

Miia R MÃ¤kelÃ¤

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7549931/publications.pdf>

Version: 2024-02-01

102
papers

4,342
citations

168829

31
h-index

139680

61
g-index

103
all docs

103
docs citations

103
times ranked

4678
citing authors

#	ARTICLE	IF	CITATIONS
1	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.	3.8	417
2	Lignin-modifying enzymes in filamentous basidiomycetes – ecological, functional and phylogenetic review. <i>Journal of Basic Microbiology</i> , 2010, 50, 5-20.	1.8	367
3	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 614-649.	2.9	340
4	Production of organic acids and oxalate decarboxylase in lignin-degrading white rot fungi. <i>Enzyme and Microbial Technology</i> , 2002, 30, 542-549.	1.6	163
5	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.	9.4	160
6	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. <i>Biotechnology for Biofuels</i> , 2016, 9, 231.	6.2	133
7	Carbohydrate-Binding Modules of Fungal Cellulases. <i>Advances in Applied Microbiology</i> , 2014, 88, 103-165.	1.3	127
8	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
9	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111
10	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.	1.3	97
11	Plant biomass degradation by fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 2-9.	0.9	91
12	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
13	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. <i>Biotechnology Advances</i> , 2019, 37, 107396.	6.0	83
14	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.	1.1	80
15	Oxalate decarboxylase: biotechnological update and prevalence of the enzyme in filamentous fungi. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 801-814.	1.7	76
16	Selective Cleavage of Lignin β -O-4 Aryl Ether Bond by β -Etherase of the White-Rot Fungus <i>Dichomitus squalens</i> . <i>ACS Sustainable Chemistry and Engineering</i> , 2018, 6, 2878-2882.	3.2	66
17	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.	1.7	59
18	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.	1.8	55

#	ARTICLE	IF	CITATIONS
19	Expression-based clustering of CAZyme-encoding genes of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2017, 18, 900.	1.2	54
20	Effect of copper, nutrient nitrogen, and wood-supplement on the production of lignin-modifying enzymes by the white-rot fungus <i>Phlebia radiata</i> . <i>Fungal Biology</i> , 2013, 117, 62-70.	1.1	52
21	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.	2.4	52
22	Uncovering the abilities of <i>Aspergillus garicus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015, 17, 3098-3109.	1.8	49
23	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.	1.5	47
24	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.	6.0	46
25	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.	0.9	42
26	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. <i>Microbiology (United Kingdom)</i> , 2017, 157, 1071-1078.	0.8	41
27	Expression and molecular properties of a new laccase of the white rot fungus <i>Phlebia radiata</i> grown on wood. <i>Current Genetics</i> , 2006, 50, 323-333.	0.8	37
28	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.	1.3	36
29	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018, 20, 4141-4156.	1.8	36
30	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.	2.0	36
31	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	1.2	35
32	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	1.5	35
33	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.	1.9	33
34	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. <i>New Biotechnology</i> , 2018, 41, 9-14.	2.4	33
35	Heterologous expression and structural characterization of two low pH laccases from a biopulping white-rot fungus <i>Physisporinus rivulosus</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 1589-1599.	1.7	32
36	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, .	1.5	32

#	ARTICLE	IF	CITATIONS
37	Transcriptional analysis of selected cellulose-acting enzymes encoding genes of the white-rot fungus <i>Dichomitus squalens</i> on spruce wood and microcrystalline cellulose. <i>Fungal Genetics and Biology</i> , 2014, 72, 91-98.	0.9	31
38	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, .	1.4	31
39	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
40	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. <i>New Biotechnology</i> , 2018, 40, 282-287.	2.4	29
41	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.	1.6	29
42	Engineering of primary carbon metabolism in filamentous fungi. <i>Biotechnology Advances</i> , 2020, 43, 107551.	6.0	28
43	<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.	2.4	27
44	<i>Agaricus bisporus</i> and related <i>Agaricus</i> species on lignocellulose: Production of manganese peroxidase and multicopper oxidases. <i>Fungal Genetics and Biology</i> , 2013, 55, 32-41.	0.9	26
45	8 Degradation and Modification of Plant Biomass by Fungi. , 2014, , 175-208.		26
46	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.	3.2	25
47	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. <i>Trends in Microbiology</i> , 2020, 28, 487-499.	3.5	25
48	Expression on wood, molecular cloning and characterization of three lignin peroxidase (LiP) encoding genes of the white rot fungus <i>Phlebia radiata</i> . <i>Current Genetics</i> , 2006, 49, 97-105.	0.8	24
49	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.	1.6	24
50	Genomic and exoproteomic diversity in plant biomass degradation approaches among <i>Aspergilli</i> . <i>Studies in Mycology</i> , 2018, 91, 79-99.	4.5	24
51	Saccharification of Lignocelluloses by Carbohydrate Active Enzymes of the White Rot Fungus <i>Dichomitus squalens</i> . <i>PLoS ONE</i> , 2015, 10, e0145166.	1.1	22
52	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.	2.4	22
53	Functional diversity in <i>Dichomitus squalens</i> monokaryons. <i>IMA Fungus</i> , 2017, 8, 17-25.	1.7	22
54	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.3	22

