HÃ¥vard Kauserud

List of Publications by Year
in descending order

132 papers	8,263 citations	61984 43 h-index	54911 84 g-index
142 all docs	142 docs citations	142 times ranked	9314 citing authors

#	Article	IF	Citations
1	ITS as an environmental DNA barcode for fungi: an in silico approach reveals potential PCR biases. BMC Microbiology, 2010, 10, 189.	3.3	792
2	Fungal community analysis by highâ€throughput sequencing of amplified markers â€“ a user's guide. New Phytologist, 2013, 199, 288-299.	7.3	747
3	The Plant Cell Wallâ€“Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	12.6	512
4	FungalTraits: a user-friendly traits database of fungi and fungus-like stramenopiles. Fungal Diversity, 2020, 105, 1-16.	12.3	387
5	<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
6	DNA metabarcodingâ€”Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology, 2019, 28, 1857-1862.	3.9	300
7	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. Molecular Ecology, 2012, 21, 1821-1833.	3.9	259
8	Changes in the rootâ€associated fungal communities along a primary succession gradient analysed by 454 pyrosequencing. Molecular Ecology, 2012, 21, 1897-1908.	3.9	172
9	Mushroom fruiting and climate change. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 3811-3814.	7.1	166
10	Don't make a mista(g)ke: is tag switching an overlooked source of error in amplicon pyrosequencing studies?. Fungal Ecology, 2012, 5, 747-749.	1.6	166
11	Climate variation effects on fungal fruiting. Fungal Ecology, 2014, 10, 20-33.	1.6	148
12	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	12.3	123
13	Environmental microbiology through the lens of high-throughput DNA sequencing: Synopsis of current platforms and bioinformatics approaches. Journal of Microbiological Methods, 2012, 91, 106-113.	1.6	115
14	Fungal palaeodiversity revealed using highâ€throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. Environmental Microbiology, 2013, 15, 1176-1189.	3.8	115
15	High diversity of root associated fungi in both alpine and arctic Dryas octopetala. BMC Plant Biology, 2010, 10, 244.	3.6	109
16	Warming-induced shift in European mushroom fruiting phenology. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14488-14493.	7.1	104
17	Modelling and predicting fungal distribution patterns using herbarium data. Journal of Biogeography, 2008, 35, 2298-2310.	3.0	102
18	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

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19	Fungi ahoy! Diversity on marine wooden substrata in the high North. Fungal Ecology, 2014, 8, 46-58.	1.6	97
20	Seasonal trends in the biomass and structure of bryophyteâ€associated fungal communities explored by 454 pyrosequencing. New Phytologist, 2012, 195, 844-856.	7.3	94
21	Drought-induced decline in Mediterranean truffle harvest. Nature Climate Change, 2012, 2, 827-829.	18.8	90
22	Towards standardization of the description and publication of nextâ€generation sequencing datasets of fungal communities. New Phytologist, 2011, 191, 314-318.	7.3	85
23	Linking climate variability to mushroom productivity and phenology. Frontiers in Ecology and the Environment, 2012, 10, 14-19.	4.0	84
24	Climate change and spring-fruiting fungi. Proceedings of the Royal Society B: Biological Sciences, 2010, 277, 1169-1177.	2.6	81
25	Different bacterial communities in ectomycorrhizae and surrounding soil. Scientific Reports, 2013, 3, 3471.	3.3	77
26	Low host specificity of rootâ€associated fungi at an Arctic site. Molecular Ecology, 2014, 23, 975-985.	3.9	77
27	High diversity of fungi associated with living parts of boreal forest bryophytes. Botany, 2008, 86, 1326-1333.	1.0	74
28	Outcrossing or inbreeding: DNA markers provide evidence for type of reproductive mode in Phellinus nigrolimitatus (Basidiomycota). Mycological Research, 2001, 105, 676-683.	2.5	71
29	Evolutionary history of Serpulaceae (Basidiomycota): molecular phylogeny, historical biogeography and evidence for a single transition of nutritional mode. BMC Evolutionary Biology, 2011, 11, 230.	3.2	64
30	Arctic rootâ€associated fungal community composition reflects environmental filtering. Molecular Ecology, 2014, 23, 649-659.	3.9	64
31	Fungal biomass associated with the phyllosphere of bryophytes and vascular plants. Mycological Research, 2009, 113, 1254-1260.	2.5	62
32	Phellinus nigrolimitatusâ€"a wood-decomposing fungus highly influenced by forestry. Forest Ecology and Management, 2004, 187, 333-343.	3.2	61
33	Asian origin and rapid global spread of the destructive dry rot fungus <i>Serpula lacrymans</i>. Molecular Ecology, 2007, 16, 3350-3360.	3.9	60
34	Mushroom's spore size and time of fruiting are strongly related: is moisture important?. Biology Letters, 2011, 7, 273-276.	2.3	58
35	Ampliconâ€pyrosequencingâ€based detection of compositional shifts in bryophyteâ€associated fungal communities along an elevation gradient. Molecular Ecology, 2013, 22, 368-383.	3.9	58
36	Fungal diversity and seasonal succession in ash leaves infected by the invasive ascomycete Hymenoscyphus fraxineus. New Phytologist, 2017, 213, 1405-1417.	7.3	58

