

Significant Alteration of Gene Expression in Wood Decaying *Phanerochaete chrysosporium* by Plant Species

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Citation Report

#	ARTICLE	IF	CITATIONS
1	iTRAQ-based quantitative secretome analysis of <i>Phanerochaete chrysosporium</i> . <i>Journal of Proteomics</i> , 2011, 75, 642-654.	1.2	73
2	Hydrolytic enzyme activity of EN113 standard basidiomycetes in the fermentation of lignocellulosic material and wood colonization. <i>Holzforschung</i> , 2012, 66, 841-847.	0.9	4
3	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnos</i> a and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 2012, 13, 444.	1.2	125
4	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259
5	Lignocellulolytic enzymes from tropical fungi: Types, substrates and applications. <i>Scientific Research and Essays</i> , 2012, 7, .	0.1	20
6	Expression and regulation of genes encoding lignocellulose-degrading activity in the genus <i>Phanerochaete</i> . <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 339-351.	1.7	47
7	Quantitative proteomic analysis of lignocellulolytic enzymes by <i>Phanerochaete chrysosporium</i> on different lignocellulosic biomass. <i>Journal of Proteomics</i> , 2012, 75, 1493-1504.	1.2	73
8	Transcriptome of an <i>Armillaria</i> root disease pathogen reveals candidate genes involved in host substrate utilization at the host-pathogen interface. <i>Forest Pathology</i> , 2013, 43, 468-477.	0.5	34
9	A phylogenetic overview of the antrodia clade (Basidiomycota, Polyporales). <i>Mycologia</i> , 2013, 105, 1391-1411.	0.8	86
10	Genomewide analysis of polysaccharides degrading enzymes in 11 white- and brown-rot Polyporales provides insight into mechanisms of wood decay. <i>Mycologia</i> , 2013, 105, 1412-1427.	0.8	110
11	Genomics of Soil- and Plant-Associated Fungi. <i>Soil Biology</i> , 2013, , .	0.6	8
12	New substrates and activity of <i>Phanerochaete chrysosporium</i> Omega glutathione transferases. <i>Biochimie</i> , 2013, 95, 336-346.	1.3	24
13	Using a grass substrate to compare decay among two clades of brown rot fungi. <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8831-8840.	1.7	13
14	Gene Expression Analysis of Copper Tolerance and Wood Decay in the Brown Rot Fungus <i>Fibroporia radiculosa</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 1523-1533.	1.4	36
15	Transcriptomic analysis of the interactions between <i>Agaricus bisporus</i> and <i>Lecanicillium fungicola</i> . <i>Fungal Genetics and Biology</i> , 2013, 55, 67-76.	0.9	19
17	Pretreatment of Lignocellulosic Biomass Using Microorganisms: Approaches, Advantages, and Limitations. , 0, , .		6
18	Xenomic networks variability and adaptation traits in wood decaying fungi. <i>Microbial Biotechnology</i> , 2013, 6, 248-263.	2.0	122
19	Redundancy among Manganese Peroxidases in <i>Pleurotus ostreatus</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 2405-2415.	1.4	48

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20	A First Insight into <i>Pycnoporus sanguineus</i> BAFC 2126 Transcriptome. <i>PLoS ONE</i> , 2013, 8, e81033.	1.1	26
21	Systematic Identification and Evolutionary Analysis of Catalytically Versatile Cytochrome P450 Monooxygenase Families Enriched in Model Basidiomycete Fungi. <i>PLoS ONE</i> , 2014, 9, e86683.	1.1	85
22	Oxalate-Metabolising Genes of the White-Rot Fungus <i>Dichomitus squalens</i> Are Differentially Induced on Wood and at High Proton Concentration. <i>PLoS ONE</i> , 2014, 9, e87959.	1.1	29
23	Influence of <i>Populus</i> Genotype on Gene Expression by the Wood Decay Fungus <i>Phanerochaete chrysosporium</i> . <i>Applied and Environmental Microbiology</i> , 2014, 80, 5828-5835.	1.4	28
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26	Inactivation of a <i>Pleurotus ostreatus</i> versatile peroxidase-encoding gene (<i>mnp2</i>) results in reduced lignin degradation. <i>Environmental Microbiology</i> , 2014, 16, 265-277.	1.8	37
27	8 Degradation and Modification of Plant Biomass by Fungi. , 2014, , 175-208.		26
28	Mode of action of brown rot decay resistance in modified wood: a review. <i>Holzforschung</i> , 2014, 68, 239-246.	0.9	95
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31	Microbial genomics, transcriptomics and proteomics: new discoveries in decomposition research using complementary methods. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 1531-1537.	1.7	49
32	Genomics, Lifestyles and Future Prospects of Wood-Decay and Litter-Decomposing Basidiomycota. <i>Advances in Botanical Research</i> , 2014, 70, 329-370.	0.5	87
33	Prevalence of transcription factors in ascomycete and basidiomycete fungi. <i>BMC Genomics</i> , 2014, 15, 214.	1.2	114
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35	Transcriptome and exoproteome analysis of utilization of plant-derived biomass by <i>Myceliophthora thermophila</i> . <i>Fungal Genetics and Biology</i> , 2014, 72, 10-20.	0.9	72
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37	Yeast Biotechnology: Teaching the Old Dog New Tricks. , 2015, , 107-116.		1

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39	Enhanced degradation of softwood versus hardwood by the white-rot fungus <i>Pycnoporus coccineus</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 216.	6.2	67
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47	Furfurylated wood: impact on <i>Postia placenta</i> gene expression and oxalate crystal formation. <i>Holzforschung</i> , 2016, 70, 947-962.	0.9	20
48	A secretomic view of woody and nonwoody lignocellulose degradation by <i>Pleurotus ostreatus</i> . <i>Biotechnology for Biofuels</i> , 2016, 9, 49.	6.2	85
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53	Gene Expression Patterns of Wood Decay Fungi <i>Postia placenta</i> and <i>Phanerochaete chrysosporium</i> Are Influenced by Wood Substrate Composition during Degradation. <i>Applied and Environmental Microbiology</i> , 2016, 82, 4387-4400.	1.4	35
54	De novo transcriptomic assembly and profiling of <i>Rigidoporus microporus</i> during saprotrophic growth on rubber wood. <i>BMC Genomics</i> , 2016, 17, 234.	1.2	12
55	Regulation of the fungal secretome. <i>Current Genetics</i> , 2016, 62, 533-545.	0.8	83
56	Gene expression metadata analysis reveals molecular mechanisms employed by <i>Phanerochaete chrysosporium</i> during lignin degradation and detoxification of plant extractives. <i>Current Genetics</i> , 2017, 63, 877-894.	0.8	34

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58	Draft genome sequence of a monokaryotic model brown-rot fungus <i>Postia</i> (<i>Rhodonia</i>) <i>placenta</i> SB12. <i>Genomics Data</i> , 2017, 14, 21-23.	1.3	19
59	Role of carbon source in the shift from oxidative to hydrolytic wood decomposition by <i>Postia placenta</i> . <i>Fungal Genetics and Biology</i> , 2017, 106, 1-8.	0.9	40
60	Transcriptome Sequencing and Comparative Analysis of <i>Piptoporus betulinus</i> in Response to Birch Sawdust Induction. <i>Forests</i> , 2017, 8, 374.	0.9	4
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