

# Henrik R Nilsson

## List of Publications by Year in descending order

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Version: 2024-02-01

138  
papers

29,747  
citations

20817

60  
h-index

16650

123  
g-index

148  
all docs

148  
docs citations

148  
times ranked

22614  
citing authors

#	ARTICLE	IF	CITATIONS
1	The curse of the uncultured fungus. <i>MycKeys</i> , 2022, 86, 177-194.	1.9	9
2	Above- and below-ground biodiversity responses to the prolonged flood pulse in central-western Amazonia, Brazil. <i>Environmental DNA</i> , 2022, 4, 533-548.	5.8	1
3	Best practices in metabarcoding of fungi: From experimental design to results. <i>Molecular Ecology</i> , 2022, 31, 2769-2795.	3.9	87
4	The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding. <i>Fungal Diversity</i> , 2022, 114, 327-386.	12.3	53
5	Dnabarcoder: An open-source software package for analysing and predicting <sc>DNA</sc> sequence similarity cutoffs for fungal sequence identification. <i>Molecular Ecology Resources</i> , 2022, 22, 2793-2809.	4.8	4
6	Assessing Biotic and Abiotic Interactions of Microorganisms in Amazonia through Co-Occurrence Networks and DNA Metabarcoding. <i>Microbial Ecology</i> , 2021, 82, 746-760.	2.8	8
7	Fusarium: more than a node or a foot-shaped basal cell. <i>Studies in Mycology</i> , 2021, 98, 100116.	7.2	134
8	Fungal taxonomy and sequence-based nomenclature. <i>Nature Microbiology</i> , 2021, 6, 540-548.	13.3	101
9	Decreased soil moisture due to warming drives phylogenetic diversity and community transitions in the tundra. <i>Environmental Research Letters</i> , 2021, 16, 064031.	5.2	10
10	Digging Up the Roots: Taxonomic and Phylogenetic Disentanglements in Corticiaceae s.s. (Corticiales). <i>Journal of Fungi</i> , 2021, 7, 1000000.	3.5	5
11	The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. <i>Fungal Diversity</i> , 2021, 111, 573-588.	12.3	42
12	Fungal functional ecology: bringing a trait-based approach to plant-associated fungi. <i>Biological Reviews</i> , 2020, 95, 409-433.	10.4	171
13	Significant taxon sampling gaps in DNA databases limit the operational use of marine macrofauna metabarcoding. <i>Marine Biodiversity</i> , 2020, 50, 1.	1.0	38
14	The Taxon Hypothesis Paradigm: On the Unambiguous Detection and Communication of Taxa. <i>Microorganisms</i> , 2020, 8, 1910.	3.6	114
15	Advancing biodiversity assessments with environmental DNA: Long-read technologies help reveal the drivers of Amazonian fungal diversity. <i>Ecology and Evolution</i> , 2020, 10, 7509-7524.	1.9	26
16	Fungal communities in groundwater springs along the volcanic zone of Iceland. <i>Inland Waters</i> , 2020, 10, 418-427.	2.2	9
17	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	12.3	387
18	When mycologists describe new species, not all relevant information is provided (clearly enough). <i>MycKeys</i> , 2020, 72, 109-128.	1.9	15

