Ronald P De Vries

List of Publications by Year
in descending order

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261 papers	21,706 citations	16791 66 h-index	12272 138 g-index
266 all docs	266 docs citations	266 times ranked	17439 citing authors

#	ARTICLE	IF	CITATIONS
1	Xylitol production from plant biomass by Aspergillus niger through metabolic engineering. Bioresource Technology, 2022, 344, 126199.	4.8	20
2	Fungal xylanolytic enzymes: Diversity and applications. Bioresource Technology, 2022, 344, 126290.	4.8	33
3	Comparative characterization of nine novel GH51, GH54 and GH62 Î±â€<scp>l</scp>â€arabinofuranosidases from <i>Penicillium subrubescens</i>. FEBS Letters, 2022, 596, 360-368.	1.3	8
4	Glycoside Hydrolase family 30 harbors fungal subfamilies with distinct polysaccharide specificities. New Biotechnology, 2022, 67, 32-41.	2.4	7
5	Fungal glycoside hydrolase family 44 xyloglucanases are restricted to the phylum Basidiomycota and show a distinct xyloglucan cleavage pattern. IScience, 2022, 25, 103666.	1.9	10
6	Detailed analysis of the D-galactose catabolic pathways in Aspergillus niger reveals complexity at both metabolic and regulatory level. Fungal Genetics and Biology, 2022, 159, 103670.	0.9	7
7	Screening of novel fungal Carbohydrate Esterase family 1 enzymes identifies three novel dual feruloyl/acetyl xylan esterases. FEBS Letters, 2022, 596, 1932-1943.	1.3	3
8	GalR, GalX and AraR coâ€regulate <scp>d</scp>â€galactose and <scp>l</scp>â€arabinose utilization in <i>Aspergillus nidulans</i>. Microbial Biotechnology, 2022, 15, 1839-1851.	2.0	4
9	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus Aspergillus niger. IScience, 2022, 25, 104065.	1.9	5
10	Carbohydrate esterase family 16 contains fungal hemicellulose acetyl esterases (HAEs) with varying specificity. New Biotechnology, 2022, 70, 28-38.	2.4	9
11	Potential Fungi Isolated From Anti-biodegradable Chinese Medicine Residue to Degrade Lignocellulose. Frontiers in Microbiology, 2022, 13, .	1.5	2
12	GH10 and GH11 endoxylanases in Penicillium subrubescens: Comparative characterization and synergy with GH51, GH54, GH62 Î±-L-arabinofuranosidases from the same fungus. New Biotechnology, 2022, 70, 84-92.	2.4	5
13	Genetic Engineering for Strain Improvement in Filamentous Fungi. , 2021, , 489-504.		4
14	Molecular engineering to improve lignocellulosic biomass based applications using filamentous fungi. Advances in Applied Microbiology, 2021, 114, 73-109.	1.3	8
15	Degradation of Homocyclic Aromatic Compounds by Fungi. , 2021, , 477-488.		0
16	Bioinformatics Approaches for Fungal Biotechnology. , 2021, , 536-554.		0
17	Discovery and Functional Analysis of a Salicylic Acid Hydroxylase from Aspergillus niger. Applied and Environmental Microbiology, 2021, 87, .	1.4	17
18	Genetic barcodes allow traceability of CRISPR/Cas9-derived Aspergillus niger strains without affecting their fitness. Current Genetics, 2021, 67, 673-684.	0.8	2

