

Michael R Thon

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.

60
papers

4,139
citations

27
h-index

62
g-index

62
ext. papers

5,096
ext. citations

6.3
avg, IF

4.67
L-index

#	Paper	IF	Citations
60	The Role of Plant Hormones in the Interaction of Species with Their Host Plants. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
59	Identification and Comparison of Secreted Effector Candidates Reveal Two Independent Lineages Pathogenic to Soybean. <i>Pathogens</i> , 2021 , 10,	4.5	1
58	A Major Effect Gene Controlling Development and Pathogenicity in Identified Through Genetic Analysis of Natural Mycelial Non-pathogenic Isolates. <i>Frontiers in Plant Science</i> , 2021 , 12, 663870	6.2	1
57	Effectors with chitinase activity (EWCA), a family of conserved, secreted fungal chitinases that suppress chitin-triggered immunity. <i>Plant Cell</i> , 2021 , 33, 1319-1340	11.6	10
56	Soybean anthracnose caused by <i>Colletotrichum</i> species: Current status and future prospects. <i>Molecular Plant Pathology</i> , 2021 , 22, 393-409	5.7	8
55	Complete Genome Sequence of the Plant-Pathogenic Fungus. <i>Molecular Plant-Microbe Interactions</i> , 2021 , MPMI07210173A	3.6	3
54	Genome Sequence Resources of , , and : Four Species Pathogenic to Soybean (). <i>Phytopathology</i> , 2020 , 110, 1497-1499	3.8	8
53	Genome sequencing of <i>Rigidoporus microporus</i> provides insights on genes important for wood decay, latex tolerance and interspecific fungal interactions. <i>Scientific Reports</i> , 2020 , 10, 5250	4.9	7
52	Nutritional factors modulating plant and fruit susceptibility to pathogens: BARD workshop, Haifa, Israel, February 25-26, 2018. <i>Phytoparasitica</i> , 2020 , 48, 317-333	1.5	
51	Dynamic Changes in the Microbiome of Rice During Shoot and Root Growth Derived From Seeds. <i>Frontiers in Microbiology</i> , 2020 , 11, 559728	5.7	9
50	Whole-Genome Sequence of the Orchid Anthracnose Pathogen <i>Colletotrichum orchidophilum</i> . <i>Molecular Plant-Microbe Interactions</i> , 2018 , 31, 979-981	3.6	13
49	Analysis of phylogeny, distribution, and pathogenicity of <i>Botryosphaeriaceae</i> species associated with gummosis of <i>Anacardium</i> in Brazil, with a new species of <i>Lasiodiplodia</i> . <i>Fungal Biology</i> , 2017 , 121, 437-451	2.8	33
48	Gapless genome assembly of <i>Colletotrichum higginsianum</i> reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , 2017 , 18, 667	4.5	53
47	The Species Complex as a Model System to Study Evolution and Host Specialization in Plant Pathogens. <i>Frontiers in Microbiology</i> , 2017 , 8, 2001	5.7	38
46	A Fungal Effector With Host Nuclear Localization and DNA-Binding Properties Is Required for Maize Anthracnose Development. <i>Molecular Plant-Microbe Interactions</i> , 2016 , 29, 83-95	3.6	33
45	Survival trade-offs in plant roots during colonization by closely related beneficial and pathogenic fungi. <i>Nature Communications</i> , 2016 , 7, 11362	17.4	130
44	Transcriptional Analysis of sp. Capable of Degrading Ochratoxin A. <i>Frontiers in Microbiology</i> , 2016 , 7, 2162	5.7	21

43	First Report of <i>Colletotrichum graminicola</i> Causing Maize Anthracnose Stalk Rot in the Alentejo Region, Portugal. <i>Plant Disease</i> , 2016 , 100, 648-648	1.5	2
42	Gene family expansions and contractions are associated with host range in plant pathogens of the genus <i>Colletotrichum</i> . <i>BMC Genomics</i> , 2016 , 17, 555	4.5	75
41	A highly conserved metalloprotease effector enhances virulence in the maize anthracnose fungus <i>Colletotrichum graminicola</i> . <i>Molecular Plant Pathology</i> , 2016 , 17, 1048-62	5.7	38
40	Genome Sequence and Annotation of <i>Colletotrichum higginsianum</i> , a Causal Agent of Crucifer Anthracnose Disease. <i>Genome Announcements</i> , 2016 , 4,		24
39	Draft whole-genome sequence of the 7/96 strain, causal agent of sunflower stem canker. <i>Genomics Data</i> , 2016 , 10, 151-152		9
38	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
37	Identification of horizontally transferred genes in the genus <i>Colletotrichum</i> reveals a steady tempo of bacterial to fungal gene transfer. <i>BMC Genomics</i> , 2015 , 16, 2	4.5	36
36	Gene expression patterns and dynamics of the colonization of common bean (<i>Phaseolus vulgaris</i> L.) by highly virulent and weakly virulent strains of <i>Fusarium oxysporum</i> . <i>Frontiers in Microbiology</i> , 2015 , 6, 234	5.7	36
35	Molecular Diversity of Anthracnose Pathogen Populations Associated with UK Strawberry Production Suggests Multiple Introductions of Three Different <i>Colletotrichum</i> Species. <i>PLoS ONE</i> , 2015 , 10, e0129140	3.7	58
34	Draft Genome Sequence of <i>Colletotrichum acutatum</i> Sensu Lato (<i>Colletotrichum fioriniae</i>). <i>Genome Announcements</i> , 2014 , 2,		41
33	Natural selection on coding and noncoding DNA sequences is associated with virulence genes in a plant pathogenic fungus. <i>Genome Biology and Evolution</i> , 2014 , 6, 2368-79	3.9	21
32	Compositions of fungal secretomes indicate a greater impact of phylogenetic history than lifestyle adaptation. <i>BMC Genomics</i> , 2014 , 15, 722	4.5	54
31	First Report of Anthracnose Stalk Rot of Maize Caused by <i>Colletotrichum graminicola</i> in Switzerland. <i>Plant Disease</i> , 2014 , 98, 694	1.5	3
30	Draft Genome Sequence of <i>Colletotrichum sublineola</i> , a Destructive Pathogen of Cultivated Sorghum. <i>Genome Announcements</i> , 2014 , 2,		35
29	First Report of Apple Bitter Rot Caused by <i>Colletotrichum godetiae</i> in the United Kingdom. <i>Plant Disease</i> , 2014 , 98, 1000	1.5	21
28	Global aspects of <i>pacC</i> regulation of pathogenicity genes in <i>Colletotrichum gloeosporioides</i> as revealed by transcriptome analysis. <i>Molecular Plant-Microbe Interactions</i> , 2013 , 26, 1345-58	3.6	70
27	Comparative phenotypic analysis and genome sequence of <i>Clostridium beijerinckii</i> SA-1, an offspring of NCIMB 8052. <i>Microbiology (United Kingdom)</i> , 2013 , 159, 2558-2570	2.9	15
26	New insights into the evolution and structure of <i>Colletotrichum</i> plant-like subtilisins (CPLSs). <i>Communicative and Integrative Biology</i> , 2013 , 6, e25727	1.7	3

