

Robin A Ohm

List of Publications by Year in descending order

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69
papers

10,396
citations

66343

42
h-index

98798

67
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78
all docs

78
docs citations

78
times ranked

10042
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	12.6	1,424
2	MycoCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	14.5	1,187
3	Convergent losses of decay mechanisms and rapid turnover of symbiosis genes in mycorrhizal mutualists. <i>Nature Genetics</i> , 2015, 47, 410-415.	21.4	870
4	Diverse Lifestyles and Strategies of Plant Pathogenesis Encoded in the Genomes of Eighteen Dothideomycetes Fungi. <i>PLoS Pathogens</i> , 2012, 8, e1003037.	4.7	595
5	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	17.5	490
6	The Genome Portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012, 40, D26-D32.	14.5	439
7	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
8	Comparative genomics of biotechnologically important yeasts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9882-9887.	7.1	302
9	Genome sequencing of four <i>Aureobasidium pullulans</i> varieties: biotechnological potential, stress tolerance, and description of new species. <i>BMC Genomics</i> , 2014, 15, 549.	2.8	262
10	Large-scale genome sequencing of mycorrhizal fungi provides insights into the early evolution of symbiotic traits. <i>Nature Communications</i> , 2020, 11, 5125.	12.8	258
11	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
12	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. <i>PLoS Genetics</i> , 2012, 8, e1003088.	3.5	226
13	Comparative Genomics of Early-Diverging Mushroom-Forming Fungi Provides Insights into the Origins of Lignocellulose Decay Capabilities. <i>Molecular Biology and Evolution</i> , 2016, 33, 959-970.	8.9	213
14	Megaphylogeny resolves global patterns of mushroom evolution. <i>Nature Ecology and Evolution</i> , 2019, 3, 668-678.	7.8	187
15	Comparative genomics and transcriptomics depict ericoid mycorrhizal fungi as versatile saprotrophs and plant mutualists. <i>New Phytologist</i> , 2018, 217, 1213-1229.	7.3	185
16	Phylogenomic Analyses Indicate that Early Fungi Evolved Digesting Cell Walls of Algal Ancestors of Land Plants. <i>Genome Biology and Evolution</i> , 2015, 7, 1590-1601.	2.5	175
17	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
18	Ectomycorrhizal ecology is imprinted in the genome of the dominant symbiotic fungus <i>Cenococcum geophilum</i> . <i>Nature Communications</i> , 2016, 7, 12662.	12.8	156

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19	Comparative genomics of <i>Mortierella elongata</i> and its bacterial endosymbiont <i>Mycoavidus cysteinexigens</i> . <i>Environmental Microbiology</i> , 2017, 19, 2964-2983.	3.8	154
20	Evolution of novel wood decay mechanisms in Agaricales revealed by the genome sequences of <i>Fistulina hepatica</i> and <i>Cylindrobasidium torrendii</i> . <i>Fungal Genetics and Biology</i> , 2015, 76, 78-92.	2.1	141
21	Comparative genomics provides insights into the lifestyle and reveals functional heterogeneity of dark septate endophytic fungi. <i>Scientific Reports</i> , 2018, 8, 6321.	3.3	138
22	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	2.1	133
23	Latent homology and convergent regulatory evolution underlies the repeated emergence of yeasts. <i>Nature Communications</i> , 2014, 5, 4471.	12.8	133
24	Transcription factor genes of <i>Schizophyllum commune</i> involved in regulation of mushroom formation. <i>Molecular Microbiology</i> , 2011, 81, 1433-1445.	2.5	127
25	Transcriptomic atlas of mushroom development reveals conserved genes behind complex multicellularity in fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7409-7418.	7.1	115
26	Prevalence of transcription factors in ascomycete and basidiomycete fungi. <i>BMC Genomics</i> , 2014, 15, 214.	2.8	114
27	Gene expression during zombie ant biting behavior reflects the complexity underlying fungal parasitic behavioral manipulation. <i>BMC Genomics</i> , 2015, 16, 620.	2.8	107
28	Genomics of wood-degrading fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 82-90.	2.1	103
29	Transcription Factor Amr1 Induces Melanin Biosynthesis and Suppresses Virulence in <i>Alternaria brassicicola</i> . <i>PLoS Pathogens</i> , 2012, 8, e1002974.	4.7	91
30	Fungi Contribute Critical but Spatially Varying Roles in Nitrogen and Carbon Cycling in Acid Mine Drainage. <i>Frontiers in Microbiology</i> , 2016, 7, 238.	3.5	66
31	The blue light receptor complex $WC\frac{1}{2}$ of <i>Schizophyllum commune</i> is involved in mushroom formation and protection against phototoxicity. <i>Environmental Microbiology</i> , 2013, 15, 943-955.	3.8	64
32	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3451-3456.	7.1	63
33	Genomics and Transcriptomics Analyses of the Oil-Accumulating Basidiomycete Yeast <i>Trichosporon oleaginosus</i> : Insights into Substrate Utilization and Alternative Evolutionary Trajectories of Fungal Mating Systems. <i>MBio</i> , 2015, 6, e00918.	4.1	63
34	Entomotoxic and nematotoxic lectins and protease inhibitors from fungal fruiting bodies. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 91-111.	3.6	60
35	Heterogenic expression of genes encoding secreted proteins at the periphery of <i>Aspergillus niger</i> colonies. <i>Environmental Microbiology</i> , 2011, 13, 216-225.	3.8	58
36	Fungal-specific transcription factor <i>AbP2</i> activates pathogenicity in <i>Alternaria brassicicola</i> . <i>Plant Journal</i> , 2013, 75, 498-514.	5.7	58

