

Ulrich GÃ¼ldener

List of Publications by Year in descending order

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69

papers

16,377

citations

81900

39

h-index

95266

68

g-index

77

all docs

77

docs citations

77

times ranked

16529

citing authors

#	ARTICLE	IF	CITATIONS
1	Transcriptome-wide association study of coronary artery disease identifies novel susceptibility genes. Basic Research in Cardiology, 2022, 117, 6.	5.9	22
2	Genetically determined intelligence and coronary artery disease risk. Clinical Research in Cardiology, 2021, 110, 211-219.	3.3	19
3	Genome sequencing, annotation and exploration of the SO ₂ -tolerant non-conventional yeast <i>Saccharomyces ludwigii</i> . BMC Genomics, 2021, 22, 131.	2.8	5
4	Identification and Functional Characterization of the Gene Cluster Responsible for Fusaproliferin Biosynthesis in <i>Fusarium proliferatum</i> . Toxins, 2021, 13, 468.	3.4	8
5	Vascular Tissue Specific miRNA Profiles Reveal Novel Correlations with Risk Factors in Coronary Artery Disease. Biomolecules, 2021, 11, 1683.	4.0	14
6	Polygenic risk for coronary artery disease in the Scottish and English population. BMC Cardiovascular Disorders, 2021, 21, 586.	1.7	6
7	Functional investigation of the coronary artery disease gene SVEP1. Basic Research in Cardiology, 2020, 115, 67.	5.9	25
8	Infection cushions of <i>Fusarium graminearum</i> are fungal arsenals for wheat infection. Molecular Plant Pathology, 2020, 21, 1070-1087.	4.2	33
9	Two Is Better Than One: Studying <i>Ustilago bromivora</i> <i>Brachypodium</i> Compatibility by Using a Hybrid Pathogen. Molecular Plant-Microbe Interactions, 2019, 32, 1623-1634.	2.6	3
10	Biochemical Characterization of the <i>Fusarium graminearum</i> Candidate ACC-Deaminases and Virulence Testing of Knockout Mutant Strains. Frontiers in Plant Science, 2019, 10, 1072.	3.6	9
11	Genome sequence of the non-conventional wine yeast <i>Hanseniaspora guilliermondii</i> UTAD222 unveils relevant traits of this species and of the <i>Hanseniaspora</i> genus in the context of wine fermentation. DNA Research, 2019, 26, 67-83.	3.4	48
12	The "PhenoBox"™, a flexible, automated, open-source plant phenotyping solution. New Phytologist, 2018, 219, 808-823.	7.3	44
13	Analysis of the global regulator Lae1 uncovers a connection between Lae1 and the histone acetyltransferase HAT1 in <i>Fusarium fujikuroi</i> . Applied Microbiology and Biotechnology, 2018, 102, 279-295.	3.6	39
14	Comparative genomic and transcriptomic analyses unveil novel features of azole resistance and adaptation to the human host in <i>Candida glabrata</i> . FEMS Yeast Research, 2018, 18, .	2.3	28
15	Elucidation of the Two H3K36me3 Histone Methyltransferases Set2 and Ash1 in <i>Fusarium fujikuroi</i> Unravels Their Different Chromosomal Targets and a Major Impact of Ash1 on Genome Stability. Genetics, 2018, 208, 153-171.	2.9	61
16	Genome Sequence of the Wine Yeast <i>Saccharomyces ludwigii</i> UTAD17. Microbiology Resource Announcements, 2018, 7, .	0.6	5
17	A New Reference Genome Shows the One-Speed Genome Structure of the Barley Pathogen <i>Ramularia collo-cygni</i> . Genome Biology and Evolution, 2018, 10, 3243-3249.	2.5	30
18	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> . Environmental Microbiology, 2018, 20, 3343-3362.	3.8	38

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19	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
20	Genome Sequence of the Nonconventional Wine Yeast <i>Hanseniaspora guilliermondii</i> UTAD222. <i>Genome Announcements</i> , 2017, 5, .	0.8	9
21	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
22	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
23	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
24	The GATA-Type Transcription Factor Csm1 Regulates Conidiation and Secondary Metabolism in <i>Fusarium fujikuroi</i> . <i>Frontiers in Microbiology</i> , 2017, 8, 1175.	3.5	35
25	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
26	Comparative transcriptome and proteome analysis reveals a global impact of the nitrogen regulators AreA and AreB on secondary metabolism in <i>Fusarium fujikuroi</i> . <i>PLoS ONE</i> , 2017, 12, e0176194.	2.5	35
27	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
28	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
29	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.	2.5	124
30	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
31	Globally distributed root endophyte <i>Phialocephala subalpina</i> links pathogenic and saprophytic lifestyles. <i>BMC Genomics</i> , 2016, 17, 1015.	2.8	54
32	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
33	<i>Fusarium</i> Mycotoxins and Their Role in Plant-Pathogen Interactions. <i>Fungal Biology</i> , 2015, , 199-233.	0.6	13
34	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.	3.8	26
35	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
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.	2.5	124