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19	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.	2.0	4
20	Revisiting a â€˜simpleâ€™ fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	2.0	10
21	Production of Protocatechuic Acid from <i>p</i> -Hydroxyphenyl (H) Units and Related Aromatic Compounds Using an Aspergillus niger Cell Factory. MBio, 2021, 12, e0039121.	1.8	14
22	Characterization of d-xylose reductase, XyrB, from Aspergillus niger. Biotechnology Reports (Amsterdam, Netherlands), 2021, 30, e00610.	2.1	5
23	Blocking utilization of major plant biomass polysaccharides leads <i>Aspergillus</i><i>niger</i> towards utilization of minor components. Microbial Biotechnology, 2021, 14, 1683-1698.	2.0	7
24	The chimeric GaaR-XlnR transcription factor induces pectinolytic activities in the presence of D-xylose in Aspergillus niger. Applied Microbiology and Biotechnology, 2021, 105, 5553-5564.	1.7	5
25	Vanillic acid and methoxyhydroquinone production from guaiacyl units and related aromatic compounds using Aspergillus niger cell factories. Microbial Cell Factories, 2021, 20, 151.	1.9	14
26	From lignocellulose to plastics: Knowledge transfer on the degradation approaches by fungi. Biotechnology Advances, 2021, 50, 107770.	6.0	33
27	The Cultivation Method Affects the Transcriptomic Response of Aspergillus niger to Growth on Sugar Beet Pulp. Microbiology Spectrum, 2021, 9, e0106421.	1.2	6
28	Carbon utilization and growth-inhibition of citrus-colonizing Phyllosticta species. Fungal Biology, 2021, 125, 815-825.	1.1	2
29	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.	1.5	16
30	Machine learning prediction of novel pectinolytic enzymes in Aspergillus niger through integrating heterogeneous (post-) genomics data. Microbial Genomics, 2021, 7, .	1.0	2
31	Recombinant production and characterization of six novel GH27 and GH36 Î±-galactosidases from Penicillium subrubescens and their synergism with a commercial mannanase during the hydrolysis of lignocellulosic biomass. Bioresource Technology, 2020, 295, 122258.	4.8	21
32	CRISPR/Cas9 technology enables the development of the filamentous ascomycete fungus Penicillium subrubescens as a new industrial enzyme producer. Enzyme and Microbial Technology, 2020, 133, 109463.	1.6	34
33	Evolutionary adaptation of <i>Aspergillus niger</i> for increased ferulic acid tolerance. Journal of Applied Microbiology, 2020, 128, 735-746.	1.4	10
34	Macroalgae Derived Fungi Have High Abilities to Degrade Algal Polymers. Microorganisms, 2020, 8, 52.	1.6	24
35	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus Dichomitus squalens. Journal of Biotechnology, 2020, 308, 35-39.	1.9	7
36	Colonies of the fungus Aspergillus niger are highly differentiated to adapt to local carbon source variation. Environmental Microbiology, 2020, 22, 1154-1166.	1.8	15

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37	Functional Validation of Two Fungal Subfamilies in Carbohydrate Esterase Family 1 by Biochemical Characterization of Esterases From Uncharacterized Branches. Frontiers in Bioengineering and Biotechnology, 2020, 8, 694.	2.0	17
38	Feruloyl Esterases for Biorefineries: Subfamily Classified Specificity for Natural Substrates. Frontiers in Bioengineering and Biotechnology, 2020, 8, 332.	2.0	39
39	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i>. DNA Research, 2020, 27, .	1.5	32
40	A comparative genomics study of 23 Aspergillus species from section Flavi. Nature Communications, 2020, 11, 1106.	5.8	125
41	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in Aspergillus niger revealed the inducer of the pathway regulator. Microbiological Research, 2020, 234, 126426.	2.5	11
42	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. Trends in Microbiology, 2020, 28, 487-499.	3.5	25
43	Evidence for ligninolytic activity of the ascomycete fungus Podospora anserina. Biotechnology for Biofuels, 2020, 13, 75.	6.2	25
44	Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7, 5.	2.5	228
45	The Current Biotechnological Status and Potential of Plant and Algal Biomass Degrading/Modifying Enzymes from Ascomycete Fungi. Grand Challenges in Biology and Biotechnology, 2020, , 81-120.	2.4	13
46	Penicillium subrubescens adapts its enzyme production to the composition of plant biomass. Bioresource Technology, 2020, 311, 123477.	4.8	15
47	Engineering of primary carbon metabolism in filamentous fungi. Biotechnology Advances, 2020, 43, 107551.	6.0	28
48	CRISPR/Cas9 facilitates rapid generation of constitutive forms of transcription factors in Aspergillus niger through specific on-site genomic mutations resulting in increased saccharification of plant biomass. Enzyme and Microbial Technology, 2020, 136, 109508.	1.6	29
49	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in Aspergillus niger. Frontiers in Bioengineering and Biotechnology, 2019, 7, 249.	2.0	19
50	Discovery of Novelp-Hydroxybenzoate-m-hydroxylase, Protocatechuate 3,4 Ring-Cleavage Dioxygenase, and Hydroxyquinol 1,2 Ring-Cleavage Dioxygenase from the Filamentous FungusAspergillus niger. ACS Sustainable Chemistry and Engineering, 2019, 7, 19081-19089.	3.2	25
51	The quest for fungal strains and their co-culture potential to improve enzymatic degradation of Chinese distillersâ€™ grain and other agricultural wastes. International Biodeterioration and Biodegradation, 2019, 144, 104765.	1.9	16
52	Myceliophthora thermophila Xyr1 is predominantly involved in xylan degradation and xylose catabolism. Biotechnology for Biofuels, 2019, 12, 220.	6.2	14
53	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. Biotechnology Advances, 2019, 37, 107396.	6.0	83
54	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus Dichomitus squalens. Microbiology Resource Announcements, 2019, 8, .	0.3	22

