

Jonathan M Palmer

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

2,383
citations

24
h-index

48
g-index

48
ext. papers

3,097
ext. citations

5.6
avg, IF

5.14
L-index

#	Paper	IF	Citations
43	Fungal communities associated with acorn woodpeckers and their excavations. <i>Fungal Ecology</i> , 2022 , 101154	4.1	0
42	Predator preferences shape the diets of arthropodivorous bats more than quantitative local prey abundance. <i>Molecular Ecology</i> , 2021 , 30, 855-873	5.7	7
41	Role of Leaf Litter in Above-Ground Wood Decay. <i>Microorganisms</i> , 2020 , 8,	4.9	2
40	Wood-colonizing fungal community response to forest restoration thinnings in a Pinus tabuliformis plantation in northern China. <i>Forest Ecology and Management</i> , 2020 , 476, 118459	3.9	1
39	Major histocompatibility complex variation is similar in little brown bats before and after white-nose syndrome outbreak. <i>Ecology and Evolution</i> , 2020 , 10, 10031-10043	2.8	2
38	Relationships among wood-boring beetles, fungi, and the decomposition of forest biomass. <i>Molecular Ecology</i> , 2019 , 28, 4971-4986	5.7	24
37	An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals. <i>Molecular Ecology Resources</i> , 2019 , 19, 176-190	8.4	49
36	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. <i>Nature Communications</i> , 2018 , 9, 35	17.4	31
35	Assembly and Phasing of Dikaryotic Genomes from Two Isolates of f. sp. , the Causal Agent of Oat Crown Rust. <i>MBio</i> , 2018 , 9,	7.8	27
34	Selenate sensitivity of a laeA mutant is restored by overexpression of the bZIP protein MetR in Aspergillus fumigatus. <i>Fungal Genetics and Biology</i> , 2018 , 117, 1-10	3.9	9
33	Incidence and taxonomic richness of mosquitoes in the diets of little brown and big brown bats. <i>Journal of Mammalogy</i> , 2018 , 99, 668-674	1.8	19
32	Draft Genome Sequence of Burkholderia cepacia ATCC 17759, a Polyhydroxybutyrate-Co-Valerate Copolymer-Producing Bacterium. <i>Genome Announcements</i> , 2018 , 6,		1
31	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data. <i>PeerJ</i> , 2018 , 6, e4925	3.1	107
30	sp. nov.: a new cold-tolerant species of yeast isolated from bats. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , 2018 , 41, 56-70	9	50
29	Characterization of PdCP1, a serine carboxypeptidase from Pseudogymnoascus destructans, the causal agent of White-nose Syndrome. <i>Biological Chemistry</i> , 2018 , 399, 1375-1388	4.5	5
28	Caspofungin exposure alters the core septin AspB interactome of Aspergillus fumigatus. <i>Biochemical and Biophysical Research Communications</i> , 2017 , 485, 221-226	3.4	5
27	Pseudogymnoascus destructans transcriptome changes during white-nose syndrome infections. <i>Virulence</i> , 2017 , 8, 1695-1707	4.7	13

26	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017 , 13, 895-901	11.7	108
25	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , 2017 , 15, e2003583	9.7	102
24	Revitalization of a Forward Genetic Screen Identifies Three New Regulators of Fungal Secondary Metabolism in the Genus. <i>MBio</i> , 2017 , 8,	7.8	29
23	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. <i>MBio</i> , 2017 , 8,	7.8	45
22	Lipoxygenase Activity Accelerates Programmed Spore Germination in. <i>Frontiers in Microbiology</i> , 2017 , 8, 831	5.7	13
21	Amplicon-Based Sequencing of Soil Fungi from Wood Preservative Test Sites. <i>Frontiers in Microbiology</i> , 2017 , 8, 1997	5.7	6
20	Characterization of Isolates from Air and Surfaces of the International Space Station. <i>MSphere</i> , 2016 , 1,	5	61
19	First Detection of Bat White-Nose Syndrome in Western North America. <i>MSphere</i> , 2016 , 1,	5	55
18	FleA Expression in <i>Aspergillus fumigatus</i> Is Recognized by Fucosylated Structures on Mucins and Macrophages to Prevent Lung Infection. <i>PLoS Pathogens</i> , 2016 , 12, e1005555	7.6	39
17	Use of Multiple Sequencing Technologies To Produce a High-Quality Genome of the Fungus <i>Pseudogymnoascus destructans</i> , the Causative Agent of Bat White-Nose Syndrome. <i>Genome Announcements</i> , 2016 , 4,		16
16	One Juliet and four Romeos: VeA and its methyltransferases. <i>Frontiers in Microbiology</i> , 2015 , 6, 1	5.7	837
15	Molecular characterization of a heterothallic mating system in <i>Pseudogymnoascus destructans</i> , the Fungus causing white-nose syndrome of bats. <i>G3: Genes, Genomes, Genetics</i> , 2014 , 4, 1755-63	3.2	28
14	A novel automethylation reaction in the <i>Aspergillus nidulans</i> LaeA protein generates S-methylmethionine. <i>Journal of Biological Chemistry</i> , 2013 , 288, 14032-14045	5.4	44
13	RsmA regulates <i>Aspergillus fumigatus</i> gliotoxin cluster metabolites including cyclo(L-Phe-L-Ser), a potential new diagnostic marker for invasive aspergillosis. <i>PLoS ONE</i> , 2013 , 8, e62591	3.7	32
12	Secondary metabolism and development is mediated by LlmF control of VeA subcellular localization in <i>Aspergillus nidulans</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003193	6	59
11	Prototype of an intertwined secondary-metabolite supercluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 17065-70	11.5	141
10	Loss of CclA, required for histone 3 lysine 4 methylation, decreases growth but increases secondary metabolite production in <i>Aspergillus fumigatus</i> . <i>PeerJ</i> , 2013 , 1, e4	3.1	50
9	Telomere position effect is regulated by heterochromatin-associated proteins and NkuA in <i>Aspergillus nidulans</i> . <i>Microbiology (United Kingdom)</i> , 2010 , 156, 3522-3531	2.9	26

8	Secondary metabolism in fungi: does chromosomal location matter?. <i>Current Opinion in Microbiology</i> , 2010 , 13, 431-6	7.9	173
7	Involvement of transposon-like elements in penicillin gene cluster regulation. <i>Fungal Genetics and Biology</i> , 2010 , 47, 423-32	3.9	51
6	H3K9 methylation regulates growth and development in <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , 2008 , 7, 2052-60		51
5	Ectomycorrhizal characterization of an American chestnut (<i>Castanea dentata</i>)-dominated community in Western Wisconsin. <i>Mycorrhiza</i> , 2008 , 19, 27-36	3.9	52
4	Preliminary characterization of little brown bats (<i>Myotis lucifugus</i>) immune MHC II DRB alleles using next-generation sequencing		2
3	An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals		3
2	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species		5
1	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data		2