

Nils HÃ¶gberg

List of Publications by Year in descending order

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Version: 2024-02-01

23
papers

2,541
citations

516561

16
h-index

642610

23
g-index

23
all docs

23
docs citations

23
times ranked

3424
citing authors

#	ARTICLE	IF	CITATIONS
1	Niche differentiation and evolution of the wood decay machinery in the invasive fungus <i>Serpula lacrymans</i> . ISME Journal, 2021, 15, 592-604.	4.4	16
2	Contrasting demographic histories revealed in two invasive populations of the dry rot fungus <i>Serpula lacrymans</i> . Molecular Ecology, 2021, 30, 2772-2789.	2.0	6
3	The fungus that came in from the cold: dry rot's pre-adapted ability to invade buildings. ISME Journal, 2018, 12, 791-801.	4.4	23
4	Draft genome of the brown-rot fungus <i>Fomitopsis pinicola</i> GR9-4. Data in Brief, 2017, 15, 496-500.	0.5	2
5	Identifying the Active Microbiome Associated with Roots and Rhizosphere Soil of Oilseed Rape. Applied and Environmental Microbiology, 2017, 83, .	1.4	141
6	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. Nature Genetics, 2015, 47, 410-415.	9.4	870
7	Transcriptomic changes in the plant pathogenic fungus <i>Rhizoctonia solani</i> AG-3 in response to the antagonistic bacteria <i>Serratia proteamaculans</i> and <i>Serratia plymuthica</i> . BMC Genomics, 2015, 16, 630.	1.2	97
8	High diversity, expanding populations and purifying selection in phytoplasmas causing coconut lethal yellowing in Mozambique. Plant Pathology, 2015, 64, 597-604.	1.2	20
9	Fungal communities associated with field grown oilseed rape (<i>Brassica napus</i> L.) – their possible role in early crop establishment. Acta Agriculturae Scandinavica - Section B Soil and Plant Science, 2013, 63, 241-252.	0.3	13
10	Non-contiguous finished genome sequence of plant-growth promoting <i>Serratia proteamaculans</i> S4. Standards in Genomic Sciences, 2013, 8, 441-449.	1.5	26
11	Evolutionary origin, worldwide dispersal, and population genetics of the dry rot fungus <i>Serpula lacrymans</i> . Fungal Biology Reviews, 2012, 26, 84-93.	1.9	16
12	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	3.5	210
13	Different crop rotation systems as drivers of change in soil bacterial community structure and yield of rice, <i>Oryza sativa</i> . Biology and Fertility of Soils, 2012, 48, 217-225.	2.3	121
14	The Plant Cell Wall's Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	6.0	512
15	Microsatellite markers for the ectomycorrhizal basidiomycete <i>Lactarius mammosus</i> . Molecular Ecology Resources, 2009, 9, 1008-1010.	2.2	5
16	Mating type distribution and genetic structure are consistent with sexual recombination in the Swedish population of <i>Phaeosphaeria nodorum</i> . Plant Pathology, 2008, 57, 634-641.	1.2	25
17	Asian origin and rapid global spread of the destructive dry rot fungus <i>Serpula lacrymans</i> . Molecular Ecology, 2007, 16, 3350-3360.	2.0	60
18	Isolation and characterization of 15 polymorphic microsatellite markers for the devastating dry rot fungus, <i>Serpula lacrymans</i> . Molecular Ecology Notes, 2006, 6, 1022-1024.	1.7	9

#	ARTICLE	IF	CITATIONS
19	Molecular phylogenetics suggest a North American link between the anthropogenic dry rot fungus <i>Serpula lacrymans</i> and its wild relative <i>S. himantioides</i> . <i>Molecular Ecology</i> , 2004, 13, 3137-3146.	2.0	23
20	Population genetics of <i>Fomitopsis rosea</i> – a wood-decay fungus of the old-growth European taiga. <i>Molecular Ecology</i> , 1999, 8, 703-710.	2.0	40
21	Population structure of the wood decay fungus <i>Fomitopsis pinicola</i> . <i>Heredity</i> , 1999, 83, 354-360.	1.2	47
22	Inter- and intraspecific variation in the ITS region of rDNA of ectomycorrhizal fungi in Fennoscandia as detected by endonuclease analysis. <i>New Phytologist</i> , 1997, 136, 313-325.	3.5	230
23	Genetic differentiation in <i>Fomitopsis pinicola</i> (Schwartz: Fr.) Karst studied by means of arbitrary primed-PCR. <i>Molecular Ecology</i> , 1995, 4, 675-680.	2.0	29