

# Michael Freitag

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

5,796  
citations

186265  
28  
h-index

189892  
50  
g-index

57  
all docs

57  
docs citations

57  
times ranked

5542  
citing authors

#	ARTICLE	IF	CITATIONS
1	Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic <i>Fusarium</i> that Includes the <i>Fusarium solani</i> Species Complex. <i>Phytopathology</i> , 2021, 111, 1064-1079.	2.2	107
2	Recent loss of the Dim2 DNA methyltransferase decreases mutation rate in repeats and changes evolutionary trajectory in a fungal pathogen. <i>PLoS Genetics</i> , 2021, 17, e1009448.	3.5	32
3	Comparative Genomics of Eight <i>Fusarium graminearum</i> Strains with Contrasting Aggressiveness Reveals an Expanded Open Pangenome and Extended Effector Content Signatures. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6257.	4.1	12
4	Genome compartmentalization predates species divergence in the plant pathogen genus <i>Zymoseptoria</i> . <i>BMC Genomics</i> , 2020, 21, 588.	2.8	34
5	Polycomb Repression without Bristles: Facultative Heterochromatin and Genome Stability in Fungi. <i>Genes</i> , 2020, 11, 638.	2.4	26
6	A metabolomics-guided approach to discover <i>Fusarium graminearum</i> metabolites after removal of a repressive histone modification. <i>Fungal Genetics and Biology</i> , 2019, 132, 103256.	2.1	30
7	Destabilization of chromosome structure by histone H3 lysine 27 methylation. <i>PLoS Genetics</i> , 2019, 15, e1008093.	3.5	75
8	Involvement of a G Protein Regulatory Circuit in Alternative Oxidase Production in <i>Neurospora crassa</i> . <i>G3: Genes, Genomes, Genetics</i> , 2019, 9, 3453-3465.	1.8	3
9	Application of the Cre/lox System to Construct Auxotrophic Markers for Quantitative Genetic Analyses in <i>Fusarium graminearum</i> . <i>Methods in Molecular Biology</i> , 2018, 1848, 235-263.	0.9	4
10	Velvet domain protein VosA represses the zinc cluster transcription factor SclB regulatory network for <i>Aspergillus nidulans</i> asexual development, oxidative stress response and secondary metabolism. <i>PLoS Genetics</i> , 2018, 14, e1007511.	3.5	29
11	Extraordinary Genome Instability and Widespread Chromosome Rearrangements During Vegetative Growth. <i>Genetics</i> , 2018, 210, 517-529.	2.9	103
12	Expression of a Structural Protein of the Mycovirus FgV-ch9 Negatively Affects the Transcript Level of a Novel Symptom Alleviation Factor and Causes Virus Infection-Like Symptoms in <i>Fusarium graminearum</i> . <i>Journal of Virology</i> , 2018, 92, .	3.4	18
13	Alternative Oxidase Transcription Factors AOD2 and AOD5 of <i>Neurospora crassa</i> Control the Expression of Genes Involved in Energy Production and Metabolism. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 449-466.	1.8	6
14	The <i>Neurospora</i> Transcription Factor ADV-1 Transduces Light Signals and Temporal Information to Control Rhythmic Expression of Genes Involved in Cell Fusion. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 129-142.	1.8	47
15	Structural reorganization of the fungal endoplasmic reticulum upon induction of mycotoxin biosynthesis. <i>Scientific Reports</i> , 2017, 7, 44296.	3.3	71
16	Centrochromatin of Fungi. <i>Progress in Molecular and Subcellular Biology</i> , 2017, 56, 85-109.	1.6	13
17	Omics Analyses of <i>Trichoderma reesei</i> CBS999.97 and QM6a Indicate the Relevance of Female Fertility to Carbohydrate-Active Enzyme and Transporter Levels. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	22
18	Histone Methylation by SET Domain Proteins in Fungi. <i>Annual Review of Microbiology</i> , 2017, 71, 413-439.	7.3	106

