## Martin Ryberg

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	27.8	1,370
2	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. Methods in Ecology and Evolution, 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. Evolutionary Bioinformatics, 2008, 4, EBO.S653.	1.2	673
4	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. PLoS ONE, 2006, 1, e59.	2.5	508
5	High-level classification of the Fungi and a tool for evolutionary ecological analyses. Fungal Diversity, 2018, 90, 135-159.	12.3	450
6	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
7	Towards global patterns in the diversity and community structure of ectomycorrhizal fungi. Molecular Ecology, 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. Biological Conservation, 2004, 117, 1-10.	4.1	246
9	The ITS region as a target for characterization of fungal communities using emerging sequencing technologies. FEMS Microbiology Letters, 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. Fungal Ecology, 2010, 3, 284-287.	1.6	194
11	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. MycoKeys, 0, 4, 37-63.	1.9	157
12	Mining metadata from unidentified ITS sequences in GenBank: A case study in Inocybe (Basidiomycota). BMC Evolutionary Biology, 2008, 8, 50.	3.2	144
13	Ranking higher taxa using divergence times: a case study in Dothideomycetes. Fungal Diversity, 2017, 84, 75-99.	12.3	138
14	The distance decay of similarity in communities of ectomycorrhizal fungi in different ecosystems and scales. Journal of Ecology, 2013, 101, 1335-1344.	4.0	124
15	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	12.3	123
16	Into and out of the tropics: global diversification patterns in a hyperdiverse clade of ectomycorrhizal fungi. Molecular Ecology, 2016, 25, 630-647.	3.9	108
17	An outlook on the fungal internal transcribed spacer sequences in GenBank and the introduction of a webâ€based tool for the exploration of fungal diversity. New Phytologist, 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. Forest Ecology and Management, 2004, 194, 235-248.	3.2	92

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19	A software pipeline for processing and identification of fungal ITS sequences. Source Code for Biology and Medicine, 2009, 4, 1.	1.7	85
20	An open source chimera checker for the fungal ITS region. Molecular Ecology Resources, 2010, 10, 1076-1081.	4.8	77
21	Asynchronous origins of ectomycorrhizal clades of Agaricales. Proceedings of the Royal Society B: Biological Sciences, 2012, 279, 2003-2011.	2.6	77
22	Approaching the taxonomic affiliation of unidentified sequences in public databasesan example from the mycorrhizal fungi. BMC Bioinformatics, 2005, 6, 178.	2.6	74
23	Ectomycorrhizal Diversity on Dryas octopetala and Salix reticulata in an Alpine Cliff Ecosystem. Arctic, Antarctic, and Alpine Research, 2009, 41, 506-514.	1.1	67
24	Fruiting body form, not nutritional mode, is the major driver of diversification in mushroom-forming fungi. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 32528-32534.	7.1	65
25	Molecular operational taxonomic units as approximations of species in the light of evolutionary models and empirical data from Fungi. Molecular Ecology, 2015, 24, 5770-5777.	3.9	63
26	Global biogeography of the ectomycorrhizal /sebacina lineage ( <scp>F</scp> ungi,) Tj ETQq0 0 0 rgBT /Overloc 2014, 23, 4168-4183.	k 10 Tf 50 4 3.9	467 Td ( <scp> 58</scp>
27	Evolution of the Toxins Muscarine and Psilocybin in a Family of Mushroom-Forming Fungi. PLoS ONE, 2013, 8, e64646.	2.5	52
28	Tidying Up International Nucleotide Sequence Databases: Ecological, Geographical and Sequence Quality Annotation of ITS Sequences of Mycorrhizal Fungi. PLoS ONE, 2011, 6, e24940.	2.5	51
29	An evolutionary perspective on morphological and ecological characters in the mushroom family Inocybaceae (Agaricomycotina, Fungi). Molecular Phylogenetics and Evolution, 2010, 55, 431-442.	2.7	49
30	Global Multilocus Sequence Type Analysis of Chlamydia trachomatis Strains from 16 Countries. Journal of Clinical Microbiology, 2015, 53, 2172-2179.	3.9	46
31	Molecular phylogenetics and taxonomy in Psathyrellaceae (Agaricales) with focus on psathyrelloid species: introduction of three new genera and 18 new species. Mycological Progress, 2015, 14, 1.	1.4	40
32	New light on names and naming of dark taxa. MycoKeys, 2018, 30, 31-39.	1.9	39
33	Weak habitat specificity in ectomycorrhizal communities associated with Salix herbacea and Salix polaris in alpine tundra. Mycorrhiza, 2011, 21, 289-296.	2.8	33
34	Partial cutting reduces species richness of fungi on woody debris in oak-rich forests. Canadian Journal of Forest Research, 2008, 38, 1807-1816.	1.7	32
35	Maintenance of High Genome Integrity over Vegetative Growth in the Fairy-Ring Mushroom Marasmius oreades. Current Biology, 2019, 29, 2758-2765.e6.	3.9	28
36	DEALING WITH INCOMPLETE TAXON SAMPLING AND DIVERSIFICATION OF A LARGE CLADE OF MUSHROOM-FORMING FUNGI. Evolution; International Journal of Organic Evolution, 2011, 65, 1862-1878.	2.3	25

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