#	ARTICLE	IF	CITATIONS
55	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.	0.9	21
56	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.	2.0	21
57	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	21
58	Recombinant production and characterization of six novel GH27 and GH36 β -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.	4.8	21
59	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.	0.9	20
60	Xylitol production from plant biomass by <i>Aspergillus niger</i> through metabolic engineering. <i>Bioresource Technology</i> , 2022, 344, 126199.	4.8	20
61	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.	0.9	19
62	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	1.2	19
63	Fungal Treatment Modifies Kraft Lignin for Lignin- and Cellulose-Based Carbon Fiber Precursors. <i>ACS Omega</i> , 2020, 5, 6130-6140.	1.6	18
64	Discovery and Functional Analysis of a Salicylic Acid Hydroxylase from <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	1.4	17
65	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.	1.3	16
66	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. <i>Cell Surface</i> , 2021, 7, 100050.	1.5	16
67	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016, 4, .	0.8	15
68	The Synthetic Potential of Fungal Feruloyl Esterases: A Correlation with Current Classification Systems and Predicted Structural Properties. <i>Catalysts</i> , 2018, 8, 242.	1.6	15
69	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.	1.8	15
70	<i>Penicillium subrubescens</i> adapts its enzyme production to the composition of plant biomass. <i>Bioresource Technology</i> , 2020, 311, 123477.	4.8	15
71	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.	2.0	14
72	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.	0.7	12

#	ARTICLE	IF	CITATIONS
73	Genome Sequence of the Basidiomycete White-Rot Fungus <i>Trametes pubescens</i> FBCC735. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
74	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018, 6, .	0.8	11
75	Role of Fungi in Wood Decay. , 2018, , .		11
76	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.	2.5	11
77	Fungal Lignin-Modifying Peroxidases and H ₂ O ₂ -Producing Enzymes. , 2021, , 247-259.		11
78	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
79	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.	2.4	10
80	Revisiting a "simple" fungal metabolic pathway reveals redundancy, complexity and diversity. <i>Microbial Biotechnology</i> , 2021, 14, 2525-2537.	2.0	10
81	Fungal Laccases and Their Potential in Bioremediation Applications. <i>Microbiology Monographs</i> , 2020, , 1-25.	0.3	10
82	Fungal glycoside hydrolase family 44 xyloglucanases are restricted to the phylum Basidiomycota and show a distinct xyloglucan cleavage pattern. <i>IScience</i> , 2022, 25, 103666.	1.9	10
83	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.	0.9	9
84	Application of CRISPR/Cas9 Tools for Genome Editing in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Biomolecules</i> , 2021, 11, 1526.	1.8	9
85	Carbohydrate esterase family 16 contains fungal hemicellulose acetyl esterases (HAEs) with varying specificity. <i>New Biotechnology</i> , 2022, 70, 28-38.	2.4	9
86	Molecular engineering to improve lignocellulosic biomass based applications using filamentous fungi. <i>Advances in Applied Microbiology</i> , 2021, 114, 73-109.	1.3	8
87	Production of Recombinant Laccase From <i>Coprinopsis cinerea</i> and Its Effect in Mediator Promoted Lignin Oxidation at Neutral pH. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 767139.	2.0	8
88	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.	1.9	7
89	Detailed analysis of the D-galactose catabolic pathways in <i>Aspergillus niger</i> reveals complexity at both metabolic and regulatory level. <i>Fungal Genetics and Biology</i> , 2022, 159, 103670.	0.9	7
90	Depolymerization of biorefinery lignin by improved laccases of the white-rot fungus <i>Obba rivulosa</i> . <i>Microbial Biotechnology</i> , 2021, 14, 2140-2151.	2.0	6

#	ARTICLE	IF	CITATIONS
91	The Cultivation Method Affects the Transcriptomic Response of <i>Aspergillus niger</i> to Growth on Sugar Beet Pulp. <i>Microbiology Spectrum</i> , 2021, 9, e0106421.	1.2	6
92	Characterization of d-xylose reductase, XyrB, from <i>Aspergillus niger</i> . <i>Biotechnology Reports</i> (Amsterdam, Netherlands), 2021, 30, e00610.	2.1	5
93	Re-routing of Sugar Catabolism Provides a Better Insight Into Fungal Flexibility in Using Plant Biomass-Derived Monomers as Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 644216.	2.0	4
94	GalR, GalX and AraR co-regulate <i>d</i> -galactose and <i>l</i> -arabinose utilization in <i>Aspergillus nidulans</i> . <i>Microbial Biotechnology</i> , 2022, 15, 1839-1851.	2.0	4
95	Plant biomass degradation by fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 1.	0.9	3
96	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. <i>Fungal Biology</i> , 2016, , 119-160.	0.3	2
97	Fungal Lignolytic Enzymes and Their Applications. , 2017, , 1049-1061.		2
98	Production of Feruloyl Esterases by <i>Aspergillus</i> Species. , 2016, , 129-144.		1
99	Organic residues from agricultural and forest companies in Brazil as useful substrates for cultivation of the edible mushroom <i>Pleurotus ostreatus</i> . <i>Letters in Applied Microbiology</i> , 2022, 74, 44-52.	1.0	1
100	Efficient Extraction Method for High Quality Fungal RNA from Complex Lignocellulosic Substrates. <i>Methods in Molecular Biology</i> , 2018, 1775, 69-73.	0.4	0
101	Applications of Fungal Cellulases. , 2021, , 295-304.		0
102	Biochemical Characterization of Recombinant Oxalate Decarboxylases of the White Rot Fungus <i>Dichomitus squalens</i> . <i>Current Biotechnology</i> , 2017, 6, 98-104.	0.2	0