

# Jonathan M Palmer

## List of Publications by Citations

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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	One Juliet and four Romeos: VeA and its methyltransferases. <i>Frontiers in Microbiology</i> , <b>2015</b> , 6, 1	5.7	837
42	Secondary metabolism in fungi: does chromosomal location matter?. <i>Current Opinion in Microbiology</i> , <b>2010</b> , 13, 431-6	7.9	173
41	Prototype of an intertwined secondary-metabolite supercluster. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2013</b> , 110, 17065-70	11.5	141
40	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , <b>2017</b> , 13, 895-901	11.7	108
39	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data. <i>PeerJ</i> , <b>2018</b> , 6, e4925	3.1	107
38	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. <i>PLoS Biology</i> , <b>2017</b> , 15, e2003583	9.7	102
37	Characterization of Isolates from Air and Surfaces of the International Space Station. <i>MSphere</i> , <b>2016</b> , 1,	5	61
36	Secondary metabolism and development is mediated by LlmF control of VeA subcellular localization in <i>Aspergillus nidulans</i> . <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003193	6	59
35	First Detection of Bat White-Nose Syndrome in Western North America. <i>MSphere</i> , <b>2016</b> , 1,	5	55
34	Ectomycorrhizal characterization of an American chestnut ( <i>Castanea dentata</i> )-dominated community in Western Wisconsin. <i>Mycorrhiza</i> , <b>2008</b> , 19, 27-36	3.9	52
33	Involvement of transposon-like elements in penicillin gene cluster regulation. <i>Fungal Genetics and Biology</i> , <b>2010</b> , 47, 423-32	3.9	51
32	H3K9 methylation regulates growth and development in <i>Aspergillus fumigatus</i> . <i>Eukaryotic Cell</i> , <b>2008</b> , 7, 2052-60		51
31	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> , <b>2013</b> , 1, e4	3.1	50
30	sp. nov.: a new cold-tolerant species of yeast isolated from bats. <i>Persoonia: Molecular Phylogeny and Evolution of Fungi</i> , <b>2018</b> , 41, 56-70	9	50
29	An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals. <i>Molecular Ecology Resources</i> , <b>2019</b> , 19, 176-190	8.4	49
28	Phylogenetics of a Fungal Invasion: Origins and Widespread Dispersal of White-Nose Syndrome. <i>MBio</i> , <b>2017</b> , 8,	7.8	45
27	A novel automethylation reaction in the <i>Aspergillus nidulans</i> LaeA protein generates S-methylmethionine. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 14032-14045	5.4	44

26	FleA Expression in <i>Aspergillus fumigatus</i> Is Recognized by Fucosylated Structures on Mucins and Macrophages to Prevent Lung Infection. <i>PLoS Pathogens</i> , <b>2016</b> , 12, e1005555	7.6	39
25	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> , <b>2013</b> , 8, e62591	3.7	32
24	Extreme sensitivity to ultraviolet light in the fungal pathogen causing white-nose syndrome of bats. <i>Nature Communications</i> , <b>2018</b> , 9, 35	17.4	31
23	Revitalization of a Forward Genetic Screen Identifies Three New Regulators of Fungal Secondary Metabolism in the Genus. <i>MBio</i> , <b>2017</b> , 8,	7.8	29
22	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> , <b>2014</b> , 4, 1755-63	3.2	28
21	Assembly and Phasing of Dikaryotic Genomes from Two Isolates of <i>f. sp.</i> , the Causal Agent of Oat Crown Rust. <i>MBio</i> , <b>2018</b> , 9,	7.8	27
20	Telomere position effect is regulated by heterochromatin-associated proteins and NkuA in <i>Aspergillus nidulans</i> . <i>Microbiology (United Kingdom)</i> , <b>2010</b> , 156, 3522-3531	2.9	26
19	Relationships among wood-boring beetles, fungi, and the decomposition of forest biomass. <i>Molecular Ecology</i> , <b>2019</b> , 28, 4971-4986	5.7	24
18	Incidence and taxonomic richness of mosquitoes in the diets of little brown and big brown bats. <i>Journal of Mammalogy</i> , <b>2018</b> , 99, 668-674	1.8	19
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> , <b>2016</b> , 4,		16
16	<i>Pseudogymnoascus destructans</i> transcriptome changes during white-nose syndrome infections. <i>Virulence</i> , <b>2017</b> , 8, 1695-1707	4.7	13
15	Lipoxygenase Activity Accelerates Programmed Spore Germination in. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 831	5.7	13
14	Selenate sensitivity of a <i>laeA</i> mutant is restored by overexpression of the bZIP protein MetR in <i>Aspergillus fumigatus</i> . <i>Fungal Genetics and Biology</i> , <b>2018</b> , 117, 1-10	3.9	9
13	Predator preferences shape the diets of arthropodivorous bats more than quantitative local prey abundance. <i>Molecular Ecology</i> , <b>2021</b> , 30, 855-873	5.7	7
12	Amplicon-Based Sequencing of Soil Fungi from Wood Preservative Test Sites. <i>Frontiers in Microbiology</i> , <b>2017</b> , 8, 1997	5.7	6
11	Caspofungin exposure alters the core septin AspB interactome of <i>Aspergillus fumigatus</i> . <i>Biochemical and Biophysical Research Communications</i> , <b>2017</b> , 485, 221-226	3.4	5
10	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species		5
9	Characterization of PdCP1, a serine carboxypeptidase from <i>Pseudogymnoascus destructans</i> , the causal agent of White-nose Syndrome. <i>Biological Chemistry</i> , <b>2018</b> , 399, 1375-1388	4.5	5

8	An improved method for utilizing high-throughput amplicon sequencing to determine the diets of insectivorous animals		3
7	Role of Leaf Litter in Above-Ground Wood Decay. <i>Microorganisms</i> , <b>2020</b> , 8,	4.9	2
6	Preliminary characterization of little brown bats ( <i>Myotis lucifugus</i> ) immune MHC II DRB alleles using next-generation sequencing		2
5	Non-biological synthetic spike-in controls and the AMPtk software pipeline improve mycobiome data		2
4	Major histocompatibility complex variation is similar in little brown bats before and after white-nose syndrome outbreak. <i>Ecology and Evolution</i> , <b>2020</b> , 10, 10031-10043	2.8	2
3	Draft Genome Sequence of <i>Burkholderia cepacia</i> ATCC 17759, a Polyhydroxybutyrate-Co-Valerate Copolymer-Producing Bacterium. <i>Genome Announcements</i> , <b>2018</b> , 6,		1
2	Wood-colonizing fungal community response to forest restoration thinnings in a <i>Pinus tabuliformis</i> plantation in northern China. <i>Forest Ecology and Management</i> , <b>2020</b> , 476, 118459	3.9	1
1	Fungal communities associated with acorn woodpeckers and their excavations. <i>Fungal Ecology</i> , <b>2022</b> , 101154	4.1	0