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List of Publications by Year in descending order

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102
papers

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citations

147801
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docs citations

103
times ranked

4252
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.	8.8	417
2	Lignin-modifying enzymes in filamentous basidiomycetes – ecological, functional and phylogenetic review. <i>Journal of Basic Microbiology</i> , 2010, 50, 5-20.	3.3	367
3	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 614-649.	6.6	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.	3.2	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.	21.4	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.	2.4	127
8	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020, 11, 1106.	12.8	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.	2.4	97
11	Plant biomass degradation by fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 2-9.	2.1	91
12	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
13	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
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.	2.5	80
15	Oxalate decarboxylase: biotechnological update and prevalence of the enzyme in filamentous fungi. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 801-814.	3.6	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.	6.7	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.	3.6	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.	3.8	55

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19	Expression-based clustering of CAZyme-encoding genes of <i>Aspergillus niger</i> . BMC Genomics, 2017, 18, 900.	2.8	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> . Fungal Biology, 2013, 117, 62-70.	2.5	52
21	Expanding the feruloyl esterase gene family of <i>Aspergillus niger</i> by characterization of a feruloyl esterase, FaeC. New Biotechnology, 2017, 37, 200-209.	4.4	52
22	Uncovering the abilities of <i>Aspergillus garicus bisporus</i> to degrade plant biomass throughout its life cycle. Environmental Microbiology, 2015, 17, 3098-3109.	3.8	49
23	In Silico Analysis of Putative Sugar Transporter Genes in <i>Aspergillus niger</i> Using Phylogeny and Comparative Transcriptomics. Frontiers in Microbiology, 2018, 9, 1045.	3.5	47
24	Developments and opportunities in fungal strain engineering for the production of novel enzymes and enzyme cocktails for plant biomass degradation. Biotechnology Advances, 2019, 37, 107361.	11.7	46
25	Comparative analysis of basidiomycete transcriptomes reveals a core set of expressed genes encoding plant biomass degrading enzymes. Fungal Genetics and Biology, 2018, 112, 40-46.	2.1	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. Microbiology (United Kingdom), 2018, 158, 107-115.	2.1	42
27	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
28	Lignocellulose-converting enzyme activity profiles correlate with molecular systematics and phylogeny grouping in the incoherent genus <i>Phlebia</i> (Polyporales, Basidiomycota). BMC Microbiology, 2015, 15, 217.	3.3	36
29	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	3.8	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. Microbial Biotechnology, 2018, 11, 869-880.	4.2	36
31	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . BMC Genomics, 2013, 14, 663.	2.8	35
32	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). Frontiers in Microbiology, 2018, 9, 3058.	3.5	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. Journal of Biotechnology, 2017, 246, 1-3.	3.8	33
34	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. New Biotechnology, 2018, 41, 9-14.	4.4	33
35	Heterologous expression and structural characterization of two low pH laccases from a biopulping white-rot fungus <i>Physiporus rivulosus</i> . Applied Microbiology and Biotechnology, 2013, 97, 1589-1599.	3.6	32
36	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . DNA Research, 2020, 27, .	3.4	32

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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.	2.1	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, .	3.1	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.	2.5	29
40	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. <i>New Biotechnology</i> , 2018, 40, 282-287.	4.4	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.	3.2	29
42	Engineering of primary carbon metabolism in filamentous fungi. <i>Biotechnology Advances</i> , 2020, 43, 107551.	11.7	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.	4.4	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.	2.1	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.	6.7	25
47	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. <i>Trends in Microbiology</i> , 2020, 28, 487-499.	7.7	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.	1.7	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.	3.3	24
50	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
51	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
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.	4.4	22
53	Functional diversity in <i>Dichomitus squalens</i> monokaryons. <i>IMA Fungus</i> , 2017, 8, 17-25.	3.8	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, .	0.6	22

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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.	2.1	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.	4.1	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, .	3.1	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.	9.6	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.	2.1	20
60	Xylitol production from plant biomass by <i>Aspergillus niger</i> through metabolic engineering. <i>Bioresource Technology</i> , 2022, 344, 126199.	9.6	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.	2.1	19
62	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016, 4, .	3.0	19
63	Fungal Treatment Modifies Kraft Lignin for Lignin- and Cellulose-Based Carbon Fiber Precursors. <i>ACS Omega</i> , 2020, 5, 6130-6140.	3.5	18
64	Discovery and Functional Analysis of a Salicylic Acid Hydroxylase from <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, .	3.1	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.	2.9	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.	3.0	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.	3.5	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.	3.8	15
70	<i>Penicillium subrubescens</i> adapts its enzyme production to the composition of plant biomass. <i>Bioresource Technology</i> , 2020, 311, 123477.	9.6	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.	4.1	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.	1.6	12

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73	Genome Sequence of the Basidiomycete White-Rot Fungus <i>Trametes pubescens</i> FBCC735. Genome Announcements, 2017, 5, .	0.8	11
74	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . Genome Announcements, 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. Microbiological Research, 2020, 234, 126426.	5.3	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. Grand Challenges in Biology and Biotechnology, 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. New Biotechnology, 2019, 51, 57-66.	4.4	10
80	Revisiting a “simple” fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	4.2	10
81	Fungal Laccases and Their Potential in Bioremediation Applications. Microbiology Monographs, 2020, , 1-25.	0.6	10
82	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
83	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. Fungal Genetics and Biology, 2018, 112, 12-20.	2.1	9
84	Application of CRISPR/Cas9 Tools for Genome Editing in the White-Rot Fungus <i>Dichomitus squalens</i> . Biomolecules, 2021, 11, 1526.	4.0	9
85	Carbohydrate esterase family 16 contains fungal hemicellulose acetyl esterases (HAEs) with varying specificity. New Biotechnology, 2022, 70, 28-38.	4.4	9
86	Molecular engineering to improve lignocellulosic biomass based applications using filamentous fungi. Advances in Applied Microbiology, 2021, 114, 73-109.	2.4	8
87	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
88	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus <i>Dichomitus squalens</i> . Journal of Biotechnology, 2020, 308, 35-39.	3.8	7
89	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
90	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

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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.	3.0	6
92	Characterization of d-xylose reductase, XyrB, from <i>Aspergillus niger</i> . <i>Biotechnology Reports</i> (Amsterdam, Netherlands), 2021, 30, e00610.	4.4	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.	4.1	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.	4.2	4
95	Plant biomass degradation by fungi. <i>Fungal Genetics and Biology</i> , 2014, 72, 1.	2.1	3
96	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. <i>Fungal Biology</i> , 2016, , 119-160.	0.6	2
97	Fungal Ligninolytic 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.	2.2	1
100	Efficient Extraction Method for High Quality Fungal RNA from Complex Lignocellulosic Substrates. <i>Methods in Molecular Biology</i> , 2018, 1775, 69-73.	0.9	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.	0.4	0