

# Miia R Mäkelä

## List of Publications by Year in descending order

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102  
papers

4,342  
citations

147801  
31  
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123424  
61  
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103  
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103  
docs citations

103  
times ranked

4252  
citing authors

#	ARTICLE	IF	CITATIONS
1	Organic residues from agricultural and forest companies in Brazil as useful substrates for cultivation of the edible mushroom <i>Pleurotus ostreatus</i> . Letters in Applied Microbiology, 2022, 74, 44-52.	2.2	1
2	Xylitol production from plant biomass by <i>Aspergillus niger</i> through metabolic engineering. Bioresource Technology, 2022, 344, 126199.	9.6	20
3	Fungal glycoside hydrolase family 44 xyloglucanases are restricted to the phylum Basidiomycota and show a distinct xyloglucan cleavage pattern. IScience, 2022, 25, 103666.	4.1	10
4	Detailed analysis of the D-galactose catabolic pathways in <i>Aspergillus niger</i> reveals complexity at both metabolic and regulatory level. Fungal Genetics and Biology, 2022, 159, 103670.	2.1	7
5	GalR, GalX and AraR co-regulate <i>Aspergillus nidulans</i> galactose and arabinose utilization in <i>Aspergillus nidulans</i> . Microbial Biotechnology, 2022, 15, 1839-1851.	4.2	4
6	Carbohydrate esterase family 16 contains fungal hemicellulose acetyl esterases (HAEs) with varying specificity. New Biotechnology, 2022, 70, 28-38.	4.4	9
7	Molecular engineering to improve lignocellulosic biomass based applications using filamentous fungi. Advances in Applied Microbiology, 2021, 114, 73-109.	2.4	8
8	Applications of Fungal Cellulases. , 2021, , 295-304.		0
9	Fungal Lignin-Modifying Peroxidases and H2O2-Producing Enzymes. , 2021, , 247-259.		11
10	Discovery and Functional Analysis of a Salicylic Acid Hydroxylase from <i>Aspergillus niger</i> . Applied and Environmental Microbiology, 2021, 87, .	3.1	17
11	Re-routing of Sugar Catabolism Provides a Better Insight Into Fungal Flexibility in Using Plant Biomass-Derived Monomers as Substrates. Frontiers in Bioengineering and Biotechnology, 2021, 9, 644216.	4.1	4
12	Revisiting a "simple" fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	4.2	10
13	Characterization of d-xylose reductase, XyrB, from <i>Aspergillus niger</i> . Biotechnology Reports (Amsterdam, Netherlands), 2021, 30, e00610.	4.4	5
14	Depolymerization of biorefinery lignin by improved laccases of the white-rot fungus <i>Obba rivulosa</i> . Microbial Biotechnology, 2021, 14, 2140-2151.	4.2	6
15	The Cultivation Method Affects the Transcriptomic Response of <i>Aspergillus niger</i> to Growth on Sugar Beet Pulp. Microbiology Spectrum, 2021, 9, e0106421.	3.0	6
16	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. Cell Surface, 2021, 7, 100050.	3.0	16
17	Application of CRISPR/Cas9 Tools for Genome Editing in the White-Rot Fungus <i>Dichomitus squalens</i> . Biomolecules, 2021, 11, 1526.	4.0	9
18	Production of Recombinant Laccase From <i>Coprinopsis cinerea</i> and Its Effect in Mediator Promoted Lignin Oxidation at Neutral pH. Frontiers in Bioengineering and Biotechnology, 2021, 9, 767139.	4.1	8