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55	Deletion of either the regulatory gene ara1 or metabolic gene xki1 in Trichoderma reesei leads to increased CAZyme gene expression on crude plant biomass. Biotechnology for Biofuels, 2019, 12, 81.	6.2	10
56	The presence of trace components significantly broadens the molecular response of Aspergillus niger to guar gum. New Biotechnology, 2019, 51, 57-66.	2.4	10
57	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.	6.0	46
58	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i>. Applied and Environmental Microbiology, 2019, 85, .	1.4	21
59	Transcriptome analysis of Aspergillus niger xlnR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. BMC Genomics, 2019, 20, 853.	1.2	5
60	Enzymatic Adaptation of Podospora anserina to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. Biotechnology Journal, 2019, 14, 1800185.	1.8	11
61	l-Arabinose induces d-galactose catabolism via the Leloir pathway in Aspergillus nidulans. Fungal Genetics and Biology, 2019, 123, 53-59.	0.9	6
62	<i>Talaromyces borbonicus</i>, sp. nov., a novel fungus from biodegraded <i>Arundo donax</i> with potential abilities in lignocellulose conversion. Mycologia, 2018, 110, 316-324.	0.8	13
63	Temporal microbiota and biochemical profiles during production and ripening of Divle Cave cheese. International Journal of Dairy Technology, 2018, 71, 99-106.	1.3	2
64	Draft Genome Sequence of the Basidiomycete White-Rot Fungus Phlebia centrifuga. Genome Announcements, 2018, 6, .	0.8	11
65	Basidiomycete Genomics. Fungal Genetics and Biology, 2018, 112, 1.	0.9	0
66	A senescence-delaying pre-culture medium for transcriptomics of Podospora anserina. Journal of Microbiological Methods, 2018, 146, 33-36.	0.7	5
67	Selective Cleavage of Lignin Î²-<i>O</i>-4 Aryl Ether Bond by Î²-Etherase of the White-Rot Fungus <i>Dichomitus squalens</i>. ACS Sustainable Chemistry and Engineering, 2018, 6, 2878-2882.	3.2	66
68	The physiology of Agaricus bisporus in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. Fungal Genetics and Biology, 2018, 112, 12-20.	0.9	9
69	<scp>ARA</scp>1 regulates not only <scp>l</scp>â€arabinose but also <scp>d</scp>â€galactose catabolism in <i>Trichoderma reesei</i>. FEBS Letters, 2018, 592, 60-70.	1.3	37
70	Draft Genome Sequence of Talaromyces adpressus. Genome Announcements, 2018, 6, .	0.8	1
71	The fungus Aspergillus niger consumes sugars in a sequential manner that is not mediated by the carbon catabolite repressor CreA. Scientific Reports, 2018, 8, 6655.	1.6	24
72	Induction of Genes Encoding Plant Cell Wall-Degrading Carbohydrate-Active Enzymes by Lignocellulose-Derived Monosaccharides and Cellobiose in the White-Rot Fungus Dichomitus squalens. Applied and Environmental Microbiology, 2018, 84, .	1.4	31

