

Martin Münsterkötter

List of Publications by Year in descending order

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Version: 2024-02-01

53
papers

8,410
citations

109321

35
h-index

161849

54
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56
all docs

56
docs citations

56
times ranked

8815
citing authors

#	ARTICLE	IF	CITATIONS
1	Chromosomal assembly and analyses of genome-wide recombination rates in the forest pathogenic fungus <i>Armillaria ostoyae</i> . <i>Heredity</i> , 2020, 124, 699-713.	2.6	17
2	Infection cushions of <i>Fusarium graminearum</i> are fungal arsenals for wheat infection. <i>Molecular Plant Pathology</i> , 2020, 21, 1070-1087.	4.2	33
3	Chitin and chitosan remodeling defines vegetative development and <i>Trichoderma</i> biocontrol. <i>PLoS Pathogens</i> , 2020, 16, e1008320.	4.7	38
4	Towards the Biological Control of Devastating Forest Pathogens from the Genus <i>Armillaria</i> . <i>Forests</i> , 2019, 10, 1013.	2.1	28
5	Genome analysis of a <i>Bacillus subtilis</i> strain reveals genetic mutations determining biocontrol properties. <i>World Journal of Microbiology and Biotechnology</i> , 2019, 35, 52.	3.6	17
6	Analysis of the global regulator <i>Lae1</i> uncovers a connection between <i>Lae1</i> and the histone acetyltransferase <i>HAT1</i> in <i>Fusarium fujikuroi</i> . <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 279-295.	3.6	39
7	Comparative genomic and transcriptomic analyses unveil novel features of azole resistance and adaptation to the human host in <i>Candida glabrata</i> . <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	28
8	Elucidation of the Two H3K36me3 Histone Methyltransferases <i>Set2</i> and <i>Ash1</i> in <i>Fusarium fujikuroi</i> Unravels Their Different Chromosomal Targets and a Major Impact of <i>Ash1</i> on Genome Stability. <i>Genetics</i> , 2018, 208, 153-171.	2.9	61
9	A New Reference Genome Shows the One-Speed Genome Structure of the Barley Pathogen <i>Ramularia collo-cygni</i> . <i>Genome Biology and Evolution</i> , 2018, 10, 3243-3249.	2.5	30
10	The <i>Gpr1</i> -regulated <i>Sur7</i> family protein <i>Sfp2</i> is required for hyphal growth and cell wall stability in the mycoparasite <i>Trichoderma atroviride</i> . <i>Scientific Reports</i> , 2018, 8, 12064.	3.3	25
11	Production and Role of Hormones During Interaction of <i>Fusarium</i> Species With Maize (<i>Zea mays</i> L.) Seedlings. <i>Frontiers in Plant Science</i> , 2018, 9, 1936.	3.6	30
12	Genome sequence of the highly weak-acid-tolerant <i>Zygosaccharomyces bailii</i> IST302, amenable to genetic manipulations and physiological studies. <i>FEMS Yeast Research</i> , 2017, 17, .	2.3	20
13	Genome expansion and lineage-specific genetic innovations in the forest pathogenic fungi <i>Armillaria</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1931-1941.	7.8	145
14	High-density genetic mapping identifies the genetic basis of a natural colony morphology mutant in the root rot pathogen <i>Armillaria ostoyae</i> . <i>Fungal Genetics and Biology</i> , 2017, 108, 44-54.	2.1	7
15	The GATA-Type Transcription Factor <i>Csm1</i> Regulates Conidiation and Secondary Metabolism in <i>Fusarium fujikuroi</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1175.	3.5	35
16	Comparative genomics of geographically distant <i>Fusarium fujikuroi</i> isolates revealed two distinct pathotypes correlating with secondary metabolite profiles. <i>PLoS Pathogens</i> , 2017, 13, e1006670.	4.7	58
17	A complete toolset for the study of <i>Ustilago bromivora</i> and <i>Brachypodium</i> sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016, 5, .	6.0	49
18	Comparison of <i>Fusarium graminearum</i> Transcriptomes on Living or Dead Wheat Differentiates Substrate-Responsive and Defense-Responsive Genes. <i>Frontiers in Microbiology</i> , 2016, 7, 1113.	3.5	48