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19	Recombinant production and characterization of six novel GH27 and GH36 $\beta$ -galactosidases from <i>Penicillium subrubescens</i> and their synergism with a commercial mannanase during the hydrolysis of lignocellulosic biomass. <i>Bioresource Technology</i> , 2020, 295, 122258.	9.6	21
20	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus <i>Dichomitus squalens</i> . <i>Journal of Biotechnology</i> , 2020, 308, 35-39.	3.8	7
21	Colonies of the fungus <i>Aspergillus niger</i> are highly differentiated to adapt to local carbon source variation. <i>Environmental Microbiology</i> , 2020, 22, 1154-1166.	3.8	15
22	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	3.4	32
23	Fungal Treatment Modifies Kraft Lignin for Lignin- and Cellulose-Based Carbon Fiber Precursors. <i>ACS Omega</i> , 2020, 5, 6130-6140.	3.5	18
24	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	12.8	125
25	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in <i>Aspergillus niger</i> revealed the inducer of the pathway regulator. <i>Microbiological Research</i> , 2020, 234, 126426.	5.3	11
26	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. <i>Trends in Microbiology</i> , 2020, 28, 487-499.	7.7	25
27	Progress and Research Needs of Plant Biomass Degradation by Basidiomycete Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 405-438.	2.4	11
28	Fungal Laccases and Their Potential in Bioremediation Applications. <i>Microbiology Monographs</i> , 2020, , 1-25.	0.6	10
29	<i>Penicillium subrubescens</i> adapts its enzyme production to the composition of plant biomass. <i>Bioresource Technology</i> , 2020, 311, 123477.	9.6	15
30	Engineering of primary carbon metabolism in filamentous fungi. <i>Biotechnology Advances</i> , 2020, 43, 107551.	11.7	28
31	CRISPR/Cas9 facilitates rapid generation of constitutive forms of transcription factors in <i>Aspergillus niger</i> through specific on-site genomic mutations resulting in increased saccharification of plant biomass. <i>Enzyme and Microbial Technology</i> , 2020, 136, 109508.	3.2	29
32	Applicability of Recombinant Laccases From the White-Rot Fungus <i>Obba rivulosa</i> for Mediator-Promoted Oxidation of Biorefinery Lignin at Low pH. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 604497.	4.1	14
33	The White-Rot Basidiomycete <i>Dichomitus squalens</i> Shows Highly Specific Transcriptional Response to Lignocellulose-Related Aromatic Compounds. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 229.	4.1	21
34	Discovery of Novel p-Hydroxybenzoate-m-hydroxylase, Protocatechuate 3,4 Ring-Cleavage Dioxygenase, and Hydroxyquinol 1,2 Ring-Cleavage Dioxygenase from the Filamentous Fungus <i>Aspergillus niger</i> . <i>ACS Sustainable Chemistry and Engineering</i> , 2019, 7, 19081-19089.	6.7	25
35	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. <i>Biotechnology Advances</i> , 2019, 37, 107396.	11.7	83
36	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	22

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37	The presence of trace components significantly broadens the molecular response of <i>Aspergillus niger</i> to guar gum. <i>New Biotechnology</i> , 2019, 51, 57-66.	4.4	10
38	Developments and opportunities in fungal strain engineering for the production of novel enzymes and enzyme cocktails for plant biomass degradation. <i>Biotechnology Advances</i> , 2019, 37, 107361.	11.7	46
39	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	21
40	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	11
41	Selective Cleavage of Lignin $\beta$ -O-4 Aryl Ether Bond by $\beta$ -Etherase of the White-Rot Fungus <i>Dichomitus squalens</i> . <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 2878-2882.	6.7	66
42	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. <i>Fungal Genetics and Biology</i> , 2018, 112, 12-20.	2.1	9
43	The fungus <i>Aspergillus niger</i> consumes sugars in a sequential manner that is not mediated by the carbon catabolite repressor CreA. <i>Scientific Reports</i> , 2018, 8, 6655.	3.3	24
44	Induction of Genes Encoding Plant Cell Wall-Degrading Carbohydrate-Active Enzymes by Lignocellulose-Derived Monosaccharides and Cellobiose in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	31
45	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. <i>New Biotechnology</i> , 2018, 40, 282-287.	4.4	29
46	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. <i>New Biotechnology</i> , 2018, 41, 9-14.	4.4	33
47	Temporal transcriptome analysis of the white-rot fungus <i>Obba rivulosa</i> shows expression of a constitutive set of plant cell wall degradation targeted genes during growth on solid spruce wood. <i>Fungal Genetics and Biology</i> , 2018, 112, 47-54.	2.1	21
48	Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes. <i>Fungal Genetics and Biology</i> , 2018, 112, 40-46.	2.1	42
49	Genomic and exoproteomic diversity in plant biomass degradation approaches among <i>Aspergilli</i> . <i>Studies in Mycology</i> , 2018, 91, 79-99.	7.2	24
50	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	3.5	35
51	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018, 20, 4141-4156.	3.8	36
52	Role of Fungi in Wood Decay. , 2018, , .		11
53	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	21.4	160
54	In Silico Analysis of Putative Sugar Transporter Genes in <i>Aspergillus niger</i> Using Phylogeny and Comparative Transcriptomics. <i>Frontiers in Microbiology</i> , 2018, 9, 1045.	3.5	47

