Daniel L Lindner

List of Publications by Year
in descending order

57 papers	3,659 citations	117453 34 h-index	149479 56 g-index
62 all docs	62 docs citations	62 times ranked	4747 citing authors

#	Article	IF	Citations
1	Wood-decay type and fungal guild dominance across a North American log transplant experiment. Fungal Ecology, 2022, 59, 101151.	0.7	8
2	Fungal communities associated with acorn woodpeckers and their excavations. Fungal Ecology, 2022, 59, 101154.	0.7	4
3	Fungal endophytes and origins of decay in beech (Fagus sylvatica) sapwood. Fungal Ecology, 2022, 59, 101161.	0.7	11
4	Diseaseâ€related population declines in bats demonstrate nonâ€exchangeability in generalist predators. Ecology and Evolution, 2022, 12, .	0.8	1
5	Predator preferences shape the diets of arthropodivorous bats more than quantitative local prey abundance. Molecular Ecology, 2021, 30, 855-873.	2.0	24
6	Coarse Woody Debris Decomposition Assessment Tool: Model validation and application. PLoS ONE, 2021, 16, e0254408.	1.1	2
7	The sexual spore pigment asperthecin is required for normal ascospore production and protection from UV light in Aspergillus nidulans. Journal of Industrial Microbiology and Biotechnology, 2021, 48, .	1.4	2
8	Fungal functional ecology: bringing a traitâ€based approach to plantâ€associated fungi. Biological Reviews, 2020, 95, 409-433.	4.7	171
9	Wood-colonizing fungal community response to forest restoration thinnings in a Pinus tabuliformis plantation in northern China. Forest Ecology and Management, 2020, 476, 118459.	1.4	6
10	Major histocompatibility complex variation is similar in little brown bats before and after whiteâ€nose syndrome outbreak. Ecology and Evolution, 2020, 10, 10031-10043.	0.8	3
11	A trait-based understanding of wood decomposition by fungi. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 11551-11558.	3.3	102
12	Identifying research needs to inform whiteâ€nose syndrome management decisions. Conservation Science and Practice, 2020, 2, e220.	0.9	21
13	Laetiporus lobatus (Basidiomycota, Polyporales), a new fungal species from Costa Rica. Phytotaxa, 2019, 408, 208-214.	0.1	1
14	Relationships among woodâ€boring beetles, fungi, and the decomposition of forest biomass. Molecular Ecology, 2019, 28, 4971-4986.	2.0	44
15	Consistent trade-offs in fungal trait expression across broad spatial scales. Nature Microbiology, 2019, 4, 846-853.	5.9	94
16	An improved method for utilizing highâ€throughput amplicon sequencing to determine the diets of insectivorous animals. Molecular Ecology Resources, 2019, 19, 176-190.	2.2	109
17	Detecting Symbioses in Complex Communities: the Fungal Symbionts of Bark and Ambrosia Beetles Within Asian Pines. Microbial Ecology, 2018, 76, 839-850.	1.4	29
18	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. Nature Communications, 2018, 9, 35.	5.8	56

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19	Characterization of PdCP1, a serine carboxypeptidase from Pseudogymnoascus destructans, the causal agent of White-nose Syndrome. Biological Chemistry, 2018, 399, 1375-1388.	1.2	6
20	Incidence and taxonomic richness of mosquitoes in the diets of little brown and big brown bats. Journal of Mammalogy, 2018, 99, 668-674.	0.6	30
21	Draft Genome Sequence of Burkholderia cepacia ATCC 17759, a Polyhydroxybutyrate-Co-Valerate Copolymer-Producing Bacterium. Genome Announcements, 2018, 6, .	0.8	1
22	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data. PeerJ, 2018, 6, e4925.	0.9	186
23	Diversity begets diversity in competition for space. Nature Ecology and Evolution, 2017, 1, 156.	3.4	79
24	A revised family-level classification of the Polyporales (Basidiomycota). Fungal Biology, 2017, 121, 798-824.	1.1	190
25	Revitalization of a Forward Genetic Screen Identifies Three New Regulators of Fungal Secondary Metabolism in the Genus Aspergillus. MBio, 2017, 8, .	1.8	47
26	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. MBio, 2017, 8, .	1.8	70
27	Use of Multiple Sequencing Technologies To Produce a High-Quality Genome of the Fungus Pseudogymnoascus destructans , the Causative Agent of Bat White-Nose Syndrome. Genome Announcements, 2016, 4, .	0.8	24
28	First Detection of Bat White-Nose Syndrome in Western North America. MSphere, 2016, 1, .	1.3	78
29	Experimental evidence of a symbiosis between red-cockaded woodpeckers and fungi. Proceedings of the Royal Society B: Biological Sciences, 2016, 283, 20160106.	1.2	38
30	Moving Beyond Too Little, Too Late: Managing Emerging Infectious Diseases in Wild Populations Requires International Policy and Partnerships. EcoHealth, 2015, 12, 404-407.	0.9	45
31	Heart rot hotel: fungal communities in red-cockaded woodpecker excavations. Fungal Ecology, 2015, 14, 33-43.	0.7	40
32	Contextâ€dependent conservation responses to emerging wildlife diseases. Frontiers in Ecology and the Environment, 2015, 13, 195-202.	1.9	147
33	THE FUNGUSTRICHOPHYTON REDELLIISP. NOV. CAUSES SKIN INFECTIONS THAT RESEMBLE WHITE-NOSE SYNDROME OF HIBERNATING BATS. Journal of Wildlife Diseases, 2015, 51, 36-47.	0.3	42
34	A Minimally Invasive Method for Sampling Nest and Roost Cavities for Fungi: a Novel Approach to Identify the Fungi Associated with Cavity-Nesting Birds. Acta Ornithologica, 2014, 49, 233-242.	0.1	12
35	Molecular Characterization of a Heterothallic Mating System in Pseudogymnoascus destructans, the Fungus Causing White-Nose Syndrome of Bats. G3: Genes, Genomes, Genetics, 2014, 4, 1755-1763.	0.8	41
36	Highly Sensitive Quantitative PCR for the Detection and Differentiation of Pseudogymnoascus destructans and Other Pseudogymnoascus Species. Applied and Environmental Microbiology, 2014, 80, 1726-1731.	1.4	46