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37	Multiple gene genealogies and AFLPs suggest cryptic speciation and long-distance dispersal in the basidiomycete Serpula himantioides (Boletales). Molecular Ecology, 2005, 15, 421-431.	3.9	55
38	High consistency between replicate 454 pyrosequencing analyses of ectomycorrhizal plant root samples. Mycorrhiza, 2012, 22, 309-315.	2.8	55
39	Hybridization among cryptic species of the cellar fungus Coniophora puteana (Basidiomycota). Molecular Ecology, 2006, 16, 389-399.	3.9	54
40	<scp>ITS</scp> all right mama: investigating the formation of chimeric sequences in the <scp>ITS</scp>2 region by <scp>DNA</scp> metabarcoding analyses of fungal mock communities of different complexities. Molecular Ecology Resources, 2017, 17, 730-741.	4.8	52
41	Relationship between basidiospore size, shape and life history characteristics: a comparison of polypores. Fungal Ecology, 2008, 1, 19-23.	1.6	49
42	Fungi Sailing the Arctic Ocean: Speciose Communities in North Atlantic Driftwood as Revealed by High-Throughput Amplicon Sequencing. Microbial Ecology, 2016, 72, 295-304.	2.8	47
43	Wood-inhabiting insects can function as targeted vectors for decomposer fungi. Fungal Ecology, 2017, 29, 76-84.	1.6	47
44	Big data integration: Pan-European fungal species observations' assembly for addressing contemporary questions in ecology and global change biology. Fungal Biology Reviews, 2017, 31, 88-98.	4.7	45
45	Climate impacts on fungal community and trait dynamics. Fungal Ecology, 2016, 22, 17-25.	1.6	44
46	Fungal communities in Scandinavian lakes along a longitudinal gradient. Fungal Ecology, 2017, 27, 36-46.	1.6	43
47	Soil depth matters: shift in composition and inter-kingdom co-occurrence patterns of microorganisms in forest soils. FEMS Microbiology Ecology, 2021, 97, .	2.7	43
48	<i>In vitro</i> evidence of root colonization suggests ecological versatility in the genus <i>Mycena</i>. New Phytologist, 2020, 227, 601-612.	7.3	41
49	Galerina Earle: A polyphyletic genus in the consortium of dark-spored agarics. Mycologia, 2005, 97, 823-837.	1.9	40
50	Primary succession of <scp><i>B</i></scp><i>istorta vivipara</i> (<scp>L</scp>.) <scp>D</scp>elabre (<scp>P</scp>olygonaceae) rootâ€associated fungi mirrors plant succession in two glacial chronosequences. Environmental Microbiology, 2015, 17, 2777-2790.	3.8	40
51	Unraveling environmental drivers of a recent increase in Swiss fungi fruiting. Global Change Biology, 2013, 19, 2785-2794.	9.5	39
52	Temporal variation of <i>Bistorta vivipara</i>â€associated ectomycorrhizal fungal communities in the High Arctic. Molecular Ecology, 2015, 24, 6289-6302.	3.9	39
53	How many DNA markers are needed to reveal cryptic fungal species?. Fungal Biology, 2015, 119, 940-945.	2.5	39
54	The influence of intraspecific sequence variation during DNA metabarcoding: A case study of eleven fungal species. Molecular Ecology Resources, 2021, 21, 1141-1148.	4.8	39