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19	Locality or habitat? Exploring predictors of biodiversity in Amazonia. <i>Ecography</i> , 2019, 42, 321-333.	4.5	32
20	Biodiversity assessments in the 21st century: the potential of insect traps to complement environmental samples for estimating eukaryotic and prokaryotic diversity using high-throughput DNA metabarcoding. <i>Genome</i> , 2019, 62, 147-159.	2.0	33
21	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	15
22	Notes, outline and divergence times of Basidiomycota. <i>Fungal Diversity</i> , 2019, 99, 105-367.	12.3	256
23	The pitfalls of biodiversity proxies: Differences in richness patterns of birds, trees and understudied diversity across Amazonia. <i>Scientific Reports</i> , 2019, 9, 19205.	3.3	23
24	Mycobiome diversity: high-throughput sequencing and identification of fungi. <i>Nature Reviews Microbiology</i> , 2019, 17, 95-109.	28.6	580
25	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. <i>Nucleic Acids Research</i> , 2019, 47, D259-D264.	14.5	2,072
26	Introducing ribosomal tandem repeat barcoding for fungi. <i>Molecular Ecology Resources</i> , 2019, 19, 118-127.	4.8	78
27	Exploring the taxonomic composition of two fungal communities on the Swedish west coast through metabarcoding. <i>Biodiversity Data Journal</i> , 2019, 7, e35332.	0.8	8
28	Solving the taxonomic identity of <i>Pseudotomentella tristis</i> s.l. (Thelephorales, Basidiomycota) – a multi-gene phylogeny and taxonomic review, integrating ecological and geographical data. <i>MycKeys</i> , 2019, 50, 1-77.	1.9	5
29	Mycobiomes of sympatric <i>Amorphophallus albispatus</i> (Araceae) and <i>Camellia sinensis</i> (Theaceae) – a case study reveals clear tissue preferences and differences in diversity and composition. <i>Mycological Progress</i> , 2018, 17, 489-500.	1.4	7
30	Relationships within <i>Capitotricha bicolor</i> (Lachnaceae, Ascomycota) as inferred from ITS rDNA sequences, including some notes on the <i>Brunnipila</i> and <i>Erioscyphella</i> clades. <i>Mycological Progress</i> , 2018, 17, 89-101.	1.4	0
31	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. <i>MycKeys</i> , 2018, 39, 29-40.	1.9	52
32	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. <i>Bioinformatics</i> , 2018, 34, 4027-4033.	4.1	36
33	<scp>Protax</scp> – fungi: a web-based tool for probabilistic taxonomic placement of fungal internal transcribed spacer sequences. <i>New Phytologist</i> , 2018, 220, 517-525.	7.3	69
34	Taxonomic annotation of public fungal ITS sequences from the built environment – a report from an April 10-11, 2017 workshop (Aberdeen, UK). <i>MycKeys</i> , 2018, 28, 65-82.	1.9	33
35	New light on names and naming of dark taxa. <i>MycKeys</i> , 2018, 30, 31-39.	1.9	39
36	High-throughput metabarcoding reveals the effect of physicochemical soil properties on soil and litter biodiversity and community turnover across Amazonia. <i>PeerJ</i> , 2018, 6, e5661.	2.0	18

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37	Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. <i>Systematic Biology</i> , 2017, 66, syw066.	5.6	42
38	Environmental impact assessment in Brazilian Amazonia: Challenges and prospects to assess biodiversity. <i>Biological Conservation</i> , 2017, 206, 161-168.	4.1	58
39	Poorly known microbial taxa dominate the microbiome of permafrost thaw ponds. <i>ISME Journal</i> , 2017, 11, 1938-1941.	9.8	32
40	Novel soil-inhabiting clades fill gaps in the fungal tree of life. <i>Microbiome</i> , 2017, 5, 42.	11.1	152
41	Morphology and phylogeny reveal a novel hydroid taxon from India: <i>Mycorrhaphoides stalpersii</i> gen. and sp. nov. <i>Nordic Journal of Botany</i> , 2017, 35, 85-94.	0.5	2
42	Critical Issues in Mycobiota Analysis. <i>Frontiers in Microbiology</i> , 2017, 8, 180.	3.5	83
43	Habitat conditions and phenological tree traits overrule the influence of tree genotype in the needle mycobiome of <i>Picea glauca</i> system at an arctic treeline ecotone. <i>New Phytologist</i> , 2016, 211, 1221-1231.	7.3	55
44	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. <i>Ecological Informatics</i> , 2016, 33, 45-50.	5.2	30
45	Digital identifiers for fungal species. <i>Science</i> , 2016, 352, 1182-1183.	12.6	24
46	Unbiased probabilistic taxonomic classification for DNA barcoding. <i>Bioinformatics</i> , 2016, 32, 2920-2927.	4.1	75
47	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. <i>Fungal Biology</i> , 2016, , 25-46.	0.6	16
48	Molecular Techniques in Mycological Studies and Sequence Data Curating: Quality Control and Challenges. <i>Fungal Biology</i> , 2016, , 47-64.	0.6	2
49	Sequence-based classification and identification of Fungi. <i>Mycologia</i> , 2016, 108, 1049-1068.	1.9	154
50	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. <i>Microbes and Environments</i> , 2015, 30, 145-150.	1.6	231
51	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. <i>Microbiome</i> , 2015, 3, 50.	11.1	175
52	metaxa2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. <i>Molecular Ecology Resources</i> , 2015, 15, 1403-1414.	4.8	426
53	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. <i>Frontiers in Microbiology</i> , 2015, 6, 1192.	3.5	49
54	Bacterial and Fungal Communities in a Degraded Ombrotrophic Peatland Undergoing Natural and Managed Re-Vegetation. <i>PLoS ONE</i> , 2015, 10, e0124726.	2.5	57