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37	Genome-Wide Analysis of <i>Corynespora cassicola</i> Leaf Fall Disease Putative Effectors. <i>Frontiers in Microbiology</i> , 2018, 9, 276.	3.5	58
38	Inactivation of <i>ku80</i> in the mushroom-forming fungus <i>Schizophyllum commune</i> increases the relative incidence of homologous recombination. <i>FEMS Microbiology Letters</i> , 2010, 310, 91-95.	1.8	54
39	Transposable Element Dynamics among Asymbiotic and Ectomycorrhizal <i>Amanita</i> Fungi. <i>Genome Biology and Evolution</i> , 2014, 6, 1564-1578.	2.5	54
40	Genomics and Development of <i>Lentinus tigrinus</i> : A White-Rot Wood-Decaying Mushroom with Dimorphic Fruiting Bodies. <i>Genome Biology and Evolution</i> , 2018, 10, 3250-3261.	2.5	53
41	Genome sequencing provides insight into the reproductive biology, nutritional mode and ploidy of the fern pathogen <i>Melampsora osmundae</i> . <i>New Phytologist</i> , 2014, 202, 554-564.	7.3	52
42	Ant-infecting <i>Ophiocordyceps</i> genomes reveal a high diversity of potential behavioral manipulation genes and a possible major role for enterotoxins. <i>Scientific Reports</i> , 2017, 7, 12508.	3.3	52
43	High-throughput targeted gene deletion in the model mushroom <i>Schizophyllum commune</i> using pre-assembled Cas9 ribonucleoproteins. <i>Scientific Reports</i> , 2019, 9, 7632.	3.3	50
44	Nucleus-specific expression in the multinuclear mushroom-forming fungus <i>Agaricus bisporus</i> reveals different nuclear regulatory programs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4429-4434.	7.1	48
45	Maturation of conidia on conidiophores of <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2017, 98, 61-70.	2.1	43
46	An efficient gene deletion procedure for the mushroom-forming basidiomycete <i>Schizophyllum commune</i> . <i>World Journal of Microbiology and Biotechnology</i> , 2010, 26, 1919-1923.	3.6	41
47	A Zinc-Finger-Family Transcription Factor, <i>AbVf19</i> , Is Required for the Induction of a Gene Subset Important for Virulence in <i>Alternaria brassicicola</i> . <i>Molecular Plant-Microbe Interactions</i> , 2012, 25, 443-452.	2.6	41
48	The role of homeodomain transcription factors in fungal development. <i>Fungal Biology Reviews</i> , 2018, 32, 219-230.	4.7	33
49	Genetic Underpinnings of Host Manipulation by <i>Ophiocordyceps</i> as Revealed by Comparative Transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2020, 10, 2275-2296.	1.8	33
50	Lipid Metabolic Versatility in <i>Malassezia</i> spp. Yeasts Studied through Metabolic Modeling. <i>Frontiers in Microbiology</i> , 2017, 8, 1772.	3.5	31
51	Draft Genome Sequence of the Animal and Human Pathogen <i>Malassezia pachydermatis</i> Strain CBS 1879. <i>Genome Announcements</i> , 2015, 3, .	0.8	30
52	The FlbA-regulated predicted transcription factor Fum21 of <i>Aspergillus niger</i> is involved in fumonisin production. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 311-322.	1.7	24
53	Genomic and Biochemical Analysis of N Glycosylation in the Mushroom-Forming Basidiomycete <i>Schizophyllum commune</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 4648-4652.	3.1	20
54	<i>Coprinopsis cinerea</i> intracellular lactonases hydrolyze quorum sensing molecules of Gram-negative bacteria. <i>Fungal Genetics and Biology</i> , 2017, 102, 49-62.	2.1	19

