 33-43.	1.4	3
2	Giant mobile elements: Agents of multivariate phenotypic evolution in fungi. <i>Current Biology</i> , 2022, 32, R234-R236.	1.8	0
3	Mechanisms of stress tolerance and their effects on the ecology and evolution of mycorrhizal fungi. <i>New Phytologist</i> , 2022, 235, 2158-2175.	3.5	34
4	Comparative genomics reveals dynamic genome evolution in host specialist ectomycorrhizal fungi. <i>New Phytologist</i> , 2021, 230, 774-792.	3.5	37
5	Disentangling the role of ectomycorrhizal fungi in plant nutrient acquisition along a Zn gradient using X-ray imaging. <i>Science of the Total Environment</i> , 2021, 801, 149481.	3.9	4
6	Fungal heavy metal adaptation through single nucleotide polymorphisms and copy number variation. <i>Molecular Ecology</i> , 2020, 29, 4157-4169.	2.0	24
7	Gene Copy Number Variation Does Not Reflect Structure or Environmental Selection in Two Recently Diverged California Populations of <i>Suillus brevipes</i> . <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 4591-4597.	0.8	2
8	Biology and applications of endophytic insect-pathogenic fungi. <i>PLoS Pathogens</i> , 2019, 15, e1007831.	2.1	46
9	Fungal diversity from communities to genes. <i>Fungal Biology Reviews</i> , 2019, 33, 225-237.	1.9	23
10	Convergent recombination cessation between mating-type genes and centromeres in selfing anther-smut fungi. <i>Genome Research</i> , 2019, 29, 944-953.	2.4	21
11	Genome-based estimates of fungal rDNA copy number variation across phylogenetic scales and ecological lifestyles. <i>Molecular Ecology</i> , 2019, 28, 721-730.	2.0	163
12	The power of discussion: Support for women at the fungal Gordon Research Conference. <i>Fungal Genetics and Biology</i> , 2018, 121, 65-67.	0.9	2
13	Survey of corticioid fungi in North American pinaceous forests reveals hyperdiversity, underpopulated sequence databases, and species that are potentially ectomycorrhizal. <i>Mycologia</i> , 2017, 109, 115-127.	0.8	31
14	Sources of Fungal Genetic Variation and Associating It with Phenotypic Diversity. <i>Microbiology Spectrum</i> , 2017, 5, .	1.2	33
15	Evolutionary strata on young mating-type chromosomes despite the lack of sexual antagonism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7067-7072.	3.3	92
16	Continental-level population differentiation and environmental adaptation in the mushroom <i>Suillus brevipes</i> . <i>Molecular Ecology</i> , 2017, 26, 2063-2076.	2.0	55
17	Scale-dependent variation in nitrogen cycling and soil fungal communities along gradients of forest composition and age in regenerating tropical dry forests. <i>New Phytologist</i> , 2016, 209, 845-854.	3.5	82
18	FUNGuild: An open annotation tool for parsing fungal community datasets by ecological guild. <i>Fungal Ecology</i> , 2016, 20, 241-248.	0.7	2,797

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19	Genetic isolation between two recently diverged populations of a symbiotic fungus. <i>Molecular Ecology</i> , 2015, 24, 2747-2758.	2.0	100
20	Clonal reproduction in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8901-8908.	3.3	104
21	Fungal evolutionary genomics provides insight into the mechanisms of adaptive divergence in eukaryotes. <i>Molecular Ecology</i> , 2014, 23, 753-773.	2.0	203
22	Endemism and functional convergence across the North American soil mycobiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 6341-6346.	3.3	482
23	Improved software detection and extraction of ITS1 and <scp>ITS</scp>2 from ribosomal <scp>ITS</scp> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919.	2.2	868
24	Independent roles of ectomycorrhizal and saprotrophic communities in soil organic matter decomposition. <i>Soil Biology and Biochemistry</i> , 2013, 57, 282-291.	4.2	203
25	Fungi at a Small Scale: Spatial Zonation of Fungal Assemblages around Single Trees. <i>PLoS ONE</i> , 2013, 8, e78295.	1.1	40
26	A note on the incidence of reverse complementary fungal ITS sequences in the public sequence databases and a software tool for their detection and reorientation. <i>Mycoscience</i> , 2011, 52, 278-282.	0.3	7
27	Serpentine soils promote ectomycorrhizal fungal diversity. <i>Molecular Ecology</i> , 2010, 19, 5566-5576.	2.0	30
28	Serpentine Soils Do Not Limit Mycorrhizal Fungal Diversity. <i>PLoS ONE</i> , 2010, 5, e11757.	1.1	40
29	Are Oaks Locally Adapted to Serpentine Soils?. <i>Northeastern Naturalist</i> , 2009, 16, 329-340.	0.1	12
30	Sources of Fungal Genetic Variation and Associating It with Phenotypic Diversity. , 0, , 635-655.		3