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55	The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. <i>Fungal Diversity</i> , 2015, 74, 3-18.	12.3	471
56	Standardizing metadata and taxonomic identification in metabarcoding studies. <i>GigaScience</i> , 2015, 4, 34.	6.4	35
57	Response to Comment on "Global diversity and geography of soil fungi". <i>Science</i> , 2015, 349, 936-936.	12.6	43
58	Global diversity and geography of soil fungi. <i>Science</i> , 2014, 346, 1256688.	12.6	2,513
59	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	12.3	123
60	One stop shop: backbone trees for important phytopathogenic genera: I (2014). <i>Fungal Diversity</i> , 2014, 67, 21-125.	12.3	241
61	14 Agaricomycetes. , 2014, , 373-429.		88
62	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, bau061-bau061.	3.0	272
63	Metaxa, Overview. , 2014, , 1-5.		1
64	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
65	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277.	3.9	2,997
66	European earthstars in Geastraceae (Geastrales, Phallomycetidae) – a systematic approach using morphology and molecular sequence data. <i>Systematics and Biodiversity</i> , 2013, 11, 437-465.	1.2	26
67	ITS1 versus ITS2 as DNA metabarcodes for fungi. <i>Molecular Ecology Resources</i> , 2013, 13, 218-224.	4.8	340
68	Nutrient enrichment increased species richness of leaf litter fungal assemblages in a tropical forest. <i>Molecular Ecology</i> , 2013, 22, 2827-2838.	3.9	61
69	Employing 454 amplicon pyrosequencing to reveal intragenomic divergence in the internal transcribed spacer rDNA region in fungi. <i>Ecology and Evolution</i> , 2013, 3, 1751-1764.	1.9	97
70	Fungal community analysis by high-throughput sequencing of amplified markers – a user's guide. <i>New Phytologist</i> , 2013, 199, 288-299.	7.3	747
71	Species complexes in <i>Hericium</i> (Russulales, Agaricomycota) and a new species - <i>Hericium rajchenbergii</i> - from southern South America. <i>Mycological Progress</i> , 2013, 12, 413-420.	1.4	21
72	Meeting Report: Fungal ITS Workshop (October 2012). <i>Standards in Genomic Sciences</i> , 2013, 8, 118-123.	1.5	34

