

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	»¿The curse of the uncultured fungus. MycoKeys, 2022, 86, 177-194.	0.8	9
2	<scp>DNA</scp> barcoding of fungal specimens using <scp>PacBio</scp> longâ€read highâ€throughput sequencing. Molecular Ecology Resources, 2022, 22, 2871-2879.	2.2	12
3	The Global Soil Mycobiome consortium dataset for boosting fungal diversity research. Fungal Diversity, 2021, 111, 573-588.	4.7	42
4	Fungal functional ecology: bringing a traitâ€based approach to plantâ€associated fungi. Biological Reviews, 2020, 95, 409-433.	4.7	171
5	Regional-Scale In-Depth Analysis of Soil Fungal Diversity Reveals Strong pH and Plant Species Effects in Northern Europe. Frontiers in Microbiology, 2020, 11, 1953.	1.5	126
6	Identifying the â€unidentifiedâ€™™ fungi: a global-scale long-read third-generation sequencing approach. Fungal Diversity, 2020, 103, 273-293.	4.7	48
7	The Taxon Hypothesis Paradigmâ€™”On the Unambiguous Detection and Communication of Taxa. Microorganisms, 2020, 8, 1910.	1.6	114
8	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
9	FungalRoot: global online database of plant mycorrhizal associations. New Phytologist, 2020, 227, 955-966.	3.5	221
10	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
11	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	4.7	387
12	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research, 2019, 47, D259-D264.	6.5	2,072
13	High-level classification of the Fungi and a tool for evolutionary ecological analyses. Fungal Diversity, 2018, 90, 135-159.	4.7	450
14	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. Advances in Ecological Research, 2018, 58, 63-99.	1.4	120
15	<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.	3.5	69
16	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
17	ToxGen: an improved reference database for the identification of type B-trichothecene genotypes inFusarium. PeerJ, 2017, 5, e2992.	0.9	18
18	Molecular Techniques in Mycological Studies and Sequence Data Curating: Quality Control and Challenges. Fungal Biology, 2016, , 47-64.	0.3	2

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	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
22	Sequence-based classification and identification of Fungi. <i>Mycologia</i> , 2016, 108, 1049-1068.	0.8	154
23	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
24	Standardizing metadata and taxonomic identification in metabarcoding studies. <i>GigaScience</i> , 2015, 4, 34.	3.3	35
25	Response to Comment on "Global diversity and geography of soil fungi". <i>Science</i> , 2015, 349, 936-936.	6.0	43
26	Global diversity and geography of soil fungi. <i>Science</i> , 2014, 346, 1256688.	6.0	2,513
27	Resistance and resilience of the forest soil microbiome to logging-associated compaction. <i>ISME Journal</i> , 2014, 8, 226-244.	4.4	293
28	Improving ITS sequence data for identification of plant pathogenic fungi. <i>Fungal Diversity</i> , 2014, 67, 11-19.	4.7	123
29	Global biogeography of the ectomycorrhizal <i>Sebacina</i> lineage (<i>Sebacina</i> spp.). <i>Journal of Biogeography</i> , 2014, 41, 1168-1183.	2.0	58
30	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.	1.4	272
31	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.	2.2	868
32	Towards a unified paradigm for sequence-based identification of fungi. <i>Molecular Ecology</i> , 2013, 22, 5271-5277.	2.0	2,997
33	ITS1 versus ITS2 as DNA metabarcodes for fungi. <i>Molecular Ecology Resources</i> , 2013, 13, 218-224.	2.2	340
34	Evolution of nutritional modes of Ceratobasidiaceae (Cantharellales, Basidiomycota) as revealed from publicly available ITS sequences. <i>Fungal Ecology</i> , 2013, 6, 256-268.	0.7	81
35	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
36	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.	1.0	12

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37	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
38	Towards standardization of the description and publication of next-generation sequencing datasets of fungal communities. New Phytologist, 2011, 191, 314-318.	3.5	85
39	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
40	Rethinking taxon sampling in the light of environmental sequencing. Cladistics, 2011, 27, 197-203.	1.5	23
41	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
42	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.	0.7	88
43	The UNITE database for molecular identification of fungi – recent updates and future perspectives. New Phytologist, 2010, 186, 281-285.	3.5	1,563
44	454 Pyrosequencing and Sanger sequencing of tropical mycorrhizal fungi provide similar results but reveal substantial methodological biases. New Phytologist, 2010, 188, 291-301.	3.5	484
45	PlutoF – a Web Based Workbench for Ecological and Taxonomic Research, with an Online Implementation for Fungal ITS Sequences. Evolutionary Bioinformatics, 2010, 6, EBO.S6271.	0.6	203
46	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
47	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.	0.7	194
48	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.	0.7	118
49	An open source chimera checker for the fungal ITS region. Molecular Ecology Resources, 2010, 10, 1076-1081.	2.2	77
50	The ITS region as a target for characterization of fungal communities using emerging sequencing technologies. FEMS Microbiology Letters, 2009, 296, 97-101.	0.7	246
51	Strong host preference of ectomycorrhizal fungi in a Tasmanian wet sclerophyll forest as revealed by DNA barcoding and taxon-specific primers. New Phytologist, 2008, 180, 479-490.	3.5	362
52	Taxonomic Reliability of DNA Sequences in Public Sequence Databases: A Fungal Perspective. PLoS ONE, 2006, 1, e59.	1.1	508
53	UNITE: a database providing web-based methods for the molecular identification of ectomycorrhizal fungi. New Phytologist, 2005, 166, 1063-1068.	3.5	912
54	Five simple guidelines for establishing basic authenticity and reliability of newly generated fungal ITS sequences. MycoKeys, 0, 4, 37-63.	0.8	157

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55	Shotgun metagenomes and multiple primer pair-barcode combinations of amplicons reveal biases in metabarcoding analyses of fungi. <i>MycoKeys</i> , 0, 10, 1-43.	0.8	409
56	Third-party Annotations: Linking PlutoF platform and the ELIXIR Contextual Data ClearingHouse for the reporting of source material annotation gaps and inaccuracies. <i>Biodiversity Information Science and Standards</i> , 0, 5, .	0.0	1
57	Top 50 most wanted fungi. <i>MycoKeys</i> , 0, 12, 29-40.	0.8	72
58	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.	0.8	8
59	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.	0.8	16
60	Read quality-based trimming of the distal ends of public fungal DNA sequences is nowhere near satisfactory. <i>MycoKeys</i> , 0, 26, 13-24.	0.8	10
61	A price tag on species. <i>Research Ideas and Outcomes</i> , 0, 8, .	1.0	1