

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	»¿The curse of the uncultured fungus. <i>MycoKeys</i> , 2022, 86, 177-194.	1.9	9
2	<i>Paxilloboletus</i> gen. nov., a new lamellate bolete genus from tropical Africa. <i>Mycological Progress</i> , 2022, 21, 243-256.	1.4	3
3	<i>Amanita</i> sect. <i>Phalloideae</i> : two interesting non-lethal species from West Africa. <i>Mycological Progress</i> , 2022, 21, 1.	1.4	5
4	Multigene phylogeny and taxonomic revision of <i>Atheliales</i> s.l.: Reinstatement of three families and one new family, <i>Lobuliciaceae</i> fam. nov.. <i>Fungal Biology</i> , 2021, 125, 239-255.	2.5	12
5	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
6	Soil fungal communities of ectomycorrhizal dominated woodlands across West Africa. <i>MycoKeys</i> , 2021, 81, 45-68.	1.9	7
7	Three new species of <i>Inosperma</i> (Agaricales, <i>Inocybaceae</i>) from Tropical Africa. <i>MycoKeys</i> , 2021, 77, 97-116.	1.9	9
8	<p>Mallocybe africana (<i>Inocybaceae</i> , Fungi), the first species of Mallocybe described from Africa</p>. <i>Phytotaxa</i> , 2021, 478, 49-60.	0.3	8
9	ARBitR: an overlap-aware genome assembly scaffolder for linked reads. <i>Bioinformatics</i> , 2021, 37, 2203-2205.	4.1	15
10	Morphology, Multilocus Phylogeny, and Toxin Analysis Reveal <i>Amanita albolimbata</i> , the First Lethal <i>Amanita</i> Species From Benin, West Africa. <i>Frontiers in Microbiology</i> , 2020, 11, 599047.	3.5	4
11	Naming the untouchable “ environmental sequences and niche partitioning as taxonomical evidence in fungi. <i>IMA Fungus</i> , 2020, 11, 23.	3.8	15
12	<i>FungalTraits</i> : a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
13	Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 32528-32534.	7.1	65
14	When mycologists describe new species, not all relevant information is provided (clearly enough). <i>MycoKeys</i> , 2020, 72, 109-128.	1.9	15
15	The genus <i>Catathelasma</i> (<i>Catathelasmataceae</i> , <i>Basidiomycota</i>) in China. <i>MycoKeys</i> , 2020, 62, 123-138.	1.9	1
16	Maintenance of High Genome Integrity over Vegetative Growth in the Fairy-Ring Mushroom <i>Marasmius oreades</i> . <i>Current Biology</i> , 2019, 29, 2758-2765.e6.	3.9	28
17	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
18	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

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19	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
20	High-level classification of the Fungi and a tool for evolutionary ecological analyses. <i>Fungal Diversity</i> , 2018, 90, 135-159.	12.3	450
21	Structure and function of the global topsoil microbiome. <i>Nature</i> , 2018, 560, 233-237.	27.8	1,370
22	New light on names and naming of dark taxa. <i>MycoKeys</i> , 2018, 30, 31-39.	1.9	39
23	Two new African siblings of <i>Pulveroboletus ravenelii</i> (Boletaceae). <i>MycoKeys</i> , 2018, 43, 115-130.	1.9	6
24	Ranking higher taxa using divergence times: a case study in Dothideomycetes. <i>Fungal Diversity</i> , 2017, 84, 75-99.	12.3	138
25	Overview of Phylogenetic Approaches to Mycorrhizal Biogeography, Diversity and Evolution. <i>Ecological Studies</i> , 2017, , 1-37.	1.2	7
26	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
27	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
28	Molecular operational taxonomic units as approximations of species in the light of evolutionary models and empirical data from Fungi. <i>Molecular Ecology</i> , 2015, 24, 5770-5777.	3.9	63
29	Global Multilocus Sequence Type Analysis of <i>Chlamydia trachomatis</i> Strains from 16 Countries. <i>Journal of Clinical Microbiology</i> , 2015, 53, 2172-2179.	3.9	46
30	Molecular phylogenetics and taxonomy in Psathyrellaceae (Agaricales) with focus on psathyrelloid species: introduction of three new genera and 18 new species. <i>Mycological Progress</i> , 2015, 14, 1.	1.4	40
31	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
32	Global biogeography of the ectomycorrhizal /sebacina lineage (<i>Fungi</i> , Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 227 Td (<i>Fungi</i>) 2014, 23, 4168-4183.	3.9	58
33	Improved software detection and extraction of ITS1 and ITS2 from ribosomal ITS 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
34	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
35	Evolution of the Toxins Muscarine and Psilocybin in a Family of Mushroom-Forming Fungi. <i>PLoS ONE</i> , 2013, 8, e64646.	2.5	52
36	Asynchronous origins of ectomycorrhizal clades of Agaricales. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2012, 279, 2003-2011.	2.6	77

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37	Towards global patterns in the diversity and community structure of ectomycorrhizal fungi. <i>Molecular Ecology</i> , 2012, 21, 4160-4170.	3.9	365
38	Tidying Up International Nucleotide Sequence Databases: Ecological, Geographical and Sequence Quality Annotation of ITS Sequences of Mycorrhizal Fungi. <i>PLoS ONE</i> , 2011, 6, e24940.	2.5	51
39	DEALING WITH INCOMPLETE TAXON SAMPLING AND DIVERSIFICATION OF A LARGE CLADE OF MUSHROOM-FORMING FUNGI. <i>Evolution; International Journal of Organic Evolution</i> , 2011, 65, 1862-1878.	2.3	25
40	Rethinking taxon sampling in the light of environmental sequencing. <i>Cladistics</i> , 2011, 27, 197-203.	3.3	23
41	Weak habitat specificity in ectomycorrhizal communities associated with <i>Salix herbacea</i> and <i>Salix polaris</i> in alpine tundra. <i>Mycorrhiza</i> , 2011, 21, 289-296.	2.8	33
42	DivBayes and SubT: exploring species diversification using Bayesian statistics. <i>Bioinformatics</i> , 2011, 27, 2439-2440.	4.1	4
43	An evolutionary perspective on morphological and ecological characters in the mushroom family Inocybaceae (Agaricomycotina, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2010, 55, 431-442.	2.7	49
44	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
45	An open source chimera checker for the fungal ITS region. <i>Molecular Ecology Resources</i> , 2010, 10, 1076-1081.	4.8	77
46	Ectomycorrhizal Diversity on <i>Dryas octopetala</i> and <i>Salix reticulata</i> in an Alpine Cliff Ecosystem. <i>Arctic, Antarctic, and Alpine Research</i> , 2009, 41, 506-514.	1.1	67
47	A software pipeline for processing and identification of fungal ITS sequences. <i>Source Code for Biology and Medicine</i> , 2009, 4, 1.	1.7	85
48	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
49	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
50	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
51	Partial cutting reduces species richness of fungi on woody debris in oak-rich forests. <i>Canadian Journal of Forest Research</i> , 2008, 38, 1807-1816.	1.7	32
52	<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
53	Intraspecific ITS Variability in the Kingdom Fungi 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
54	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. <i>PLoS ONE</i> , 2006, 1, e59.	2.5	508

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55	Approaching the taxonomic affiliation of unidentified sequences in public databases—an example from the mycorrhizal fungi. <i>BMC Bioinformatics</i> , 2005, 6, 178.	2.6	74
56	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
57	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
58	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
59	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
60	Phylommand - a command line software package for phylogenetics. <i>F1000Research</i> , 0, 5, 2903.	1.6	2