25	Horizontal transfer of a subtilisin gene from plants into an ancestor of the plant pathogenic fungal genus <i>Colletotrichum</i> . <i>PLoS ONE</i> , 2013 , 8, e59078	3.7	24
24	Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , 2012 , 44, 1060-5	36.3	564
23	Supervised protein family classification and new family construction. <i>Journal of Computational Biology</i> , 2012 , 19, 957-67	1.7	1
22	Plant defense mechanisms are activated during biotrophic and necrotrophic development of <i>Colletotricum graminicola</i> in maize. <i>Plant Physiology</i> , 2012 , 158, 1342-58	6.6	129
21	Identification of positive selection in disease response genes within members of the Poaceae. <i>Plant Signaling and Behavior</i> , 2012 , 7, 1667-75	2.5	6
20	Comparative genome sequence analysis underscores mycoparasitism as the ancestral life style of <i>Trichoderma</i> . <i>Genome Biology</i> , 2011 , 12, R40	18.3	448
19	Identifying gene clusters within localized regions in multiple genomes. <i>Journal of Computational Biology</i> , 2010 , 17, 657-68	1.7	2
18	PoGO: Prediction of Gene Ontology terms for fungal proteins. <i>BMC Bioinformatics</i> , 2010 , 11, 215	3.6	12
17	A bound on modeling error in observable operator models and an associated learning algorithm. <i>Neural Computation</i> , 2009 , 21, 2687-712	2.9	2
16	Making the error-controlling algorithm of observable operator models constructive. <i>Neural Computation</i> , 2009 , 21, 3460-86	2.9	
15	Root infection and systemic colonization of maize by <i>Colletotrichum graminicola</i> . <i>Applied and Environmental Microbiology</i> , 2008 , 74, 823-32	4.8	83
14	Gene function prediction using protein domain probability and hierarchical Gene Ontology information 2008 ,		3
13	Identifying clusters of functionally related genes in genomes. <i>Bioinformatics</i> , 2007 , 23, 1053-60	7.2	96
12	A systematic analysis of T-DNA insertion events in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2007 , 44, 1050-64	3.9	52
11	The role of transposable element clusters in genome evolution and loss of synteny in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Genome Biology</i> , 2006 , 7, R16	18.3	66
10	Bioinformatic analysis of expressed sequence tags derived from a compatible <i>Alternaria brassicicola</i> - <i>Brassica oleracea</i> interaction. <i>Molecular Plant Pathology</i> , 2006 , 7, 113-24	5.7	25
9	Automatic Annotation of Protein Functional Class from Sparse and Imbalanced Data Sets. <i>Lecture Notes in Computer Science</i> , 2006 , 65-77	0.9	4
8	Novel G-protein-coupled receptor-like proteins in the plant pathogenic fungus <i>Magnaporthe grisea</i> . <i>Genome Biology</i> , 2005 , 6, R24	18.3	159

7	The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , 2005 , 434, 980-6	50.4	1202
6	BAC end sequences and a physical map reveal transposable element content and clustering patterns in the genome of <i>Magnaporthe grisea</i> . <i>Fungal Genetics and Biology</i> , 2004 , 41, 657-66	3.9	24
5	Gene discovery and gene expression in the rice blast fungus, <i>Magnaporthe grisea</i> : analysis of expressed sequence tags. <i>Molecular Plant-Microbe Interactions</i> , 2004 , 17, 1337-47	3.6	76
4	The rice blast pathosystem as a case study for the development of new tools and raw materials for genome analysis of fungal plant pathogens. <i>New Phytologist</i> , 2003 , 159, 53-61	9.8	17
3	Partial β -tubulin gene sequences for evolutionary studies in the Basidiomycotina. <i>Mycologia</i> , 1999 , 91, 468-474	2.4	57
2	Partial beta-Tubulin Gene Sequences for Evolutionary Studies in the Basidiomycotina. <i>Mycologia</i> , 1999 , 91, 468	2.4	43
1	Evidence for two independent lineages of shiitake of the americas (<i>Lentinula boryana</i>) based on rDNA and beta-tubulin gene sequences. <i>Molecular Phylogenetics and Evolution</i> , 1999 , 13, 520-4	4.1	15