

Martin Munsterkotter

List of Publications by Citations

Source: <https://exaly.com/author-pdf/2415522/martin-munsterkotter-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006 , 444, 97-101	50.4	867
53	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
52	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
51	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 2002 , 30, 31-4	20.1	655
50	MIPS: analysis and annotation of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004 , 32, D41-4	20.1	430
49	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
48	MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006 , 34, D436-41	20.1	280
47	MIPS: analysis and annotation of proteins from whole genomes in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D169-72	20.1	278
46	Pathogenicity determinants in smut fungi revealed by genome comparison. <i>Science</i> , 2010 , 330, 1546-8	33.3	249
45	CYGD: the Comprehensive Yeast Genome Database. <i>Nucleic Acids Research</i> , 2005 , 33, D364-8	20.1	242
44	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
43	MIPS: analysis and annotation of genome information in 2007. <i>Nucleic Acids Research</i> , 2008 , 36, D196-201	20.1	123
42	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
41	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003 , 31, 1121-35	20.1	101
40	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
39	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
38	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009 , 37, D408-11	20.1	85

37	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
36	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
35	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
34	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
33	MitoP2, an integrated database on mitochondrial proteins in yeast and man. <i>Nucleic Acids Research</i> , 2004 , 32, D459-62	20.1	68
32	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	4.8	61
31	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
30	Transcriptome responses to aluminum stress in roots of aspen (<i>Populus tremula</i>). <i>BMC Plant Biology</i> , 2010 , 10, 185	5.3	43
29	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
28	Elucidation of the Two H3K36me3 Histone Methyltransferases Set2 and Ash1 in Unravels Their Different Chromosomal Targets and a Major Impact of Ash1 on Genome Stability. <i>Genetics</i> , 2018 , 208, 153-171	4	40
27	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
26	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
25	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
24	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
23	A complete toolset for the study of and sp. as a fungal-temperate grass pathosystem. <i>ELife</i> , 2016 , 5,	8.9	36
22	Globally distributed root endophyte <i>Phialocephala subalpina</i> links pathogenic and saprophytic lifestyles. <i>BMC Genomics</i> , 2016 , 17, 1015	4.5	28
21	The posttranscriptional machinery of <i>Ustilago maydis</i> . <i>Fungal Genetics and Biology</i> , 2008 , 45 Suppl 1, S40-6	3.9	27
20	The GATA-Type Transcription Factor Csm1 Regulates Conidiation and Secondary Metabolism in. <i>Frontiers in Microbiology</i> , 2017 , 8, 1175	5.7	26

19	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
18	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
17	Natriumdinitridoborat mit dem linear gebauten, symmetrischen BN ₂₃ -Anion. <i>Journal of the Less Common Metals</i> , 1990 , 162, L17-L22		23
16	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
15	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
14	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
13	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
12	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
11	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
10	Chitin and chitosan remodeling defines vegetative development and <i>Trichoderma</i> biocontrol. <i>PLoS Pathogens</i> , 2020 , 16, e1008320	7-6	16
9	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
8	Towards the Biological Control of Devastating Forest Pathogens from the Genus <i>Armillaria</i> . <i>Forests</i> , 2019 , 10, 1013	2.8	13
7	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
6	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
5	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
4	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
3	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
2	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

- 1 Looking for biomarkers of Hg exposure by transcriptome analysis in the aquatic plant *Elodea nuttallii*. *E3S Web of Conferences*, **2013**, 1, 29004 0.5