

Lena Studt

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

1,673
citations

393982

19
h-index

433756

31
g-index

34
all docs

34
docs citations

34
times ranked

1772
citing authors

#	ARTICLE	IF	CITATIONS
1	Secondary Metabolite Gene Regulation in Mycotoxigenic <i>Fusarium</i> Species: A Focus on Chromatin. <i>Toxins</i> , 2022, 14, 96.	1.5	12
2	Biosynthesis of Fusapyrone Depends on the H3K9 Methyltransferase, FmKmt1, in <i>Fusarium mangiferae</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, .	0.9	13
3	Cyclic, Hydrophobic Hexapeptide Fusahexin Is the Product of a Nonribosomal Peptide Synthetase in <i>Fusarium graminearum</i> . <i>Journal of Natural Products</i> , 2021, 84, 2070-2080.	1.5	8
4	The H4K20 methyltransferase Kmt5 is involved in secondary metabolism and stress response in phytopathogenic <i>Fusarium</i> species. <i>Fungal Genetics and Biology</i> , 2021, 155, 103602.	0.9	13
5	A novel fungal gene regulation system based on inducible VPR-dCas9 and nucleosome map-guided sgRNA positioning. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 9801-9822.	1.7	12
6	Effect of H2A.Z deletion is rescued by compensatory mutations in <i>Fusarium graminearum</i> . <i>PLoS Genetics</i> , 2020, 16, e1009125.	1.5	10
7	Evidence of a Demethylase-Independent Role for the H3K4-Specific Histone Demethylases in <i>Aspergillus nidulans</i> and <i>Fusarium graminearum</i> Secondary Metabolism. <i>Frontiers in Microbiology</i> , 2019, 10, 1759.	1.5	23
8	Fusaoctaxin A, an Example of a Two-Step Mechanism for Non-Ribosomal Peptide Assembly and Maturation in Fungi. <i>Toxins</i> , 2019, 11, 277.	1.5	17
9	The putative H3K36 demethylase BcKDM1 affects virulence, stress responses and photomorphogenesis in <i>Botrytis cinerea</i> . <i>Fungal Genetics and Biology</i> , 2019, 123, 14-24.	0.9	23
10	Regulation of a novel <i>Fusarium</i> cytokinin in <i>Fusarium pseudograminearum</i> . <i>Fungal Biology</i> , 2019, 123, 255-266.	1.1	9
11	Set1 and Kdm5 are antagonists for H3K4 methylation and regulators of the major conidiation-specific transcription factor gene <i>ABA1</i> in <i>Fusarium fujikuroi</i> . <i>Environmental Microbiology</i> , 2018, 20, 3343-3362.	1.8	38
12	High-throughput format for the phenotyping of fungi on solid substrates. <i>Scientific Reports</i> , 2017, 7, 4289.	1.6	22
13	Comparative transcriptome and proteome analysis reveals a global impact of the nitrogen regulators <i>AreA</i> and <i>AreB</i> on secondary metabolism in <i>Fusarium fujikuroi</i> . <i>PLoS ONE</i> , 2017, 12, e0176194.	1.1	35
14	Mechanistic Characterisation of Two Sesquiterpene Cyclases from the Plant Pathogenic Fungus <i>Fusarium fujikuroi</i> . <i>Angewandte Chemie - International Edition</i> , 2016, 55, 8748-8751.	7.2	63
15	Mechanistische Charakterisierung von zwei Sesquiterpen-Cyclasen aus dem phytopathogenen Pilz <i>Fusarium fujikuroi</i> . <i>Angewandte Chemie</i> , 2016, 128, 8890-8893.	1.6	19
16	Knockdown of the methyltransferase Kmt6 relieves H3K27me3 and results in induction of cryptic and otherwise silent secondary metabolite gene clusters in <i>Fusarium fujikuroi</i> . <i>Environmental Microbiology</i> , 2016, 18, 4037-4054.	1.8	109
17	Sound of silence: the beauvericin cluster in <i>Fusarium fujikuroi</i> is controlled by cluster-specific and global regulators mediated by H3K27 modification. <i>Environmental Microbiology</i> , 2016, 18, 4282-4302.	1.8	45
18	Two separate key enzymes and two pathway-specific transcription factors are involved in fusaric acid biosynthesis in <i>Fusarium fujikuroi</i> . <i>Environmental Microbiology</i> , 2016, 18, 936-956.	1.8	64

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19	Lack of the COMPASS Component Ccl1 Reduces H3K4 Trimethylation Levels and Affects Transcription of Secondary Metabolite Genes in Two Plant-Pathogenic <i>Fusarium</i> Species. <i>Frontiers in Microbiology</i> , 2016, 07, 2144.	1.5	42
20	Genetic engineering, high resolution mass spectrometry and nuclear magnetic resonance spectroscopy elucidate the bikaverin biosynthetic pathway in <i>Fusarium fujikuroi</i> . <i>Fungal Genetics and Biology</i> , 2015, 84, 26-36.	0.9	27
21	The global regulator <i>FfSge1</i> is required for expression of secondary metabolite gene clusters but not for pathogenicity in <i>Fusarium fujikuroi</i> . <i>Environmental Microbiology</i> , 2015, 17, 2690-2708.	1.8	26
22	Gibberellins and the Red Pigments Bikaverin and Fusarubin. <i>Fungal Biology</i> , 2014, , 209-238.	0.3	9
23	Genetic Manipulation of the <i>Fusarium fujikuroi</i> Fusarin Gene Cluster Yields Insight into the Complex Regulation and Fusarin Biosynthetic Pathway. <i>Chemistry and Biology</i> , 2013, 20, 1055-1066.	6.2	107
24	Signaling Governed by G Proteins and cAMP Is Crucial for Growth, Secondary Metabolism and Sexual Development in <i>Fusarium fujikuroi</i> . <i>PLoS ONE</i> , 2013, 8, e58185.	1.1	52
25	Deciphering the Cryptic Genome: Genome-wide Analyses of the Rice Pathogen <i>Fusarium fujikuroi</i> Reveal Complex Regulation of Secondary Metabolism and Novel Metabolites. <i>PLoS Pathogens</i> , 2013, 9, e1003475.	2.1	406
26	Two Histone Deacetylases, FfHda1 and FfHda2, Are Important for <i>Fusarium fujikuroi</i> Secondary Metabolism and Virulence. <i>Applied and Environmental Microbiology</i> , 2013, 79, 7719-7734.	1.4	112
27	A Functional Bikaverin Biosynthesis Gene Cluster in Rare Strains of <i>Botrytis cinerea</i> Is Positively Controlled by VELVET. <i>PLoS ONE</i> , 2013, 8, e53729.	1.1	69
28	Biosynthesis of Fusarubins Accounts for Pigmentation of <i>Fusarium fujikuroi</i> Perithecia. <i>Applied and Environmental Microbiology</i> , 2012, 78, 4468-4480.	1.4	169
29	Bioassay-guided fractionation of a thymol-deprived hydrophilic thyme extract and its antispasmodic effect. <i>Journal of Ethnopharmacology</i> , 2012, 141, 848-853.	2.0	32
30	Segregation of secondary metabolite biosynthesis in hybrids of <i>Fusarium fujikuroi</i> and <i>Fusarium proliferatum</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 567-577.	0.9	14
31	The Sfp-Type 4-Phosphopantetheinyl Transferase Ppt1 of <i>Fusarium fujikuroi</i> Controls Development, Secondary Metabolism and Pathogenicity. <i>PLoS ONE</i> , 2012, 7, e37519.	1.1	59