Henrik R Nilsson

List of Publications by Year
in descending order

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	Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for <i>Fungi</i>. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6241-6246.	7.1	4,012
2	Towards a unified paradigm for sequenceâ€based identification of fungi. Molecular Ecology, 2013, 22, 5271-5277.	3.9	2,997
3	Global diversity and geography of soil fungi. Science, 2014, 346, 1256688.	12.6	2,513
4	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research, 2019, 47, D259-D264.	14.5	2,072
5	The UNITE database for molecular identification of fungi â€“ recent updates and future perspectives. New Phytologist, 2010, 186, 281-285.	7.3	1,563
6	UNITE: a database providing webâ€based methods for the molecular identification of ectomycorrhizal fungi. New Phytologist, 2005, 166, 1063-1068.	7.3	912
7	454 Pyrosequencing analyses of forest soils reveal an unexpectedly high fungal diversity. New Phytologist, 2009, 184, 449-456.	7.3	908
8	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
9	Fungal community analysis by highâ€throughput sequencing of amplified markers â€“ a user's guide. New Phytologist, 2013, 199, 288-299.	7.3	747
10	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
11	Mycobiome diversity: high-throughput sequencing and identification of fungi. Nature Reviews Microbiology, 2019, 17, 95-109.	28.6	580
12	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. PLoS ONE, 2006, 1, e59.	2.5	508
13	454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. New Phytologist, 2010, 188, 291-301.	7.3	484
14	The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity, 2015, 74, 3-18.	12.3	471
15	<scp>metaxa</scp>2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. Molecular Ecology Resources, 2015, 15, 1403-1414.	4.8	426
16	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. MycoKeys, 0, 10, 1-43.	1.9	409
17	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
18	A subgroup of plant aquaporins facilitate the bi-directional diffusion of As(OH)3 and Sb(OH)3across membranes. BMC Biology, 2008, 6, 26.	3.8	379

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19	Contributions of rpb2 and tef1 to the phylogeny of mushrooms and allies (Basidiomycota, Fungi). Molecular Phylogenetics and Evolution, 2007, 43, 430-451.	2.7	341
20	<scp>ITS</scp>1 versus <scp>ITS</scp>2 as <scp>DNA</scp> metabarcodes for fungi. Molecular Ecology Resources, 2013, 13, 218-224.	4.8	340
21	Current state and perspectives of fungal DNA barcoding and rapid identification procedures. Applied Microbiology and Biotechnology, 2010, 87, 99-108.	3.6	339
22	Progress in molecular and morphological taxon discovery in Fungi and options for formal classification of environmental sequences. Fungal Biology Reviews, 2011, 25, 38-47.	4.7	296
23	Finding needles in haystacks: linking scientific names, reference specimens and molecular data for Fungi. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau061-bau061.	3.0	272
24	Significant and persistent impact of timber harvesting on soil microbial communities in Northern coniferous forests. ISME Journal, 2012, 6, 2199-2218.	9.8	259
25	Notes, outline and divergence times of Basidiomycota. Fungal Diversity, 2019, 99, 105-367.	12.3	256
26	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
27	One stop shop: backbones trees for important phytopathogenic genera: I (2014). Fungal Diversity, 2014, 67, 21-125.	12.3	241
28	A Comprehensive, Automatically Updated Fungal ITS Sequence Dataset for Reference-Based Chimera Control in Environmental Sequencing Efforts. Microbes and Environments, 2015, 30, 145-150.	1.6	231
29	PlutoFâ€"a Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. Evolutionary Bioinformatics, 2010, 6, EBO.S6271.	1.2	203
30	Preserving Accuracy in GenBank. Science, 2008, 319, 1616-1616.	12.6	198
31	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
32	Unravelling Soil Fungal Communities from Different Mediterranean Land-Use Backgrounds. PLoS ONE, 2012, 7, e34847.	2.5	194
33	Microbiomes of the dust particles collected from the International Space Station and Spacecraft Assembly Facilities. Microbiome, 2015, 3, 50.	11.1	175
34	Fungal functional ecology: bringing a traitâ€based approach to plantâ€associated fungi. Biological Reviews, 2020, 95, 409-433.	10.4	171
35	Soil fungal community structure along a soil health gradient in pea fields examined using deep amplicon sequencing. Soil Biology and Biochemistry, 2012, 46, 26-32.	8.8	170
36	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. MycoKeys, 0, 4, 37-63.	1.9	157