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19	A Matter of Scale and Dimensions: Chromatin of Chromosome Landmarks in the Fungi. , 2017, 5, 571-597.		18
20	Translation Initiation from Conserved Non-AUG Codons Provides Additional Layers of Regulation and Coding Capacity. MBio, 2017, 8, .	4.1	25
21	Profiling Changes in Histone Post-translational Modifications by Top-Down Mass Spectrometry. Methods in Molecular Biology, 2017, 1507, 153-168.	0.9	8
22	The kinetochore interaction network (KIN) of ascomycetes. Mycologia, 2016, 108, 485-505.	1.9	14
23	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> . Environmental Microbiology, 2016, 18, 4037-4054.	3.8	109
24	Genome-Wide Chromatin Immunoprecipitation Sequencing Analysis of the <i>Penicillium chrysogenum</i> Velvet Protein PcVelA Identifies Methyltransferase PcLlmA as a Novel Downstream Regulator of Fungal Development. MSphere, 2016, 1, .	2.9	9
25	Normal chromosome conformation depends on subtelomeric facultative heterochromatin in <i>Neurospora crassa</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15048-15053.	7.1	55
26	<i>Neurospora</i> chromosomes are organized by blocks of importin alpha-dependent heterochromatin that are largely independent of H3K9me3. Genome Research, 2016, 26, 1069-1080.	5.5	64
27	Genome-wide identification of target genes of a mating-type domain transcription factor reveals functions beyond sexual development. Molecular Microbiology, 2015, 96, 1002-1022.	2.5	45
28	Histone modifications rather than the novel regional centromeres of <i>Zygomycetes tritici</i> distinguish core and accessory chromosomes. Epigenetics and Chromatin, 2015, 8, 41.	3.9	139
29	Endogenous Small RNA Mediates Meiotic Silencing of a Novel DNA Transposon. G3: Genes, Genomes, Genetics, 2015, 5, 1949-1960.	1.8	34
30	Chromatin analyses of <i>Zygomycetes tritici</i> : Methods for chromatin immunoprecipitation followed by high-throughput sequencing (ChIP-seq). Fungal Genetics and Biology, 2015, 79, 63-70.	2.1	35
31	Genome Sequence and Annotation of <i>Trichoderma parareesei</i> , the Ancestor of the Cellulase Producer <i>Trichoderma reesei</i> . Genome Announcements, 2015, 3, .	0.8	28
32	Genome-Wide Characterization of Light-Regulated Genes in <i>Neurospora crassa</i> . G3: Genes, Genomes, Genetics, 2014, 4, 1731-1745.	1.8	82
33	Epigenetic Control of Effector Gene Expression in the Plant Pathogenic Fungus <i>Leptosphaeria maculans</i> . PLoS Genetics, 2014, 10, e1004227.	3.5	209
34	Increase in cellular triacylglycerol content and emergence of large ER-associated lipid droplets in the absence of CDP-DG synthase function. Molecular Biology of the Cell, 2014, 25, 4083-4095.	2.1	13
35	Analysis of clock-regulated genes in <i>Neurospora</i> reveals widespread posttranscriptional control of metabolic potential. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 16995-17002.	7.1	131
36	Heterochromatin Controls H2A Localization in <i>Neurospora crassa</i> . Eukaryotic Cell, 2014, 13, 990-1000.	3.4	26

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37	Variability of chromosome structure in pathogenic fungi of the <i>Ascomycota</i> and <i>Basidiomycota</i> . <i>Current Opinion in Microbiology</i> , 2014, 20, 19-26.	5.1	78
38	Thermal Stress Triggers Broad <i>Pocillopora damicornis</i> Transcriptomic Remodeling, while <i>Vibrio coralliilyticus</i> Infection Induces a More Targeted Immuno-Suppression Response. <i>PLoS ONE</i> , 2014, 9, e107672.	2.5	80
39	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.	6.0	107
40	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.	4.7	406
41	The <i>Fusarium graminearum</i> Histone H3 K27 Methyltransferase KMT6 Regulates Development and Expression of Secondary Metabolite Gene Clusters. <i>PLoS Genetics</i> , 2013, 9, e1003916.	3.5	233
42	Genome resequencing reveals multiscale geographic structure and extensive linkage disequilibrium in the forest tree <i>Populus trichocarpa</i> . <i>New Phytologist</i> , 2012, 196, 713-725.	7.3	173
43	Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , 2010, 464, 367-373.	27.8	1,442
44	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
45	The fungus <i>Neurospora crassa</i> displays telomeric silencing mediated by multiple sirtuins and by methylation of histone H3 lysine 9. <i>Epigenetics and Chromatin</i> , 2008, 1, 5.	3.9	72
46	Controlling DNA methylation: many roads to one modification. <i>Current Opinion in Genetics and Development</i> , 2005, 15, 191-199.	3.3	100
47	DNA Methylation Is Independent of RNA Interference in <i>Neurospora</i> . <i>Science</i> , 2004, 304, 1939-1939.	12.6	116
48	GFP as a tool to analyze the organization, dynamics and function of nuclei and microtubules in <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2004, 41, 897-910.	2.1	306
49	HP1 Is Essential for DNA Methylation in <i>Neurospora</i> . <i>Molecular Cell</i> , 2004, 13, 427-434.	9.7	207
50	A cytosine methyltransferase homologue is essential for repeat-induced point mutation in <i>Neurospora crassa</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8802-8807.	7.1	228
51	A Matter of Scale and Dimensions: Chromatin of Chromosome Landmarks in the Fungi. <i>Genetics</i> , 2000, 155, 571-597.		0