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37	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
38	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
39	Plant-Symbiotic Fungi as Chemical Engineers: Multi-Genome Analysis of the <i>Clavicipitaceae</i> Reveals Dynamics of Alkaloid Loci. <i>PLoS Genetics</i> , 2013, 9, e1003323.	3.5	344
40	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
41	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	3.5	902
42	Endophytic Life Strategies Decoded by Genome and Transcriptome Analyses of the Mutualistic Root Symbiont <i>Piriformospora indica</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002290.	4.7	361
43	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
44	Transcriptome analysis of nitrate assimilation in <i>Aspergillus nidulans</i> reveals connections to nitric oxide metabolism. <i>Molecular Microbiology</i> , 2010, 78, 720-738.	2.5	78
45	Pathogenicity Determinants in Smut Fungi Revealed by Genome Comparison. <i>Science</i> , 2010, 330, 1546-1548.	12.6	301
46	PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411.	14.5	97
47	Conidial germination in the filamentous fungus <i>Fusarium graminearum</i> . <i>Fungal Genetics and Biology</i> , 2008, 45, 389-399.	2.1	180
48	Gene expression shifts during perithecial development in <i>Gibberella zeae</i> (anamorph <i>Fusarium</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 344, 1146-1156.	2.1	103
49	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
50	Gene Disruption in the Budding Yeast <i>Saccharomyces cerevisiae</i> . , 2006, 313, 129-144.		28
51	Development of a <i>Fusarium graminearum</i> Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. <i>Fungal Genetics and Biology</i> , 2006, 43, 316-325.	2.1	164
52	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
53	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
54	MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006, 34, D436-D441.	14.5	305

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55	The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. Nucleic Acids Research, 2004, 32, 5539-5545.	14.5	988
56	Characterization of the <i>Saccharomyces cerevisiae</i> Fol1 Protein: Starvation for C1 Carrier Induces Pseudohyphal Growth. Molecular Biology of the Cell, 2004, 15, 3811-3828.	2.1	39
57	MIPS: analysis and annotation of proteins from whole genomes. Nucleic Acids Research, 2004, 32, 41D-44.	14.5	522
58	CYGD: the Comprehensive Yeast Genome Database. Nucleic Acids Research, 2004, 33, D364-D368.	14.5	288
59	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. Nucleic Acids Research, 2003, 31, 1121-1135.	14.5	118
60	A second set of loxP marker cassettes for Cre-mediated multiple gene knockouts in budding yeast. Nucleic Acids Research, 2002, 30, 23e-23.	14.5	855
61	MIPS: a database for genomes and protein sequences. Nucleic Acids Research, 2002, 30, 31-34.	14.5	724
62	Functional profiling of the <i>Saccharomyces cerevisiae</i> genome. Nature, 2002, 418, 387-391.	27.8	3,938
63	Molecular Analysis of the <i>Saccharomyces cerevisiae</i> YHR076w Gene. IUBMB Life, 2000, 50, 371-377.	3.4	9
64	Functional analysis of 150 deletion mutants in <i>Saccharomyces cerevisiae</i> by a systematic approach. Molecular Genetics and Genomics, 1999, 262, 683-702.	2.4	143
65	A fast method to diagnose chromosome and plasmid loss in <i>Saccharomyces cerevisiae</i> strains. , 1999, 15, 1009-1019.		19
66	Systematic analysis of <i>S. cerevisiae</i> chromosome VIII genes. Yeast, 1999, 15, 1775-1796.	1.7	42
67	The nucleotide sequence of <i>Saccharomyces cerevisiae</i> chromosome XIV and its evolutionary implications. Nature, 1997, 387, 93-98.	27.8	65
68	Sequence Analysis of the 33â€‰kb Long Region Between ORC5 and SUI1 from the Left Arm of Chromosome XIV from <i>Saccharomyces cerevisiae</i> . , 1997, 13, 849-860.		9
69	A new efficient gene disruption cassette for repeated use in budding yeast. Nucleic Acids Research, 1996, 24, 2519-2524.	14.5	1,512