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37	Sequence-based classification and identification of Fungi. Mycologia, 2016, 108, 1049-1068.	1.9	154
38	Novel soil-inhabiting clades fill gaps in the fungal tree of life. Microbiome, 2017, 5, 42.	11.1	152
39	Mining metadata from unidentified ITS sequences in GenBank: A case study in Inocybe (Basidiomycota). BMC Evolutionary Biology, 2008, 8, 50.	3.2	144
40	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. Mycologia, 2006, 98, 896-905.	1.9	143
41	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. Mycologia, 2006, 98, 937-948.	1.9	135
42	Fusarium: more than a node or a foot-shaped basal cell. Studies in Mycology, 2021, 98, 100116.	7.2	134
43	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	12.3	123
44	V-Xtractor: An open-source, high-throughput software tool to identify and extract hypervariable regions of small subunit (16S/18S) ribosomal RNA gene sequences. Journal of Microbiological Methods, 2010, 83, 250-253.	1.6	118
45	The Taxon Hypothesis Paradigmâ€"On the Unambiguous Detection and Communication of Taxa. Microorganisms, 2020, 8, 1910.	3.6	114
46	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
47	Fungal taxonomy and sequence-based nomenclature. Nature Microbiology, 2021, 6, 540-548.	13.3	101
48	Employing 454 amplicon pyrosequencing to reveal intragenomic divergence in the internal transcribed spacer <scp>rDNA</scp> region in fungi. Ecology and Evolution, 2013, 3, 1751-1764.	1.9	97
49	The cantharelloid clade: dealing with incongruent gene trees and phylogenetic reconstruction methods. Mycologia, 2006, 98, 937-948.	1.9	89
50	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. Antonie Van Leeuwenhoek, 2011, 100, 471-475.	1.7	88
51	Pyrosequencing-Derived Bacterial, Archaeal, and Fungal Diversity of Spacecraft Hardware Destined for Mars. Applied and Environmental Microbiology, 2012, 78, 5912-5922.	3.1	88
52	14 Agaricomycetes. , 2014, , 373-429.		88
53	Best practices in metabarcoding of fungi: From experimental design to results. Molecular Ecology, 2022, 31, 2769-2795.	3.9	87
54	A software pipeline for processing and identification of fungal ITS sequences. Source Code for Biology and Medicine, 2009, 4, 1.	1.7	85

