

# Kessy Abarenkov

## List of Publications by Year in descending order

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Version: 2024-02-01

61  
papers

19,025  
citations

81839

39  
h-index

161767

54  
g-index

66  
all docs

66  
docs citations

66  
times ranked

16420  
citing authors

#	ARTICLE	IF	CITATIONS
1	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277.	2.0	2,997
2	Global diversity and geography of soil fungi. <i>Science</i> , 2014, 346, 1256688.	6.0	2,513
3	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. <i>Nucleic Acids Research</i> , 2019, 47, D259-D264.	6.5	2,072
4	The UNITE database for molecular identification of fungi – recent updates and future perspectives. <i>New Phytologist</i> , 2010, 186, 281-285.	3.5	1,563
5	UNITE: a database providing web-based methods for the molecular identification of ectomycorrhizal fungi. <i>New Phytologist</i> , 2005, 166, 1063-1068.	3.5	912
6	Improved software detection and extraction of ITS1 and <i>ITS2</i> from ribosomal <i>ITS</i> sequences of fungi and other eukaryotes for analysis of environmental sequencing data. <i>Methods in Ecology and Evolution</i> , 2013, 4, 914-919.	2.2	868
7	Fungal community analysis by high-throughput sequencing of amplified markers – a user's guide. <i>New Phytologist</i> , 2013, 199, 288-299.	3.5	747
8	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. <i>PLoS ONE</i> , 2006, 1, e59.	1.1	508
9	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.	3.5	484
10	High-level classification of the Fungi and a tool for evolutionary ecological analyses. <i>Fungal Diversity</i> , 2018, 90, 135-159.	4.7	450
11	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycKeys</i> , 0, 10, 1-43.	0.8	409
12	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. <i>Fungal Diversity</i> , 2020, 105, 1-16.	4.7	387
13	Strong host preference of ectomycorrhizal fungi in a Tasmanian wet sclerophyll forest as revealed by DNA barcoding and taxon-specific primers. <i>New Phytologist</i> , 2008, 180, 479-490.	3.5	362
14	<i>ITS1</i> versus <i>ITS2</i> as <i>DNA</i> metabarcodes for fungi. <i>Molecular Ecology Resources</i> , 2013, 13, 218-224.	2.2	340
15	Tree diversity and species identity effects on soil fungi, protists and animals are context dependent. <i>ISME Journal</i> , 2016, 10, 346-362.	4.4	307
16	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <i>ISME Journal</i> , 2014, 8, 226-244.	4.4	293
17	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.	1.4	272
18	Stochastic distribution of small soil eukaryotes resulting from high dispersal and drift in a local environment. <i>ISME Journal</i> , 2016, 10, 885-896.	4.4	256

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19	The ITS region as a target for characterization of fungal communities using emerging sequencing technologies. <i>FEMS Microbiology Letters</i> , 2009, 296, 97-101.	0.7	246
20	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.	0.7	231
21	FungalRoot: global online database of plant mycorrhizal associations. <i>New Phytologist</i> , 2020, 227, 955-966.	3.5	221
22	PlutoFâ€”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.	0.6	203
23	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.	0.7	194
24	Fungal functional ecology: bringing a traitâ€”based approach to plantâ€”associated fungi. <i>Biological Reviews</i> , 2020, 95, 409-433.	4.7	171
25	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. <i>MycoKeys</i> , 0, 4, 37-63.	0.8	157
26	Sequence-based classification and identification of Fungi. <i>Mycologia</i> , 2016, 108, 1049-1068.	0.8	154
27	Regional-Scale In-Depth Analysis of Soil Fungal Diversity Reveals Strong pH and Plant Species Effects in Northern Europe. <i>Frontiers in Microbiology</i> , 2020, 11, 1953.	1.5	126
28	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	4.7	123
29	Why We Need Sustainable Networks Bridging Countries, Disciplines, Cultures and Generations for Aquatic Biomonitoring 2.0: A Perspective Derived From the DNAqua-Net COST Action. <i>Advances in Ecological Research</i> , 2018, 58, 63-99.	1.4	120
30	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.	0.7	118
31	The Taxon Hypothesis Paradigmâ€”On the Unambiguous Detection and Communication of Taxa. <i>Microorganisms</i> , 2020, 8, 1910.	1.6	114
32	Determining threshold values for barcoding fungi: lessons from <i>Cortinarius</i> (Basidiomycota), a highly diverse and widespread ectomycorrhizal genus. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw045.	1.3	94
33	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.	0.7	88
34	Towards standardization of the description and publication of nextâ€”generation sequencing datasets of fungal communities. <i>New Phytologist</i> , 2011, 191, 314-318.	3.5	85
35	Evolution of nutritional modes of <i>Ceratobasidiaceae</i> (Cantharellales, Basidiomycota) as revealed from publicly available ITS sequences. <i>Fungal Ecology</i> , 2013, 6, 256-268.	0.7	81
36	An open source chimera checker for the fungal ITS region. <i>Molecular Ecology Resources</i> , 2010, 10, 1076-1081.	2.2	77