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55	Impact of maturation and growth temperature on cell-size distribution, heat-resistance, compatible solute composition and transcription profiles of <i>Penicillium roqueforti</i> conidia. <i>Food Research International</i> , 2020, 136, 109287.	6.2	18
56	H3K4me2 ChIP-Seq reveals the epigenetic landscape during mushroom formation and novel developmental regulators of <i>Schizophyllum commune</i> . <i>Scientific Reports</i> , 2021, 11, 8178.	3.3	13
57	Telomere-to-telomere assembled and centromere annotated genomes of the two main subspecies of the button mushroom <i>Agaricus bisporus</i> reveal especially polymorphic chromosome ends. <i>Scientific Reports</i> , 2020, 10, 14653.	3.3	12
58	Expression profile analysis reveals that <i>Aspergillus fumigatus</i> but not <i>Aspergillus niger</i> makes type II epithelial lung cells less immunological alert. <i>BMC Genomics</i> , 2018, 19, 534.	2.8	11
59	Transcriptional Responses of the Bdtf1-Deletion Mutant to the Phytoalexin Brassinin in the Necrotrophic Fungus <i>Alternaria brassicicola</i> . <i>Molecules</i> , 2014, 19, 10717-10732.	3.8	10
60	The Transcription Factor Roc1 Is a Key Regulator of Cellulose Degradation in the Wood-Decaying Mushroom <i>Schizophyllum commune</i> . <i>MBio</i> , 2022, 13, .	4.1	10
61	First evidence of cholinesterase-like activity in Basidiomycota. <i>PLoS ONE</i> , 2019, 14, e0216077.	2.5	9
62	FlbA-Regulated Gene <i>rpnR</i> Is Involved in Stress Resistance and Impacts Protein Secretion when <i>Aspergillus niger</i> Is Grown on Xylose. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	9
63	Degradative Capacity of Two Strains of <i>Rhodonía placenta</i> : From Phenotype to Genotype. <i>Frontiers in Microbiology</i> , 2020, 11, 1338.	3.5	9
64	Cycling in degradation of organic polymers and uptake of nutrients by a litter-degrading fungus. <i>Environmental Microbiology</i> , 2021, 23, 224-238.	3.8	6
65	Genome sequences of 24 <i>Aspergillus niger sensu stricto</i> strains to study strain diversity, heterokaryon compatibility, and sexual reproduction. <i>G3: Genes, Genomes, Genetics</i> , 0, , .	1.8	4
66	High sorbic acid resistance of <i>Penicillium roqueforti</i> is mediated by the SORBUS gene cluster. <i>PLoS Genetics</i> , 2022, 18, e1010086.	3.5	4
67	Production of β -1,3-L-arabinofuranosidase active on substituted xylan does not improve compost degradation by <i>Agaricus bisporus</i> . <i>PLoS ONE</i> , 2018, 13, e0201090.	2.5	3
68	9 Fungal Genomics. , 2020, , 207-224.		0
69	Targeted gene knock-in reduces variation between transformants in the mushroom-forming fungus <i>Schizophyllum commune</i> . <i>Open Research Europe</i> , 0, 1, 140.	2.0	0