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73	Incorporating molecular data in fungal systematics: a guide for aspiring researchers. <i>Current Research in Environmental and Applied Mycology</i> , 2013, 3, 1-32.	0.6	65
74	Pyrosequencing-Derived Bacterial, Archaeal, and Fungal Diversity of Spacecraft Hardware Destined for Mars. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5912-5922.	3.1	88
75	Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. <i>ISME Journal</i> , 2012, 6, 2199-2218.	9.8	259
76	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 6241-6246.	7.1	4,012
77	Megraft: a software package to graft ribosomal small subunit (16S/18S) fragments onto full-length sequences for accurate species richness and sequencing depth analysis in pyrosequencing-length metagenomes and similar environmental datasets. <i>Research in Microbiology</i> , 2012, 163, 407-412.	2.1	12
78	Unravelling Soil Fungal Communities from Different Mediterranean Land-Use Backgrounds. <i>PLoS ONE</i> , 2012, 7, e34847.	2.5	194
79	Morphology, anatomy, and molecular studies of the ectomycorrhiza formed axenically by the fungus <i>Sistotrema</i> sp. (Basidiomycota). <i>Mycological Progress</i> , 2012, 11, 817-826.	1.4	14
80	Soil fungal community structure along a soil health gradient in pea fields examined using deep amplicon sequencing. <i>Soil Biology and Biochemistry</i> , 2012, 46, 26-32.	8.8	170
81	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
82	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATÅ© Alignments for Environmental ITS Data. <i>PLoS ONE</i> , 2011, 6, e19039.	2.5	32
83	Towards standardization of the description and publication of next-generation sequencing datasets of fungal communities. <i>New Phytologist</i> , 2011, 191, 314-318.	7.3	85
84	V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets. <i>FEMS Microbiology Letters</i> , 2011, 319, 140-145.	1.8	12
85	Rethinking taxon sampling in the light of environmental sequencing. <i>Cladistics</i> , 2011, 27, 197-203.	3.3	23
86	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.	0.8	7
87	Metaxa: a software tool for automated detection and discrimination among ribosomal small subunit (12S/16S/18S) sequences of archaea, bacteria, eukaryotes, mitochondria, and chloroplasts in metagenomes and environmental sequencing datasets. <i>Antonie Van Leeuwenhoek</i> , 2011, 100, 471-475.	1.7	88
88	Progress in molecular and morphological taxon discovery in Fungi and options for formal classification of environmental sequences. <i>Fungal Biology Reviews</i> , 2011, 25, 38-47.	4.7	296
89	DivBayes and SubT: exploring species diversification using Bayesian statistics. <i>Bioinformatics</i> , 2011, 27, 2439-2440.	4.1	4
90	Molecular Identification of Fungi: Rationale, Philosophical Concerns, and the UNITE Database. <i>The Open Applied Informatics Journal</i> , 2011, 5, 81-86.	1.0	20

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91	Current state and perspectives of fungal DNA barcoding and rapid identification procedures. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 99-108.	3.6	339
92	The white-rotting genus <i>Phanerochaete</i> is polyphyletic and distributed throughout the phleboid clade of the Polyporales (Basidiomycota). <i>Fungal Diversity</i> , 2010, 42, 107-118.	12.3	57
93	The UNITE database for molecular identification of fungi – recent updates and future perspectives. <i>New Phytologist</i> , 2010, 186, 281-285.	7.3	1,563
94	454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. <i>New Phytologist</i> , 2010, 188, 291-301.	7.3	484
95	Phylogeny and taxonomy of the genus <i>Vuilleminia</i> (Basidiomycota) based on molecular and morphological evidence, with new insights into Corticiales. <i>Taxon</i> , 2010, 59, 1519-1534.	0.7	25
96	PlutoF – a Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. <i>Evolutionary Bioinformatics</i> , 2010, 6, EBO.S6271.	1.2	203
97	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
98	V-Xtractor: An open-source, high-throughput software tool to identify and extract hypervariable regions of small subunit (16S/18S) ribosomal RNA gene sequences. <i>Journal of Microbiological Methods</i> , 2010, 83, 250-253.	1.6	118
99	An open source chimera checker for the fungal ITS region. <i>Molecular Ecology Resources</i> , 2010, 10, 1076-1081.	4.8	77
100	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
101	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
102	A phylogenetic approach to detect selection on the target site of the antifouling compound irgarol in tolerant periphyton communities. <i>Environmental Microbiology</i> , 2009, 11, 2065-2077.	3.8	15
103	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
104	454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. <i>New Phytologist</i> , 2009, 184, 449-456.	7.3	908
105	A subgroup of plant aquaporins facilitate the bi-directional diffusion of As(OH) <sub>3</sub> and Sb(OH) <sub>3</sub> across membranes. <i>BMC Biology</i> , 2008, 6, 26.	3.8	379
106	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
107	<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
108	Preserving Accuracy in GenBank. <i>Science</i> , 2008, 319, 1616-1616.	12.6	198