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55	The Synthetic Potential of Fungal Feruloyl Esterases: A Correlation with Current Classification Systems and Predicted Structural Properties. <i>Catalysts</i> , 2018, 8, 242.	3.5	15
56	Characterization of a feruloyl esterase from <i>Aspergillus terreus</i> facilitates the division of fungal enzymes from Carbohydrate Esterase family 1 of the carbohydrate-active enzymes (CAZy) database. <i>Microbial Biotechnology</i> , 2018, 11, 869-880.	4.2	36
57	Efficient Extraction Method for High Quality Fungal RNA from Complex Lignocellulosic Substrates. <i>Methods in Molecular Biology</i> , 2018, 1775, 69-73.	0.9	0
58	The draft genome sequence of the ascomycete fungus <i>Penicillium subrubescens</i> reveals a highly enriched content of plant biomass related CAZymes compared to related fungi. <i>Journal of Biotechnology</i> , 2017, 246, 1-3.	3.8	33
59	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	8.8	417
60	Genome Sequence of the Basidiomycete White-Rot Fungus <i>Trametes pubescens</i> FBCC735. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
61	Cultivation of <i>Podospora anserina</i> on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. <i>New Biotechnology</i> , 2017, 37, 162-171.	4.4	22
62	Occurrence and function of enzymes for lignocellulose degradation in commercial <i>Agaricus bisporus</i> cultivation. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4363-4369.	3.6	59
63	Expanding the feruloyl esterase gene family of <i>Aspergillus niger</i> by characterization of a feruloyl esterase, FaeC. <i>New Biotechnology</i> , 2017, 37, 200-209.	4.4	52
64	The molecular response of the white-rot fungus <i>Dichomitus squalens</i> to wood and non-woody biomass as examined by transcriptome and exoproteome analyses. <i>Environmental Microbiology</i> , 2017, 19, 1237-1250.	3.8	55
65	Genetic transformation of the white-rot fungus <i>Dichomitus squalens</i> using a new commercial protoplasting cocktail. <i>Journal of Microbiological Methods</i> , 2017, 143, 38-43.	1.6	12
66	Fungal Ligninolytic Enzymes and Their Applications. , 2017, , 1049-1061.		2
67	Expression-based clustering of CAZyme-encoding genes of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2017, 18, 900.	2.8	54
68	Functional diversity in <i>Dichomitus squalens</i> monokaryons. <i>IMA Fungus</i> , 2017, 8, 17-25.	3.8	22
69	Biochemical Characterization of Recombinant Oxalate Decarboxylases of the White Rot Fungus <i>Dichomitus squalens</i> . <i>Current Biotechnology</i> , 2017, 6, 98-104.	0.4	0
70	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	19
71	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. <i>Fungal Biology</i> , 2016, , 119-160.	0.6	2
72	<i>Penicillium subrubescens</i> is a promising alternative for <i>Aspergillus niger</i> in enzymatic plant biomass saccharification. <i>New Biotechnology</i> , 2016, 33, 834-841.	4.4	27

