

Martin Munsterkötter

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.

54
papers

6,741
citations

32
h-index

56
g-index

56
ext. papers

7,869
ext. citations

10.7
avg, IF

4.74
L-index

#	Paper	IF	Citations
54	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	3.6	7
53	Infection cushions of <i>Fusarium graminearum</i> are fungal arsenals for wheat infection. <i>Molecular Plant Pathology</i> , 2020 , 21, 1070-1087	5.7	14
52	Chitin and chitosan remodeling defines vegetative development and <i>Trichoderma</i> biocontrol. <i>PLoS Pathogens</i> , 2020 , 16, e1008320	7.6	16
51	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	4.4	9
50	Towards the Biological Control of Devastating Forest Pathogens from the Genus <i>Armillaria</i> . <i>Forests</i> , 2019 , 10, 1013	2.8	13
49	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	5.7	17
48	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,	3.1	21
47	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	4.9	17
46	Production and Role of Hormones During Interaction of Species With Maize (L.) Seedlings. <i>Frontiers in Plant Science</i> , 2018 , 9, 1936	6.2	20
45	Elucidation of the Two H3K36me3 Histone Methyltransferases <i>Set2</i> and <i>Ash1</i> in Unravels Their Different Chromosomal Targets and a Major Impact of <i>Ash1</i> on Genome Stability. <i>Genetics</i> , 2018 , 208, 153-171	4	40
44	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	3.9	12
43	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,	3.1	11
42	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	12.3	85
41	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	7.6	39
40	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	3.9	3
39	The GATA-Type Transcription Factor <i>Csm1</i> Regulates Conidiation and Secondary Metabolism in. <i>Frontiers in Microbiology</i> , 2017 , 8, 1175	5.7	26
38	A Tale of Genome Compartmentalization: The Evolution of Virulence Clusters in Smut Fungi. <i>Genome Biology and Evolution</i> , 2016 , 8, 681-704	3.9	85

37	A complete toolset for the study of and sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016 , 5,	8.9	36
36	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	5.7	20
35	Comparative "Omics" 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	3.9	81
34	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	4.5	21
33	Globally distributed root endophyte <i>Phialocephala subalpina</i> links pathogenic and saprophytic lifestyles. <i>BMC Genomics</i> , 2016 , 17, 1015	4.5	28
32	Hxt1, a monosaccharide transporter and sensor required for virulence of the maize pathogen <i>Ustilago maydis</i> . <i>New Phytologist</i> , 2015 , 206, 1086-1100	9.8	39
31	Molecular analysis of <i>Coxiella burnetii</i> in Germany reveals evolution of unique clonal clusters. <i>International Journal of Medical Microbiology</i> , 2014 , 304, 868-76	3.7	24
30	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	4.5	39
29	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	3.7	80
28	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, 8825-34	10.3	38
27	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	7.6	321
26	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	
25	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, 1733-45	11.6	125
24	FGDB: revisiting the genome annotation of the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2011 , 39, D637-9	20.1	73
23	Pathogenicity determinants in smut fungi revealed by genome comparison. <i>Science</i> , 2010 , 330, 1546-8	33.3	249
22	Transcriptome responses to aluminum stress in roots of aspen (<i>Populus tremula</i>). <i>BMC Plant Biology</i> , 2010 , 10, 185	5.3	43
21	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009 , 37, D408-11	20.1	85
20	The posttranscriptional machinery of <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2008 , 45 Suppl 1, S40-6	3.9	27

19	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D196-2010.1	10.1	123
18	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	4.5	11
17	The <i>Fusarium graminearum</i> genome reveals a link between localized polymorphism and pathogen specialization. <i>Science</i> , 2007 , 317, 1400-2	33.3	668
16	FGDB: a comprehensive fungal genome resource on the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2006 , 34, D456-8	20.1	69
15	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D169-72	20.1	278
14	MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006 , 34, D436-41	20.1	280
13	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006 , 444, 97-101	50.4	867
12	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2005 , 33, D364-8	20.1	242
11	The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004 , 32, 5539-45	20.1	862
10	MitoP2, an integrated database on mitochondrial proteins in yeast and man. <i>Nucleic Acids Research</i> , 2004 , 32, D459-62	20.1	68
9	MIPS: analysis and annotation of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004 , 32, D41-4	20.1	430
8	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003 , 31, 1121-35	20.1	101
7	Systematic analysis of sporulation phenotypes in 624 non-lethal homozygous deletion strains of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2002 , 19, 403-22	3.4	42
6	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 2002 , 30, 31-4	20.1	655
5	Transcriptional regulation of the yeast PHO8 promoter in comparison to the coregulated PHO5 promoter. <i>Journal of Biological Chemistry</i> , 2000 , 275, 22678-85	5.4	24
4	Chromatin remodelling at the PHO8 promoter requires SWI-SNF and SAGA at a step subsequent to activator binding. <i>EMBO Journal</i> , 1999 , 18, 6407-14	13	113
3	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, 2629-39	4.8	61
2	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, 4479-86	20.1	59

- 1 Natriumdinitridoborat mit dem linear gebauten, symmetrischen BN_2B^- Anion. *Journal of the Less Common Metals*, **1990**, 162, L17-L22