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55	Substantial compositional turnover of fungal communities in an alpine ridgeâ€toâ€snowbed gradient. Molecular Ecology, 2013, 22, 5040-5052.	3.9	38
56	Arctic fungal communities associated with roots of Bistorta vivipara do not respond to the same fineâ€scale edaphic gradients as the aboveground vegetation. New Phytologist, 2015, 205, 1587-1597.	7.3	37
57	Fungal communities influence decomposition rates of plant litter from two dominant tree species. Fungal Ecology, 2018, 32, 1-8.	1.6	35
58	Continentalâ€scale macrofungal assemblage patterns correlate with climate, soil carbon and nitrogen deposition. Journal of Biogeography, 2018, 45, 1942-1953.	3.0	35
59	Analysis of Environmental 18S Ribosomal RNA Sequences reveals Unknown Diversity of the Cosmopolitan Phylum Telonemia. Protist, 2007, 158, 173-180.	1.5	34
60	Fungarium specimens: a largely untapped source in global change biology and beyond. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20170392.	4.0	34
61	Ribosomal DNA variation, recombination and inheritance in the basidiomycete Trichaptum abietinum: implications for reticulate evolution. Heredity, 2003, 91, 163-172.	2.6	33
62	Molecular characterization of airborne fungal spores in boreal forests of contrasting human disturbance. Mycologia, 2005, 97, 1215-1224.	1.9	33
63	Multiple cryptic species with divergent substrate affinities in the Serpula himantioides species complex. Fungal Biology, 2011, 115, 54-61.	2.5	33
64	Genetics of self/nonself recognition in Serpula lacrymans. Fungal Genetics and Biology, 2006, 43, 503-510.	2.1	32
65	Accelerated nrDNA evolution and profound AT bias in the medicinal fungus Cordyceps sinensis. Mycological Research, 2007, 111, 409-415.	2.5	31
66	Ectomycorrhizal and saprotrophic fungi respond differently to longâ€term experimentally increased snow depth in the High Arctic. MicrobiologyOpen, 2016, 5, 856-869.	3.0	30
67	Explaining European fungal fruiting phenology with climate variability. Ecology, 2018, 99, 1306-1315.	3.2	29
68	Links between Genetic Groups, Indole Alkaloid Profiles and Ecology within the Grass-Parasitic Claviceps purpurea Species Complex. Toxins, 2015, 7, 1431-1456.	3.4	28
69	Planktonic protistan communities in lakes along a large-scale environmental gradient. FEMS Microbiology Ecology, 2017, 93, fiw231.	2.7	28
70	Openâ€source data reveal how collectionsâ€based fungal diversity is sensitive to global change. Applications in Plant Sciences, 2019, 7, e01227.	2.1	28
71	Host- and tissue-specificity of moss-associated Galerina and Mycena determined from amplicon pyrosequencing data. Fungal Ecology, 2013, 6, 179-186.	1.6	27
72	Genetic structure of Fennoscandian populations of the threatened wood-decay fungus Fomitopsis rosea (Basidiomycota). Mycological Research, 2003, 107, 155-163.	2.5	25