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37	Molecular phylogeny, morphology, pigment chemistry and ecology in Hygrophoraceae (Agaricales). Fungal Diversity, 2014, 64, 1-99.	4.7	108
38	Improving ITS sequence data for identification of plant pathogenic fungi. Fungal Diversity, 2014, 67, 11-19.	4.7	123
39	Disturbance and diversity of wood-inhabiting fungi: effects of canopy gaps and downed woody debris. Biodiversity and Conservation, 2014, 23, 2155-2172.	1.2	72
40	A phylogenetic overview of the antrodia clade (Basidiomycota, Polyporales). Mycologia, 2013, 105, 1391-1411.	0.8	86
41	Phylogenetic evaluation of Geomyces and allies reveals no close relatives of Pseudogymnoascus destructans, comb. nov., inÂbat hibernacula of eastern North America. Fungal Biology, 2013, 117, 638-649.	1.1	228
42	Distribution and Environmental Persistence of the Causative Agent of White-Nose Syndrome, Geomyces destructans, in Bat Hibernacula of the Eastern United States. Applied and Environmental Microbiology, 2013, 79, 1293-1301.	1.4	135
43	A culture-based survey of fungi in soil from bat hibernacula in the eastern United States and its implications for detection of Geomyces destructans, the causal agent of bat white-nose syndrome. Mycologia, 2013, 105, 237-252.	0.8	95
44	Bat white-nose syndrome: a real-time TaqMan polymerase chain reaction test targeting the intergenic spacer region ofGeomyces destructans. Mycologia, 2013, 105, 253-259.	0.8	127
45	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.	0.8	97
46	Wood-inhabiting, polyporoid fungi in aspen-dominated forests managed for biomass in the U.S. Lake States. Fungal Ecology, 2012, 5, 600-609.	0.7	26
47	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.	0.7	166
48	Taxonomy of Pseudolagarobasidium (Polyporales, Basidiomycota). Fungal Diversity, 2012, 55, 155-169.	4.7	7
49	Initial fungal colonizer affects mass loss and fungal community development in Picea abies logs 6yr after inoculation. Fungal Ecology, 2011, 4, 449-460.	0.7	81
50	Intragenomic variation in the ITS rDNA region obscures phylogenetic relationships and inflates estimates of operational taxonomic units in genus Laetiporus. Mycologia, 2011, 103, 731-740.	0.8	155
51	DNA-based detection of the fungal pathogen Geomyces destructans in soils from bat hibernacula. Mycologia, 2011, 103, 241-246.	0.8	76
52	Relationships among North American and Japanese Laetiporus isolates inferred from molecular phylogenetics and single-spore incompatibility reactions. Mycologia, 2010, 102, 911-917.	0.8	15
53	Effects of cloning and root-tip size on observations of fungal ITS sequences fromPicea glaucaroots. Mycologia, 2009, 101, 157-165.	0.8	55
54	Ectomycorrhizal characterization of an American chestnut (Castanea dentata)-dominated community in Western Wisconsin. Mycorrhiza, 2008, 19, 27-36.	1.3	66

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55	Molecular phylogeny of Laetiporus and other brown rot polypore genera in North America. Mycologia, 2008, 100, 417-430.	0.8	68
56	Species diversity of polyporoid and corticioid fungi in northern hardwood forests with differing management histories. Mycologia, 2006, 98, 195-217.	0.8	23
57	Species diversity of polyporoid and corticioid fungi in northern hardwood forests with differing management histories. Mycologia, 2006, 98, 195-217.	0.8	33