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19	Comparative Genomics of the <i>Fusarium fujikuroi</i> Species Complex Highlights Differences in Genetic Potential and Metabolite Synthesis. <i>Genome Biology and Evolution</i> , 2016, 8, 3574-3599.	2.5	124
20	Comparative genomics to explore phylogenetic relationship, cryptic sexual potential and host specificity of <i>Rhynchosporium</i> species on grasses. <i>BMC Genomics</i> , 2016, 17, 953.	2.8	33
21	Globally distributed root endophyte <i>Phialocephala subalpina</i> links pathogenic and saprophytic lifestyles. <i>BMC Genomics</i> , 2016, 17, 1015.	2.8	54
22	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. <i>Genome Biology and Evolution</i> , 2016, 8, 681-704.	2.5	125
23	<i>Hxt1</i> , a monosaccharide transporter and sensor required for virulence of the maize pathogen <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2015, 206, 1086-1100.	7.3	55
24	Molecular analysis of <i>Coxiella burnetii</i> in Germany reveals evolution of unique clonal clusters. <i>International Journal of Medical Microbiology</i> , 2014, 304, 868-876.	3.6	36
25	The Genome Sequence of the Highly Acetic Acid-Tolerant <i>Zygosaccharomyces bailii</i> -Derived Interspecies Hybrid Strain ISA1307, Isolated From a Sparkling Wine Plant. <i>DNA Research</i> , 2014, 21, 299-313.	3.4	62
26	The <i>Fusarium graminearum</i> Genome Reveals More Secondary Metabolite Gene Clusters and Hints of Horizontal Gene Transfer. <i>PLoS ONE</i> , 2014, 9, e110311.	2.5	124
27	Analysis of the <i>Elodea nuttallii</i> Transcriptome in Response to Mercury and Cadmium Pollution: Development of Sensitive Tools for Rapid Ecotoxicological Testing. <i>Environmental Science & Technology</i> , 2013, 47, 8825-8834.	10.0	41
28	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
29	Looking for biomarkers of Hg exposure by transcriptome analysis in the aquatic plant <i>Elodea nuttallii</i> . <i>E3S Web of Conferences</i> , 2013, 1, 29004.	0.5	0
30	Genome Comparison of Barley and Maize Smut Fungi Reveals Targeted Loss of RNA Silencing Components and Species-Specific Presence of Transposable Elements. <i>Plant Cell</i> , 2012, 24, 1733-1745.	6.6	159
31	FGDB: revisiting the genome annotation of the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2011, 39, D637-D639.	14.5	81
32	Transcriptome responses to aluminum stress in roots of aspen (<i>Populus tremula</i>). <i>BMC Plant Biology</i> , 2010, 10, 185.	3.6	48
33	Pathogenicity Determinants in Smut Fungi Revealed by Genome Comparison. <i>Science</i> , 2010, 330, 1546-1548.	12.6	301
34	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	14.5	97
35	The posttranscriptional machinery of <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, S40-S46.	2.1	29
36	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2007, 36, D196-D201.	14.5	156

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37	The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402.	12.6	837
38	The fungus <i>Ustilago maydis</i> and humans share disease-related proteins that are not found in <i>Saccharomyces cerevisiae</i> . <i>BMC Genomics</i> , 2007, 8, 473.	2.8	15
39	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	27.8	1,113
40	FGDB: a comprehensive fungal genome resource on the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2006, 34, D456-D458.	14.5	77
41	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D169-D172.	14.5	348
42	MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006, 34, D436-D441.	14.5	305
43	The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004, 32, 5539-5545.	14.5	988
44	MitoP2, an integrated database on mitochondrial proteins in yeast and man. <i>Nucleic Acids Research</i> , 2004, 32, 459D-462.	14.5	75
45	MIPS: analysis and annotation of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004, 32, 41D-44.	14.5	522
46	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2004, 33, D364-D368.	14.5	288
47	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003, 31, 1121-1135.	14.5	118
48	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 2002, 30, 31-34.	14.5	724
49	Systematic analysis of sporulation phenotypes in 624 non-lethal homozygous deletion strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2002, 19, 403-422.	1.7	51
50	Transcriptional Regulation of the Yeast PHO8 Promoter in Comparison to the Coregulated PHO5 Promoter. <i>Journal of Biological Chemistry</i> , 2000, 275, 22678-22685.	3.4	27
51	Chromatin remodelling at the PHO8 promoter requires SWI5 and SAGA at a step subsequent to activator binding. <i>EMBO Journal</i> , 1999, 18, 6407-6414.	7.8	117
52	Cooperative Pho2-Pho4 Interactions at the PHO5 Promoter Are Critical for Binding of Pho4 to UASp1 and for Efficient Transactivation by Pho4 at UASp2. <i>Molecular and Cellular Biology</i> , 1998, 18, 2629-2639.	2.3	68
53	The Homeodomain Protein Pho2 and the Basic-Helix-Loop-Helix Protein Pho4 Bind DNA Cooperatively at the Yeast PHO5 Promoter. <i>Nucleic Acids Research</i> , 1996, 24, 4479-4486.	14.5	68