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73	Host and tissue variations overshadow the response of boreal mossâ€associated fungal communities to increased nitrogen load. Molecular Ecology, 2017, 26, 571-588.	3.9	25
74	Exclusion of invertebrates influences saprotrophic fungal community and wood decay rate in an experimental field study. Functional Ecology, 2018, 32, 2571-2582.	3.6	25
75	Spruce and beech as local determinants of forest fungal community structure in litter, humus and mineral soil. FEMS Microbiology Ecology, 2019, 95, .	2.7	24
76	Fungal sporocarps house diverse and host-specific communities of fungicolous fungi. ISME Journal, 2021, 15, 1445-1457.	9.8	24
77	Molecular phylogenetics suggest a North American link between the anthropogenic dry rot fungus Serpula lacrymans and its wild relative S. himantioides. Molecular Ecology, 2004, 13, 3137-3146.	3.9	23
78	The fungus that came in from the cold: dry rotâ€™s pre-adapted ability to invade buildings. ISME Journal, 2018, 12, 791-801.	9.8	23
79	A single ectomycorrhizal plant root system includes a diverse and spatially structured fungal community. Mycorrhiza, 2019, 29, 167-180.	2.8	22
80	Population structure of the endangered wood decay fungus Phellinus nigrolimitatus (Basidiomycota). Canadian Journal of Botany, 2002, 80, 597-606.	1.1	21
81	Molecular characterization of airborne fungal spores in boreal forests of contrasting human disturbance. Mycologia, 2005, 97, 1215-1224.	1.9	21
82	Does warming by open-top chambers induce change in the root-associated fungal community of the arctic dwarf shrub Cassiope tetragona (Ericaceae)?. Mycorrhiza, 2017, 27, 513-524.	2.8	21
83	Forestry impacts on the hidden fungal biodiversity associated with bryophytes. FEMS Microbiology Ecology, 2014, 90, 313-325.	2.7	20
84	Altitudinal upwards shifts in fungal fruiting in the Alps. Proceedings of the Royal Society B: Biological Sciences, 2020, 287, 20192348.	2.6	20
85	Widespread vegetative compatibility groups in the dry-rot fungusSerpula lacrymans. Mycologia, 2004, 96, 232-239.	1.9	19
86	GalerinaEarle: A polyphyletic genus in the consortium of dark-spored agarics. Mycologia, 2005, 97, 823-837.	1.9	19
87	Traitâ€dependent distributional shifts in fruiting of common British fungi. Ecography, 2018, 41, 51-61.	4.5	19
88	Soil compartments (bulk soil, litter, root and rhizosphere) as main drivers of soil protistan communities distribution in forests with different nitrogen deposition. Soil Biology and Biochemistry, 2022, 168, 108628.	8.8	19
89	Extremely low AFLP variation in the European dry rot fungus (Serpula lacrymans): implications for self/nonself-recognition. Mycological Research, 2004, 108, 1264-1270.	2.5	18
90	Multilocus sequencing reveals multiple geographically structured lineages of Coniophora arida and C. olivacea (Boletales) in North America. Mycologia, 2007, 99, 705-713.	1.9	17

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91	Two invasive populations of the dry rot fungus<i>Serpula lacrymans</i>show divergent population genetic structures. Molecular Ecology, 2010, 19, 706-715.	3.9	17
92	Species delimitation, bioclimatic range, and conservation status of the threatened lichen Fuscopannaria confusa. Lichenologist, 2012, 44, 565-575.	0.8	17
93	Sequence clustering threshold has little effect on the recovery of microbial community structure. Molecular Ecology Resources, 2018, 18, 1064-1076.	4.8	17
94	Microsatellite markers show decreasing diversity but unchanged level of clonality in<i>Dryas octopetala</i>(Rosaceae) with increasing latitude. American Journal of Botany, 2010, 97, 988-997.	1.7	16
95	Evolutionary origin, worldwide dispersal, and population genetics of the dry rot fungus Serpula lacrymans. Fungal Biology Reviews, 2012, 26, 84-93.	4.7	16
96	Revealing hidden insectâ€"fungus interactions; moderately specialized, modular and anti-nested detritivore networks. Proceedings of the Royal Society B: Biological Sciences, 2018, 285, 20172833.	2.6	16
97	Community composition of arctic root-associated fungi mirrors host plant phylogeny. FEMS Microbiology Ecology, 2020, 96, .	2.7	16
98	Molecular Characterization of Sexual Diversity in a Population of <i>Serpula lacrymans</i>, a Tetrapolar Basidiomycete. G3: Genes, Genomes, Genetics, 2013, 3, 145-152.	1.8	15
99	Widespread Vegetative Compatibility Groups in the Dry-Rot Fungus Serpula lacrymans. Mycologia, 2004, 96, 232.	1.9	14
100	Pronounced ecological separation between two closely related lineages of the polyporous fungus Gloeoporus taxicola. Mycological Research, 2007, 111, 778-786.	2.5	14
101	Yeasts dominate soil fungal communities in three lowland Neotropical rainforests. Environmental Microbiology Reports, 2017, 9, 668-675.	2.4	14
102	Fineâ€scale spatiotemporal dynamics of fungal fruiting: prevalence, amplitude, range and continuity. Ecography, 2017, 40, 947-959.	4.5	14
103	Congruency in fungal phenology patterns across dataset sources and scales. Fungal Ecology, 2018, 32, 9-17.	1.6	14
104	Biogeography of plant rootâ€associated fungal communities in the North Atlantic region mirrors climatic variability. Journal of Biogeography, 2019, 46, 1532-1546.	3.0	14
105	Fungal community dynamics across a forestâ€"alpine ecotone. Molecular Ecology, 2021, 30, 4926-4938.	3.9	13
106	Multilocus sequencing reveals multiple geographically structured lineages of Coniophora arida and C. olivacea (Boletales) in North America. Mycologia, 2007, 99, 705-713.	1.9	12
107	Mycorrhizal fungal communities in coastal sand dunes and heaths investigated by pyrosequencing analyses. Mycorrhiza, 2015, 25, 447-456.	2.8	12
108	Analysing indoor mycobiomes through a largeâ€scale citizen science study in Norway. Molecular Ecology, 2021, 30, 2689-2705.	3.9	12