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37	Top 50 most wanted fungi. MycoKeys, 0, 12, 29-40.	0.8	72
38	<sc>Protax</sc>â€“fungi: a webâ€“based tool for probabilistic taxonomic placement of fungal internal transcribed spacer sequences. New Phytologist, 2018, 220, 517-525.	3.5	69
39	Global biogeography of the ectomycorrhizal /sebacina lineage (<sc>F</sc>ungi,) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 667 2014, 23, 4168-4183.	2.0	58
40	Tidying Up International Nucleotide Sequence Databases: Ecological, Geographical and Sequence Quality Annotation of ITS Sequences of Mycorrhizal Fungi. PLoS ONE, 2011, 6, e24940.	1.1	51
41	Identifying the â€“unidentifiedâ€™ fungi: a global-scale long-read third-generation sequencing approach. Fungal Diversity, 2020, 103, 273-293.	4.7	48
42	Response to Comment on â€œGlobal diversity and geography of soil fungiâ€• Science, 2015, 349, 936-936.	6.0	43
43	The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. Fungal Diversity, 2021, 111, 573-588.	4.7	42
44	Mycorrhizal symbionts of <i>Pisonia grandis</i> and <i>P. sechellarum</i> in Seychelles: identification of mycorrhizal fungi and description of new <i>Tomentella</i> species. Mycologia, 2010, 102, 522-533.	0.8	38
45	Standardizing metadata and taxonomic identification in metabarcoding studies. GigaScience, 2015, 4, 34.	3.3	35
46	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.	0.8	33
47	Rethinking taxon sampling in the light of environmental sequencing. Cladistics, 2011, 27, 197-203.	1.5	23
48	Alien ectomycorrhizal plants differ in their ability to interact with co-introduced and native ectomycorrhizal fungi in novel sites. ISME Journal, 2020, 14, 2336-2346.	4.4	19
49	ToxGen: an improved reference database for the identification of type B-trichothecene genotypes in Fusarium. PeerJ, 2017, 5, e2992.	0.9	18
50	Early successional ectomycorrhizal fungi are more likely to naturalize outside their native range than other ectomycorrhizal fungi. New Phytologist, 2020, 227, 1289-1293.	3.5	17
51	Annotating public fungal ITS sequences from the built environment according to the MlxS-Built Environment standard â€“ a report from a May 23-24, 2016 workshop (Gothenburg, Sweden). MycoKeys, 0, 16, 1-15.	0.8	16
52	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.	0.7	12
53	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.	1.0	12
54	<sc>DNA</sc> barcoding of fungal specimens using <sc>PacBio</sc> longâ€“read highâ€“throughput sequencing. Molecular Ecology Resources, 2022, 22, 2871-2879.	2.2	12

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55	Read quality-based trimming of the distal ends of public fungal DNA sequences is nowhere near satisfactory. MycoKeys, 0, 26, 13-24.	0.8	10
56	«¿The curse of the uncultured fungus. MycoKeys, 2022, 86, 177-194.	0.8	9
57	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.	0.8	8
58	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.	0.3	7
59	Molecular Techniques in Mycological Studies and Sequence Data Curating: Quality Control and Challenges. Fungal Biology, 2016, , 47-64.	0.3	2
60	Third-party Annotations: Linking PlutoF platform and the ELIXIR Contextual Data ClearingHouse for the reporting of source material annotation gaps and inaccuracies. Biodiversity Information Science and Standards, 0, 5, .	0.0	1
61	A price tag on species. Research Ideas and Outcomes, 0, 8, .	1.0	1