Philipp Wiemann

List of Publications by Year
in descending order

35 papers	3,401 citations	279798 23 h-index	377865 34 g-index
36 all docs	36 docs citations	36 times ranked	4295 citing authors

#	Article	IF	Citations
1	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, .	3.0	2
2	Secreted Secondary Metabolites Reduce Bacterial Wilt Severity of Tomato in Bacterialâ€"Fungal Co-Infections. Microorganisms, 2021, 9, 2123.	3.6	4
3	Identification of the Antifungal Metabolite Chaetoglobosin P From Discosia rubi Using a Cryptococcus neoformans Inhibition Assay: Insights Into Mode of Action and Biosynthesis. Frontiers in Microbiology, 2020, 11, 1766.	3.5	4
4	Acrophiarin (antibiotic S31794 /Fâ€1) from Penicillium arenicola shares biosynthetic features with both Aspergillus â€•and Leotiomycete â€type echinocandins. Environmental Microbiology, 2020, 22, 2292-2311.	3.8	5
5	Gastrointestinal microbiota alteration induced by Mucor circinelloides in a murine model. Journal of Microbiology, 2019, 57, 509-520.	2.8	18
6	Abstract 998: HEx: A computational and synthetic biology platform applied to oncology drug discovery. , 2019, , .		0
7	CoIN: co-inducible nitrate expression system for secondary metabolites in Aspergillus nidulans. Fungal Biology and Biotechnology, 2018, 5, 6.	5.1	29
8	A possible role for fumagillin in cellular damage during host infection by Aspergillus fumigatus. Virulence, 2018, 9, 1548-1561.	4.4	37
9	Conserved Responses in a War of Small Molecules between a Plant-Pathogenic Bacterium and Fungi. MBio, 2018, 9, .	4.1	73
10	A Bcl-2 Associated Athanogene (bagA) Modulates Sexual Development and Secondary Metabolism in the Filamentous Fungus Aspergillus nidulans. Frontiers in Microbiology, 2018, 9, 1316.	3.5	13
11	Contribution of ATPase copper transporters in animal but not plant virulence of the crossover pathogen Aspergillus flavus. Virulence, 2018, 9, 1273-1286.	4.4	29
12	Aspergillus fumigatus Copper Export Machinery and Reactive Oxygen Intermediate Defense Counter Host Copper-Mediated Oxidative Antimicrobial Offense. Cell Reports, 2017, 19, 1008-1021.	6.4	95
13	Revitalization of a Forward Genetic Screen Identifies Three New Regulators of Fungal Secondary Metabolism in the Genus Aspergillus. MBio, 2017, 8, .	4.1	47
14	Drivers of genetic diversity in secondary metabolic gene clusters within a fungal species. PLoS Biology, 2017, 15, e2003583.	5.6	187
15	TrpE feedback mutants reveal roadblocks and conduits toward increasing secondary metabolism in Aspergillus fumigatus. Fungal Genetics and Biology, 2016, 89, 102-113.	2.1	24
16	The art of design. Fungal Genetics and Biology, 2016, 89, 1-2.	2.1	5
17	Enhancing Nonribosomal Peptide Biosynthesis in Filamentous Fungi. Methods in Molecular Biology, 2016, 1401, 149-160.	0.9	12
18	Evolution of Chemical Diversity in a Group of Non-Reduced Polyketide Gene Clusters: Using Phylogenetics to Inform the Search for Novel Fungal Natural Products. Toxins, 2015, 7, 3572-3607.	3.4	27

#	Article	IF	Citations
19	Genetic engineering, high resolution mass spectrometry and nuclear magnetic resonance spectroscopy elucidate the bikaverin biosynthetic pathway in Fusarium fujikuroi. Fungal Genetics and Biology, 2015, 84, 26-36.	2.1	27
20	An update to polyketide synthase and non-ribosomal synthetase genes and nomenclature in Fusarium. Fungal Genetics and Biology, 2015, 75, 20-29.	2.1	123
21	Minimum Information about a Biosynthetic Gene cluster. Nature Chemical Biology, 2015, 11, 625-631.	8.0	715
22	Perturbations in small molecule synthesis uncovers an iron-responsive secondary metabolite network in Aspergillus fumigatus. Frontiers in Microbiology, 2014, 5, 530.	3.5	59
23	Illumina identification of RsrA, a conserved C2H2 transcription factor coordinating the NapA mediated oxidative stress signaling pathway in Aspergillus. BMC Genomics, 2014, 15, 1011.	2.8	25
24	Strategies for mining fungal natural products. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 301-313.	3.0	168
25	Genetic Manipulation of the Fusarium fujikuroi Fusarin Gene Cluster Yields Insight into the Complex Regulation and Fusarin Biosynthetic Pathway. Chemistry and Biology, 2013, 20, 1055-1066.	6.0	107
26	Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen Fusarium fujikuroi Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. PLoS Pathogens, 2013, 9, e1003475.	4.7	406
27	Prototype of an intertwined secondary-metabolite supercluster. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 17065-17070.	7.1	174
28	A Sensing Role of the Glutamine Synthetase in the Nitrogen Regulation Network in Fusarium fujikuroi. PLoS ONE, 2013, 8, e80740.	2.5	26
29	Biosynthesis of Fusarubins Accounts for Pigmentation of Fusarium fujikuroi Perithecia. Applied and Environmental Microbiology, 2012, 78, 4468-4480.	3.1	169
30	New Approach via Gene Knockout and Single-Step Chemical Reaction for the Synthesis of Isotopically Labeled Fusarin C as an Internal Standard for the Analysis of this Fusarium Mycotoxin in Food and Feed Samples. Journal of Agricultural and Food Chemistry, 2012, 60, 8350-8355.	5.2	18
31	Lae1 regulates expression of multiple secondary metabolite gene clusters in Fusarium verticillioides. Fungal Genetics and Biology, 2012, 49, 602-612.	2.1	114
32	Genetic evidence for natural productâ€mediated plantâ€"plant allelopathy in rice (Oryza sativa). New Phytologist, 2012, 193, 570-575.	7.3	146
33	The Sfp-Type 4â€²-Phosphopantetheinyl Transferase Ppt1 of Fusarium fujikuroi Controls Development, Secondary Metabolism and Pathogenicity. PLoS ONE, 2012, 7, e37519.	2.5	59
34	FfVel1 and FfLae1, components of a velvetâ€like complex in Fusarium fujikuroi, affect differentiation, secondary metabolism and virulence. Molecular Microbiology, 2010, 77, 972-994.	2.5	234
35	Biosynthesis of the red pigment bikaverin in Fusarium fujikuroi: genes, their function and regulation. Molecular Microbiology, 2009, 72, 931-946.	2.5	209