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55	Towards standardization of the description and publication of nextâ€generation sequencing datasets of fungal communities. New Phytologist, 2011, 191, 314-318.	7.3	85
56	Critical Issues in Mycobiota Analysis. Frontiers in Microbiology, 2017, 8, 180.	3.5	83
57	An overview of the higher level classification of Pucciniomycotina based on combined analyses of nuclear large and small subunit rDNA sequences. Mycologia, 2006, 98, 896-905.	1.9	80
58	Introducing ribosomal tandem repeat barcoding for fungi. Molecular Ecology Resources, 2019, 19, 118-127.	4.8	78
59	An open source chimera checker for the fungal ITS region. Molecular Ecology Resources, 2010, 10, 1076-1081.	4.8	77
60	Unbiased probabilistic taxonomic classification for DNA barcoding. Bioinformatics, 2016, 32, 2920-2927.	4.1	75
61	Approaching the taxonomic affiliation of unidentified sequences in public databases--an example from the mycorrhizal fungi. BMC Bioinformatics, 2005, 6, 178.	2.6	74
62	Top 50 most wanted fungi. MycoKeys, 0, 12, 29-40.	1.9	72
63	<scp>Protax</scp>â€fungi: a webâ€based tool for probabilistic taxonomic placement of fungal internal transcribed spacer sequences. New Phytologist, 2018, 220, 517-525.	7.3	69
64	Incorporating molecular data in fungal systematics: a guide for aspiring researchers. Current Research in Environmental and Applied Mycology, 2013, 3, 1-32.	0.6	65
65	Automated Phylogenetic Taxonomy: An Example in the Homobasidiomycetes (Mushroom-Forming) Tj ETQq1 1 0.784314 rgBT /Overlo	5.6	63
66	Nutrient enrichment increased species richness of leaf litter fungal assemblages in a tropical forest. Molecular Ecology, 2013, 22, 2827-2838.	3.9	61
67	Environmental impact assessment in Brazilian Amazonia: Challenges and prospects to assess biodiversity. Biological Conservation, 2017, 206, 161-168.	4.1	58
68	The white-rotting genus Phanerochaete is polyphyletic and distributed throughout the phleboid clade of the Polyporales (Basidiomycota). Fungal Diversity, 2010, 42, 107-118.	12.3	57
69	Bacterial and Fungal Communities in a Degraded Ombrotrophic Peatland Undergoing Natural and Managed Re-Vegetation. PLoS ONE, 2015, 10, e0124726.	2.5	57
70	Habitat conditions and phenological tree traits overrule the influence of tree genotype in the needle mycobiomeâ€“<i><scp>P</scp>icea glauca</i> system at an arctic treeline ecotone. New Phytologist, 2016, 211, 1221-1231.	7.3	55
71	The numbers of fungi: contributions from traditional taxonomic studies and challenges of metabarcoding. Fungal Diversity, 2022, 114, 327-386.	12.3	53
72	Great differences in performance and outcome of high-throughput sequencing data analysis platforms for fungal metabarcoding. MycoKeys, 2018, 39, 29-40.	1.9	52

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73	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
74	Metagenomic sequencing of marine periphyton: taxonomic and functional insights into biofilm communities. Frontiers in Microbiology, 2015, 6, 1192.	3.5	49
75	Response to Comment on â€œGlobal diversity and geography of soil fungiâ€• Science, 2015, 349, 936-936.	12.6	43
76	Toward a Self-Updating Platform for Estimating Rates of Speciation and Migration, Ages, and Relationships of Taxa. Systematic Biology, 2017, 66, syw066.	5.6	42
77	The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. Fungal Diversity, 2021, 111, 573-588.	12.3	42
78	New light on names and naming of dark taxa. MycoKeys, 2018, 30, 31-39.	1.9	39
79	Fruiting body-guided molecular identification of root-tip mantle mycelia provides strong indications of ectomycorrhizal associations in two species of Sistotrema (Basidiomycota). Mycological Research, 2006, 110, 1426-1432.	2.5	38
80	Significant taxon sampling gaps in DNA databases limit the operational use of marine macrofauna metabarcoding. Marine Biodiversity, 2020, 50, 1.	1.0	38
81	Metaxa2 Database Builder: enabling taxonomic identification from metagenomic or metabarcoding data using any genetic marker. Bioinformatics, 2018, 34, 4027-4033.	4.1	36
82	Phylogeography of Hyphoderma setigerum (Basidiomycota) in the Northern Hemisphere. Mycological Research, 2003, 107, 645-652.	2.5	35
83	Standardizing metadata and taxonomic identification in metabarcoding studies. GigaScience, 2015, 4, 34.	6.4	35
84	Meeting Report: Fungal ITS Workshop (October 2012). Standards in Genomic Sciences, 2013, 8, 118-123.	1.5	34
85	Taxonomic annotation of public fungal ITS sequences from the built environment â€“ a report from an April 10â€“11, 2017 workshop (Aberdeen, UK). MycoKeys, 2018, 28, 65-82.	1.9	33
86	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. Genome, 2019, 62, 147-159.	2.0	33
87	Tasting Soil Fungal Diversity with Earth Tongues: Phylogenetic Test of SATÃ© Alignments for Environmental ITS Data. PLoS ONE, 2011, 6, e19039.	2.5	32
88	Poorly known microbial taxa dominate the microbiome of permafrost thaw ponds. ISME Journal, 2017, 11, 1938-1941.	9.8	32
89	Locality or habitat? Exploring predictors of biodiversity in Amazonia. Ecography, 2019, 42, 321-333.	4.5	32
90	The Peniophorella praetermissa species complex (Basidiomycota). Mycological Research, 2007, 111, 1366-1376.	2.5	30

