

Martin Ryberg

List of Publications by Year in descending order

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Version: 2024-02-01

60
papers

7,526
citations

147801

31
h-index

138484

58
g-index

66
all docs

66
docs citations

66
times ranked

8908
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370
2	Improved software detection and extraction of ITS1 and <sc>ITS</sc>2 from ribosomal <sc>ITS</sc> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919.	5.2	868
3	Intraspecific <i>ITS</i> Variability in the Kingdom <i>Fungi</i> as Expressed in the International Sequence Databases and Its Implications for Molecular Species Identification. <i>Evolutionary Bioinformatics</i> , 2008, 4, EBO.S653.	1.2	673
4	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. <i>PLoS ONE</i> , 2006, 1, e59.	2.5	508
5	High-level classification of the Fungi and a tool for evolutionary ecological analyses. <i>Fungal Diversity</i> , 2018, 90, 135-159.	12.3	450
6	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
7	Towards global patterns in the diversity and community structure of ectomycorrhizal fungi. <i>Molecular Ecology</i> , 2012, 21, 4160-4170.	3.9	365
8	Relative importance of coarse and fine woody debris for the diversity of wood-inhabiting fungi in temperate broadleaf forests. <i>Biological Conservation</i> , 2004, 117, 1-10.	4.1	246
9	The ITS region as a target for characterization of fungal communities using emerging sequencing technologies. <i>FEMS Microbiology Letters</i> , 2009, 296, 97-101.	1.8	246
10	An open source software package for automated extraction of ITS1 and ITS2 from fungal ITS sequences for use in high-throughput community assays and molecular ecology. <i>Fungal Ecology</i> , 2010, 3, 284-287.	1.6	194
11	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycKeys</i> , 0, 4, 37-63.	1.9	157
12	Mining metadata from unidentified ITS sequences in GenBank: A case study in <i>Inocybe</i> (Basidiomycota). <i>BMC Evolutionary Biology</i> , 2008, 8, 50.	3.2	144
13	Ranking higher taxa using divergence times: a case study in Dothideomycetes. <i>Fungal Diversity</i> , 2017, 84, 75-99.	12.3	138
14	The distance decay of similarity in communities of ectomycorrhizal fungi in different ecosystems and scales. <i>Journal of Ecology</i> , 2013, 101, 1335-1344.	4.0	124
15	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
16	Into and out of the tropics: global diversification patterns in a hyperdiverse clade of ectomycorrhizal fungi. <i>Molecular Ecology</i> , 2016, 25, 630-647.	3.9	108
17	An outlook on the fungal internal transcribed spacer sequences in GenBank and the introduction of a web-based tool for the exploration of fungal diversity. <i>New Phytologist</i> , 2009, 181, 471-477.	7.3	107
18	Dead wood in semi-natural temperate broadleaved woodland: contribution of coarse and fine dead wood, attached dead wood and stumps. <i>Forest Ecology and Management</i> , 2004, 194, 235-248.	3.2	92

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37	Rethinking taxon sampling in the light of environmental sequencing. <i>Cladistics</i> , 2011, 27, 197-203.	3.3	23
38	Host genetic variation strongly influences the microbiome structure and function in fungal fruiting bodies. <i>Environmental Microbiology</i> , 2018, 20, 1641-1650.	3.8	23
39	<i>Pseudolagarobasidium</i> (Basidiomycota): on the reinstatement of a genus of parasitic, saprophytic, and endophytic resupinate fungi. <i>Botany</i> , 2008, 86, 1319-1325.	1.0	17
40	The genome and microbiome of a dikaryotic fungus (<i>Inocybe terrigena</i> , Inocybaceae) revealed by metagenomics. <i>Environmental Microbiology Reports</i> , 2018, 10, 155-166.	2.4	17
41	Long- and short-read metabarcoding technologies reveal similar spatiotemporal structures in fungal communities. <i>Molecular Ecology Resources</i> , 2021, 21, 1833-1849.	4.8	16
42	Annotating public fungal ITS sequences from the built environment according to the MlXs-Built Environment standard – a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). <i>MycKeys</i> , 0, 16, 1-15.	1.9	16
43	Naming the untouchable – environmental sequences and niche partitioning as taxonomical evidence in fungi. <i>IMA Fungus</i> , 2020, 11, 23.	3.8	15
44	ARBitR: an overlap-aware genome assembly scaffolder for linked reads. <i>Bioinformatics</i> , 2021, 37, 2203-2205.	4.1	15
45	When mycologists describe new species, not all relevant information is provided (clearly enough). <i>MycKeys</i> , 2020, 72, 109-128.	1.9	15
46	Complex effects of mammalian grazing on extramatrical mycelial biomass in the Scandes forest-tundra ecotone. <i>Ecology and Evolution</i> , 2018, 8, 1019-1030.	1.9	13
47	Multigene phylogeny and taxonomic revision of Atheliales s.l.: Reinstatement of three families and one new family, Lobuliciaceae fam. nov.. <i>Fungal Biology</i> , 2021, 125, 239-255.	2.5	12
48	Three new species of <i>Inosperma</i> (Agaricales, Inocybaceae) from Tropical Africa. <i>MycKeys</i> , 2021, 77, 97-116.	1.9	9
49	The curse of the uncultured fungus. <i>MycKeys</i> , 2022, 86, 177-194.	1.9	9
50	Dating the emergence of truffle-like fungi in Australia, by using an augmented meta-analysis. <i>Australian Systematic Botany</i> , 2016, 29, 284.	0.9	8
51	<i>Mallocybe africana</i> (Inocybaceae, Fungi), the first species of <i>Mallocybe</i> described from Africa. <i>Phytotaxa</i> , 2021, 478, 49-60.	0.3	8
52	Soil fungal communities of ectomycorrhizal dominated woodlands across West Africa. <i>MycKeys</i> , 2021, 81, 45-68.	1.9	7
53	Overview of Phylogenetic Approaches to Mycorrhizal Biogeography, Diversity and Evolution. <i>Ecological Studies</i> , 2017, , 1-37.	1.2	7
54	Two new African siblings of <i>Pulveroboletus ravenelii</i> (Boletaceae). <i>MycKeys</i> , 2018, 43, 115-130.	1.9	6

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55	Amanita sect. Phalloideae: two interesting non-lethal species from West Africa. Mycological Progress, 2022, 21, 1.	1.4	5
56	DivBayes and SubT: exploring species diversification using Bayesian statistics. Bioinformatics, 2011, 27, 2439-2440.	4.1	4
57	Morphology, Multilocus Phylogeny, and Toxin Analysis Reveal Amanita albolimbata, the First Lethal Amanita Species From Benin, West Africa. Frontiers in Microbiology, 2020, 11, 599047.	3.5	4
58	Paxilloboletus gen. nov., a new lamellate bolete genus from tropical Africa. Mycological Progress, 2022, 21, 243-256.	1.4	3
59	Phylommand - a command line software package for phylogenetics. F1000Research, 0, 5, 2903.	1.6	2
60	The genus Catathelasma (Catathelasmataceae, Basidiomycota) in China. MycoKeys, 2020, 62, 123-138.	1.9	1