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73	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. New Biotechnology, 2018, 40, 282-287.	2.4	29
74	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. New Biotechnology, 2018, 41, 9-14.	2.4	33
75	Temporal transcriptome analysis of the white-rot fungus Obba rivulosa shows expression of a constitutive set of plant cell wall degradation targeted genes during growth on solid spruce wood. Fungal Genetics and Biology, 2018, 112, 47-54.	0.9	21
76	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.	0.9	42
77	The gold-standard genome of <i>Aspergillus niger</i> NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. Studies in Mycology, 2018, 91, 61-78.	4.5	62
78	Duplications and losses of genes encoding known elements of the stress defence system of the Aspergilli contribute to the evolution of these filamentous fungi but do not directly influence their environmental stress tolerance. Studies in Mycology, 2018, 91, 23-36.	4.5	21
79	Genomic and exoproteomic diversity in plant biomass degradation approaches among Aspergilli. Studies in Mycology, 2018, 91, 79-99.	4.5	24
80	Fungal Stress Database (FSD)â€“â€“a repository of fungal stress physiological data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	13
81	Genomic and Genetic Insights Into a Cosmopolitan Fungus, Paecilomyces variotii (Eurotiales). Frontiers in Microbiology, 2018, 9, 3058.	1.5	35
82	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	1.8	36
83	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	2.5	20
84	The obligate alkalophilic sodaâ€·lake fungus Sodiomyces alkalinus has shifted to a protein diet. Molecular Ecology, 2018, 27, 4808-4819.	2.0	20
85	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. Nature Genetics, 2018, 50, 1688-1695.	9.4	160
86	Improved Hemicellulase Production by Genetic Modification of Carbon Catabolite Repression and Xylanolitic Activation in Aspergillus niger. Current Biotechnology, 2018, 7, 10-18.	0.2	7
87	Physiological background of the remarkably high Cd²⁺ tolerance of the <i>Aspergillus fumigatus</i> Af293 strain. Journal of Basic Microbiology, 2018, 58, 957-967.	1.8	10
88	On the origin of vanillyl alcohol oxidases. Fungal Genetics and Biology, 2018, 116, 24-32.	0.9	28
89	In Silico Analysis of Putative Sugar Transporter Genes in Aspergillus niger Using Phylogeny and Comparative Transcriptomics. Frontiers in Microbiology, 2018, 9, 1045.	1.5	47
90	The Synthetic Potential of Fungal Feruloyl Esterases: A Correlation with Current Classification Systems and Predicted Structural Properties. Catalysts, 2018, 8, 242.	1.6	15

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91	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in Aspergillus nidulans. BMC Genomics, 2018, 19, 214.	1.2	11
92	Characterization of a feruloyl esterase from <i>Aspergillus terreus</i> facilitates the division of fungal enzymes from Carbohydrate Esterase family 1 of the carbohydrateâ€active enzymes (CAZy) database. Microbial Biotechnology, 2018, 11, 869-880.	2.0	36
93	Introduction: Overview of Fungal Genomics. Methods in Molecular Biology, 2018, 1775, 1-7.	0.4	0
94	Evolutionary Adaptation to Generate Mutants. Methods in Molecular Biology, 2018, 1775, 133-137.	0.4	1
95	Role of Microbial Cultures and Enzymes During Cheese Production and Ripening. Advances in Medical Technologies and Clinical Practice Book Series, 2018, , 182-203.	0.3	3
96	Secretion of small proteins is speciesâ€specific within <i>Aspergillus</i> sp. Microbial Biotechnology, 2017, 10, 323-329.	2.0	23
97	Mixed colonies of Aspergillus niger and Aspergillus oryzae cooperatively degrading wheat bran. Fungal Genetics and Biology, 2017, 102, 31-37.	0.9	23
98	The draft genome sequence of the ascomycete fungus Penicillium subrubescens reveals a highly enriched content of plant biomass related CAZymes compared to related fungi. Journal of Biotechnology, 2017, 246, 1-3.	1.9	33
99	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
100	Genome Sequence of the Basidiomycete White-Rot Fungus Trametes pubescens FBCC735. Genome Announcements, 2017, 5, .	0.8	11
101	Cultivation of Podospora anserina on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. New Biotechnology, 2017, 37, 162-171.	2.4	22
102	Characterisation of three fungal glucuronoyl esterases on glucuronic acid ester model compounds. Applied Microbiology and Biotechnology, 2017, 101, 5301-5311.	1.7	23
103	The pathway intermediate 2â€ketoâ€3â€deoxyâ€Lâ€galactonate mediates the induction of genes involved in Dâ€galacturonic acid utilization in <i>Aspergillus niger</i>. FEBS Letters, 2017, 591, 1408-1418.	1.3	25
104	Occurrence and function of enzymes for lignocellulose degradation in commercial Agaricus bisporus cultivation. Applied Microbiology and Biotechnology, 2017, 101, 4363-4369.	1.7	59
105	Regulators of plant biomass degradation in ascomycetous fungi. Biotechnology for Biofuels, 2017, 10, 152.	6.2	202
106	Hydrolytic potential of five fungal supernatants to enhance a commercial enzyme cocktail. Biotechnology Letters, 2017, 39, 1403-1411.	1.1	20
107	Microbial Interactions. Fungal Genetics and Biology, 2017, 102, 1-3.	0.9	0
108	Expanding the feruloyl esterase gene family of Aspergillus niger by characterization of a feruloyl esterase, FaeC. New Biotechnology, 2017, 37, 200-209.	2.4	52