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91	Metaxa2 Diversity Tools: Easing microbial community analysis with Metaxa2. Ecological Informatics, 2016, 33, 45-50.	5.2	30
92	galaxie--CGI scripts for sequence identification through automated phylogenetic analysis. Bioinformatics, 2004, 20, 1447-1452.	4.1	27
93	European earthstars in Geastraceae (Geastrales, Phallomycetidae) â€" a systematic approach using morphology and molecular sequence data. Systematics and Biodiversity, 2013, 11, 437-465.	1.2	26
94	Advancing biodiversity assessments with environmental DNA: Longâ€read technologies help reveal the drivers of Amazonian fungal diversity. Ecology and Evolution, 2020, 10, 7509-7524.	1.9	26
95	Phylogeny and taxonomy of the genus <i>Vuilleminia</i> (Basidiomycota) based on molecular and morphological evidence, with new insights into Corticiales. Taxon, 2010, 59, 1519-1534.	0.7	25
96	Digital identifiers for fungal species. Science, 2016, 352, 1182-1183.	12.6	24
97	Rethinking taxon sampling in the light of environmental sequencing. Cladistics, 2011, 27, 197-203.	3.3	23
98	The pitfalls of biodiversity proxies: Differences in richness patterns of birds, trees and understudied diversity across Amazonia. Scientific Reports, 2019, 9, 19205.	3.3	23
99	Species complexes in Hericium (Russulales, Agaricomycota) and a new species - Hericium rajchenbergii - from southern South America. Mycological Progress, 2013, 12, 413-420.	1.4	21
100	Molecular Identification of Fungi: Rationale, Philosophical Concerns, and the UNITE Database. The Open Applied Informatics Journal, 2011, 5, 81-86.	1.0	20
101	Phylogenetic studies in<i>Hypochnicium</i>(Basidiomycota), with special emphasis on species from New Zealand. New Zealand Journal of Botany, 2007, 45, 139-150.	1.1	18
102	High-throughput metabarcoding reveals the effect of physicochemical soil properties on soil and litter biodiversity and community turnover across Amazonia. PeerJ, 2018, 6, e5661.	2.0	18
103	<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
104	Unexpected high species diversity among European stalked puffballs â€" a contribution to the phylogeny and taxonomy of the genus Tulostoma (Agaricales). MycoKeys, 0, 21, 33-88.	1.9	17
105	Future Perspectives and Challenges of Fungal Systematics in the Age of Big Data. Fungal Biology, 2016, , 25-46.	0.6	16
106	Annotating public fungal ITS sequences from the built environment according to the MIxS-Built Environment standard â€" a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). MycoKeys, 0, 16, 1-15.	1.9	16
107	A phylogenetic approach to detect selection on the target site of the antifouling compound irgarol in tolerant periphyton communities. Environmental Microbiology, 2009, 11, 2065-2077.	3.8	15
108	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15