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109	Large-scale fungal strain sequencing unravels the molecular diversity in mating loci maintained by long-term balancing selection. PLoS Genetics, 2022, 18, e1010097.	3.5	12
110	A phylogeographic survey of a circumboreal polypore indicates introgression among ecologically differentiated cryptic lineages. Fungal Ecology, 2013, 6, 119-128.	1.6	11
111	Coming up short: Identifying substrate and geographic biases in fungal sequence databases. Fungal Ecology, 2018, 36, 75-80.	1.6	11
112	Warming drives a â€˜hummockificationâ€™ of microbial communities associated with decomposing mycorrhizal fungal necromass in peatlands. New Phytologist, 2022, 234, 2032-2043.	7.3	11
113	Shift in tree species changes the belowground biota of boreal forests. New Phytologist, 2022, 234, 2073-2087.	7.3	10
114	Isolation and characterization of 15 polymorphic microsatellite markers for the devastating dry rot fungus, Serpula lacrymans. Molecular Ecology Notes, 2006, 6, 1022-1024.	1.7	9
115	Spatiotemporal variation of the indoor mycobiome in daycare centers. Microbiome, 2021, 9, 220.	11.1	9
116	High variability in a mating type linked region in the dry rot fungus Serpula lacrymans caused by frequency-dependent selection?. BMC Genetics, 2010, 11, 64.	2.7	7
117	Population structure of Serpula lacrymans in Europe with an outlook to the French population. Mycologia, 2014, 106, 889-895.	1.9	7
118	Contrasting demographic histories revealed in two invasive populations of the dry rot fungus <i>Serpula lacrymans</i>. Molecular Ecology, 2021, 30, 2772-2789.	3.9	6
119	Establishment of spruce plantations in native birch forests reduces soil fungal diversity. FEMS Microbiology Ecology, 2021, 97, .	2.7	6
120	DNA metabarcoding reveals host-specific communities of arthropods residing in fungal fruit bodies. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20212622.	2.6	6
121	Legacies of invertebrate exclusion and tree secondary metabolites control fungal communities in dead wood. Molecular Ecology, 2022, 31, 3241-3253.	3.9	6
122	Microsatellite markers for <i>Bistorta vivipara</i> (Polygonaceae). American Journal of Botany, 2012, 99, e226-9.	1.7	5
123	Glacier retreat in the High Arctic: opportunity or threat for ectomycorrhizal diversity?. FEMS Microbiology Ecology, 2020, 96, .	2.7	5
124	Contrasting genetic structuring in the closely related basidiomycetes Trichaptum abietinum and Trichaptum fuscoviolaceum (Hymenochaetales). Fungal Biology, 2021, 125, 269-275.	2.5	5
125	Reply to Gange et al.: Climate-driven changes in the fungal fruiting season in the United Kingdom. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E335.	7.1	4
126	Widespread vegetative compatibility groups in the dry-rot fungus Serpula lacrymans. Mycologia, 2004, 96, 232-9.	1.9	4

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127	Secondary metabolites and nutrients explain fungal community composition in aspen wood. Fungal Ecology, 2021, , 101115.	1.6	3
128	Population genomics of a forest fungus reveals high gene flow and climate adaptation signatures. Molecular Ecology, 2022, 31, 1963-1979.	3.9	3
129	Regional and local population structure of the pioneer wood-decay fungus Trichaptum abietinum. Mycologia, 2003, 95, 416-25.	1.9	3
130	Microsatellite markers for <i>Hylocomium splendens</i> (Hylocomiaceae). American Journal of Botany, 2012, 99, e344-6.	1.7	2
131	Population structure of Serpula lacrymans in Europe with an outlook to the French population. Mycologia, 2014, 106, 889-895.	1.9	2
132	The Indoor Mycobiomes of Daycare Centers Are Affected by Occupancy and Climate. Applied and Environmental Microbiology, 2022, 88, AEM0211321.	3.1	2