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109	The molecular response of the whiteâ€rot fungus <scp><i>D</i></scp><i>ichomitus squalens</i> to wood and nonâ€woody biomass as examined by transcriptome and exoproteome analyses. Environmental Microbiology, 2017, 19, 1237-1250.	1.8	55
110	Combinatorial control of gene expression in Aspergillus niger grown on sugar beet pectin. Scientific Reports, 2017, 7, 12356.	1.6	64
111	Genetic transformation of the white-rot fungus Dichomitus squalens using a new commercial protoplasting cocktail. Journal of Microbiological Methods, 2017, 143, 38-43.	0.7	12
112	High resolution visualization and exoâ€proteomics reveal the physiological role of XlnR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i>. Environmental Microbiology, 2017, 19, 4587-4598.	1.8	6
113	N -acetylglucosamine, the building block of chitin, inhibits growth of Neurospora crassa. Fungal Genetics and Biology, 2017, 107, 1-11.	0.9	29
114	In vivo functional analysis of L-rhamnose metabolic pathway in Aspergillus niger: a tool to identify the potential inducer of RhaR. BMC Microbiology, 2017, 17, 214.	1.3	18
115	Fungal Ligninolytic Enzymes and Their Applications. , 2017, , 1049-1061.		2
116	Expression-based clustering of CAZyme-encoding genes of Aspergillus niger. BMC Genomics, 2017, 18, 900.	1.2	54
117	Mold-Ripened and Raw Milk Cheeses. , 2017, , 353-361.		2
118	Functional diversity in Dichomitus squalens monokaryons. IMA Fungus, 2017, 8, 17-25.	1.7	22
119	A novel <scp>l</scp>â€arabinoseâ€responsive regulator discovered in the riceâ€blast fungus <i>Pyricularia oryzae</i> (<i>Magnaporthe oryzae</i>). FEBS Letters, 2016, 590, 550-558.	1.3	22
120	Fungal Ligninolytic Enzymes and Their Applications. Microbiology Spectrum, 2016, 4, .	1.2	19
121	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	1.8	175
122	Characterization and biotechnological application of recombinant xylanases from Aspergillus nidulans. International Journal of Biological Macromolecules, 2016, 91, 60-67.	3.6	35
123	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. Fungal Biology, 2016, , 119-160.	0.3	2
124	Volatile compound profiling of Turkish Divle Cave cheese during production and ripening. Journal of Dairy Science, 2016, 99, 5120-5131.	1.4	37
125	Penicillium subrubescens is a promising alternative for Aspergillus niger in enzymatic plant biomass saccharification. New Biotechnology, 2016, 33, 834-841.	2.4	27
126	Protease and lipase activities of fungal and bacterial strains derived from an artisanal raw ewe's milk cheese. International Journal of Food Microbiology, 2016, 237, 17-27.	2.1	72