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109	When mycologists describe new species, not all relevant information is provided (clearly enough). MycoKeys, 2020, 72, 109-128.	1.9	15
110	Morphology, anatomy, and molecular studies of the ectomycorrhiza formed axenically by the fungus Sistotrema sp. (Basidiomycota). Mycological Progress, 2012, 11, 817-826.	1.4	14
111	Morphologic and molecular data help adopting the insect-pathogenic nephridiophagids (Nephridiophagidae) among the early diverging fungal lineages, close to the Chytridiomycota. MycoKeys, 0, 25, 31-50.	1.9	14
112	Phylogeny of the<i>Hypochnicium punctulatum</i>complex as inferred from ITS sequence data. Mycologia, 2003, 95, 54-60.	1.9	12
113	V-REVCOMP: automated high-throughput detection of reverse complementary 16S rRNA gene sequences in large environmental and taxonomic datasets. FEMS Microbiology Letters, 2011, 319, 140-145.	1.8	12
114	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. Research in Microbiology, 2012, 163, 407-412.	2.1	12
115	The UNITE Database for Molecular Identification and for Communicating Fungal Species. Biodiversity Information Science and Standards, 0, 3, .	0.0	11
116	Decreased soil moisture due to warming drives phylogenetic diversity and community transitions in the tundra. Environmental Research Letters, 2021, 16, 064031.	5.2	10
117	Read quality-based trimming of the distal ends of public fungal DNA sequences is nowhere near satisfactory. MycoKeys, 0, 26, 13-24.	1.9	10
118	Phylogeny of the Hypochnicium punctulatum Complex as Inferred from ITS Sequence Data. Mycologia, 2003, 95, 54.	1.9	9
119	Fungal communities in groundwater springs along the volcanic zone of Iceland. Inland Waters, 2020, 10, 418-427.	2.2	9
120	ï»¿The curse of the uncultured fungus. MycoKeys, 2022, 86, 177-194.	1.9	9
121	Assessing Biotic and Abiotic Interactions of Microorganisms in Amazonia through Co-Occurrence Networks and DNA Metabarcoding. Microbial Ecology, 2021, 82, 746-760.	2.8	8
122	Exploring the taxonomic composition of two fungal communities on the Swedish west coast through metabarcoding. Biodiversity Data Journal, 2019, 7, e35332.	0.8	8
123	Detection of signal recognition particle (SRP) RNAs in the nuclear ribosomal internal transcribed spacer 1 (ITS1) of three lineages of ectomycorrhizal fungi (Agaricomycetes, Basidiomycota). MycoKeys, 0, 13, 21-33.	1.9	8
124	galaxieEST: addressing EST identity through automated phylogenetic analysis. BMC Bioinformatics, 2004, 5, 87.	2.6	7
125	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. Mycoscience, 2011, 52, 278-282.	0.8	7
126	Mycobiomes of sympatric Amorphophallus albispathus (Araceae) and Camellia sinensis (Theaceae) â€“ a case study reveals clear tissue preferences and differences in diversity and composition. Mycological Progress, 2018, 17, 489-500.	1.4	7

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127	Digging Up the Roots: Taxonomic and Phylogenetic Disentanglements in Corticiaceae s.s. (Corticiales,) Tj ETQq1 1 0.784314 rgBT /Over	3.5	5
128	Solving the taxonomic identity of Pseudotomentella tristis s.l. (Thelephorales, Basidiomycota) â€" a multi-gene phylogeny and taxonomic review, integrating ecological and geographical data. MycoKeys, 2019, 50, 1-77.	1.9	5
129	DivBayes and SubT: exploring species diversification using Bayesian statistics. Bioinformatics, 2011, 27, 2439-2440.	4.1	4
130	Dnabarcoder: An openâ€source software package for analysing and predicting <scp>DNA</scp> sequence similarity cutoffs for fungal sequence identification. Molecular Ecology Resources, 2022, 22, 2793-2809.	4.8	4
131	ï»¿Evidence for further non-coding RNA genes in the fungal rDNA region. MycoKeys, 0, 90, 203-213.	1.9	3
132	Molecular Techniques in Mycological Studies and Sequence Data Curating: Quality Control and Challenges. Fungal Biology, 2016, , 47-64.	0.6	2
133	Morphology and phylogeny reveal a novel hydnoid taxon from India: <i>Mycorrhaphoides stalpersii</i> gen. and sp. nov. Nordic Journal of Botany, 2017, 35, 85-94.	0.5	2
134	Metaxa, Overview. , 2014, , 1-5.		1
135	Aboveâ€and belowâ€ground biodiversity responses to the prolonged flood pulse in centralâ€western Amazonia, Brazil. Environmental DNA, 2022, 4, 533-548.	5.8	1
136	A price tag on species. Research Ideas and Outcomes, 0, 8, .	1.0	1
137	Relationships within Capitotricha bicolor (Lachnaceae, Ascomycota) as inferred from ITS rDNA sequences, including some notes on the Brunnipila and Erioscyphella clades. Mycological Progress, 2018, 17, 89-101.	1.4	0
138	Mapping and Publishing Sequence-Derived Data through Biodiversity Data Platforms. Biodiversity Information Science and Standards, 0, 4, .	0.0	0