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73	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. <i>Biotechnology for Biofuels</i> , 2016, 9, 231.	6.2	133
74	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
75	Production of Feruloyl Esterases by <i>Aspergillus</i> Species. , 2016, , 129-144.		1
76	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015, 17, 3098-3109.	3.8	49
77	Lignocellulose-converting enzyme activity profiles correlate with molecular systematics and phylogeny grouping in the incoherent genus <i>Phlebia</i> (Polyporales, Basidiomycota). <i>BMC Microbiology</i> , 2015, 15, 217.	3.3	36
78	Saccharification of Lignocelluloses by Carbohydrate Active Enzymes of the White Rot Fungus <i>Dichomitus squalens</i> . <i>PLoS ONE</i> , 2015, 10, e0145166.	2.5	22
79	Aromatic Metabolism of Filamentous Fungi in Relation to the Presence of Aromatic Compounds in Plant Biomass. <i>Advances in Applied Microbiology</i> , 2015, 91, 63-137.	2.4	97
80	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111
81	Fungal colonisation and moisture uptake of torrefied wood, charcoal, and thermally treated pellets during storage. <i>European Journal of Wood and Wood Products</i> , 2015, 73, 709-717.	2.9	16
82	Mitochondrial Genome of <i>Phlebia radiata</i> Is the Second Largest (156 kbp) among Fungi and Features Signs of Genome Flexibility and Recent Recombination Events. <i>PLoS ONE</i> , 2014, 9, e97141.	2.5	80
83	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.	2.5	29
84	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 614-649.	6.6	340
85	8 Degradation and Modification of Plant Biomass by Fungi. , 2014, , 175-208.		26
86	Biochemical and molecular characterization of an atypical manganese peroxidase of the litter-decomposing fungus <i>Agrocybe praecox</i> . <i>Fungal Genetics and Biology</i> , 2014, 72, 131-136.	2.1	19
87	Genomics, Lifestyles and Future Prospects of Wood-Decay and Litter-Decomposing Basidiomycota. <i>Advances in Botanical Research</i> , 2014, 70, 329-370.	1.1	87
88	Carbohydrate-Binding Modules of Fungal Cellulases. <i>Advances in Applied Microbiology</i> , 2014, 88, 103-165.	2.4	127
89	Plant biomass degradation by fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 1.	2.1	3
90	An improved and reproducible protocol for the extraction of high quality fungal RNA from plant biomass substrates. <i>Fungal Genetics and Biology</i> , 2014, 72, 201-206.	2.1	20

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91	Plant biomass degradation by fungi. Fungal Genetics and Biology, 2014, 72, 2-9.	2.1	91
92	Transcriptional analysis of selected cellulose-acting enzymes encoding genes of the white-rot fungus <i>Dichomitus squalens</i> on spruce wood and microcrystalline cellulose. Fungal Genetics and Biology, 2014, 72, 91-98.	2.1	31
93	Heterologous expression and structural characterization of two low pH laccases from a biopulping white-rot fungus <i>Physisporinus rivulosus</i> . Applied Microbiology and Biotechnology, 2013, 97, 1589-1599.	3.6	32
94	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . BMC Genomics, 2013, 14, 663.	2.8	35
95	<i>Agaricus bisporus</i> and related <i>Agaricus</i> species on lignocellulose: Production of manganese peroxidase and multicopper oxidases. Fungal Genetics and Biology, 2013, 55, 32-41.	2.1	26
96	Effect of copper, nutrient nitrogen, and wood-supplement on the production of lignin-modifying enzymes by the white-rot fungus <i>Phlebia radiata</i> . Fungal Biology, 2013, 117, 62-70.	2.5	52
97	Oxalate decarboxylase: biotechnological update and prevalence of the enzyme in filamentous fungi. Applied Microbiology and Biotechnology, 2010, 87, 801-814.	3.6	76
98	Lignin-modifying enzymes in filamentous basidiomycetes – ecological, functional and phylogenetic review. Journal of Basic Microbiology, 2010, 50, 5-20.	3.3	367
99	Oxalate decarboxylase of the white-rot fungus <i>Dichomitus squalens</i> demonstrates a novel enzyme primary structure and non-induced expression on wood and in liquid cultures. Microbiology (United Kingdom), 2010, 150, 1843-1853. Over	1.7	24
100	Expression on wood, molecular cloning and characterization of three lignin peroxidase (LiP) encoding genes of the white rot fungus <i>Phlebia radiata</i> . Current Genetics, 2006, 49, 97-105.	1.7	24
101	Expression and molecular properties of a new laccase of the white rot fungus <i>Phlebia radiata</i> grown on wood. Current Genetics, 2006, 50, 323-333.	1.7	37
102	Production of organic acids and oxalate decarboxylase in lignin-degrading white rot fungi. Enzyme and Microbial Technology, 2002, 30, 542-549.	3.2	163