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109	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
110	Phylogenetic studies in <i>Hypochnicium</i> (Basidiomycota), with special emphasis on species from New Zealand. <i>New Zealand Journal of Botany</i> , 2007, 45, 139-150.	1.1	18
111	Contributions of <i>rpb2</i> and <i>tef1</i> to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). <i>Molecular Phylogenetics and Evolution</i> , 2007, 43, 430-451.	2.7	341
112	The <i>Peniophorella praetermissa</i> species complex (Basidiomycota). <i>Mycological Research</i> , 2007, 111, 1366-1376.	2.5	30
113	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. <i>Mycologia</i> , 2006, 98, 937-948.	1.9	89
114	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. <i>Mycologia</i> , 2006, 98, 896-905.	1.9	80
115	Fruiting body-guided molecular identification of root-tip mantle mycelia provides strong indications of ectomycorrhizal associations in two species of <i>Sistotrema</i> (Basidiomycota). <i>Mycological Research</i> , 2006, 110, 1426-1432.	2.5	38
116	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. <i>PLoS ONE</i> , 2006, 1, e59.	2.5	508
117	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. <i>Mycologia</i> , 2006, 98, 896-905.	1.9	143
118	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. <i>Mycologia</i> , 2006, 98, 937-948.	1.9	135
119	UNITE: a database providing web-based methods for the molecular identification of ectomycorrhizal fungi. <i>New Phytologist</i> , 2005, 166, 1063-1068.	7.3	912
120	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
121	Automated Phylogenetic Taxonomy: An Example in the Homobasidiomycetes (Mushroom-Forming) <i>Tj ETQq1 1 0.784314 rgBTJ/Overl</i>	5.6	63
122	galaxie--CGI scripts for sequence identification through automated phylogenetic analysis. <i>Bioinformatics</i> , 2004, 20, 1447-1452.	4.1	27
123	galaxieEST: addressing EST identity through automated phylogenetic analysis. <i>BMC Bioinformatics</i> , 2004, 5, 87.	2.6	7
124	Phylogeography of <i>Hyphoderma setigerum</i> (Basidiomycota) in the Northern Hemisphere. <i>Mycological Research</i> , 2003, 107, 645-652.	2.5	35
125	Phylogeny of the <i>Hypochnicium punctulatum</i> Complex as Inferred from ITS Sequence Data. <i>Mycologia</i> , 2003, 95, 54.	1.9	9
126	Phylogeny of the <i>Hypochnicium punctulatum</i> complex as inferred from ITS sequence data. <i>Mycologia</i> , 2003, 95, 54-60.	1.9	12



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127	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 0, 4, 37-63.	1.9	157
128	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycoKeys</i> , 0, 10, 1-43.	1.9	409
129	The UNITE Database for Molecular Identification and for Communicating Fungal Species. <i>Biodiversity Information Science and Standards</i> , 0, 3, .	0.0	11
130	Top 50 most wanted fungi. <i>MycoKeys</i> , 0, 12, 29-40.	1.9	72
131	Detection of signal recognition particle (SRP) RNAs in the nuclear ribosomal internal transcribed spacer 1 (ITS1) of three lineages of ectomycorrhizal fungi (Agaricomycetes, Basidiomycota). <i>MycoKeys</i> , 0, 13, 21-33.	1.9	8
132	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). <i>MycoKeys</i> , 0, 16, 1-15.	1.9	16
133	Unexpected high species diversity among European stalked puffballs – a contribution to the phylogeny and taxonomy of the genus <i>Tulostoma</i> (Agaricales). <i>MycoKeys</i> , 0, 21, 33-88.	1.9	17
134	Morphologic and molecular data help adopting the insect-pathogenic nephridiophagids (Nephridiophagidae) among the early diverging fungal lineages, close to the Chytridiomycota. <i>MycoKeys</i> , 0, 25, 31-50.	1.9	14
135	Read quality-based trimming of the distal ends of public fungal DNA sequences is nowhere near satisfactory. <i>MycoKeys</i> , 0, 26, 13-24.	1.9	10
136	Mapping and Publishing Sequence-Derived Data through Biodiversity Data Platforms. <i>Biodiversity Information Science and Standards</i> , 0, 4, .	0.0	0
137	A price tag on species. <i>Research Ideas and Outcomes</i> , 0, 8, .	1.0	1
138	Evidence for further non-coding RNA genes in the fungal rDNA region. <i>MycoKeys</i> , 0, 90, 203-213.	1.9	3