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127	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. Biotechnology for Biofuels, 2016, 9, 231.	6.2	133
128	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. Genome Announcements, 2016, 4, .	0.8	15
129	Generic names in Magnaporthales. IMA Fungus, 2016, 7, 155-159.	1.7	98
130	Current challenges of research on filamentous fungi in relation to human welfare and a sustainable bio-economy: a white paper. Fungal Biology and Biotechnology, 2016, 3, 6.	2.5	208
131	Cooperation of <i>Aspergillus nidulans</i> enzymes increases plant polysaccharide saccharification. Biotechnology Journal, 2016, 11, 988-992.	1.8	8
132	Sexual crossing of thermophilic fungus Myceliophthora heterothallica improved enzymatic degradation of sugar beet pulp. Biotechnology for Biofuels, 2016, 9, 41.	6.2	6
133	The transcriptional activator GaaR of <i>AspergillusÂniger</i> is required for release and utilization of <scp>dâ€</scp>galacturonic acid from pectin. FEBS Letters, 2016, 590, 1804-1815.	1.3	64
134	Enhancing saccharification of wheat straw by mixing enzymes from genetically-modified Trichoderma reesei and Aspergillus niger. Biotechnology Letters, 2016, 38, 65-70.	1.1	24
135	Improving cellulase production by Aspergillus niger using adaptive evolution. Biotechnology Letters, 2016, 38, 969-974.	1.1	28
136	The diversity and evolution of microbiota in traditional Turkish Divle Cave cheese during ripening. International Dairy Journal, 2016, 58, 50-53.	1.5	43
137	Production of Feruloyl Esterases by Aspergillus Species. , 2016, , 129-144.		1
138	Evolutionary Adaptation as a Tool to Generate Targeted Mutant Strains as Evidence by Increased Inulinase Production in Aspergillus oryzae. , 2016, , 189-196.		2
139	Spatial differentiation of gene expression in Aspergillus niger colony grown for sugar beet pulp utilization. Scientific Reports, 2015, 5, 13592.	1.6	15
140	Uncovering the abilities of <scp><i>A</i></scp><i>garicus bisporus</i> to degrade plant biomass throughout its life cycle. Environmental Microbiology, 2015, 17, 3098-3109.	1.8	49
141	Compost Grown Agaricus bisporus Lacks the Ability to Degrade and Consume Highly Substituted Xylan Fragments. PLoS ONE, 2015, 10, e0134169.	1.1	19
142	Disruption of photoautotrophic intertidal mats by filamentous fungi. Environmental Microbiology, 2015, 17, 2910-2921.	1.8	13
143	Aromatic Metabolism of Filamentous Fungi in Relation to the Presence of Aromatic Compounds in Plant Biomass. Advances in Applied Microbiology, 2015, 91, 63-137.	1.3	97
144	Sugar Catabolism in Aspergillus and Other Fungi Related to the Utilization of Plant Biomass. Advances in Applied Microbiology, 2015, 90, 1-28.	1.3	46

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145	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3451-3456.	3.3	63
146	The interaction of induction and repression mechanisms in the regulation of galacturonic acid-induced genes in Aspergillus niger. Fungal Genetics and Biology, 2015, 82, 32-42.	0.9	24
147	Accumulation of recalcitrant xylan in mushroom-compost is due to a lack of xylan substituent removing enzyme activities of Agaricus bisporus. Carbohydrate Polymers, 2015, 132, 359-368.	5.1	6
148	The influence of pretreatment methods on saccharification of sugarcane bagasse by an enzyme extract from Chrysoporthe cubensis and commercial cocktails: A comparative study. Bioresource Technology, 2015, 192, 670-676.	4.8	49
149	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. Biotechnology for Biofuels, 2015, 8, 107.	6.2	111
150	<scp><i>B</i></scp><i>acillus subtilis</i> attachment to <scp><i>A</i></scp><i>spergillus niger</i> hyphae results in mutually altered metabolism. Environmental Microbiology, 2015, 17, 2099-2113.	1.8	112
151	FluG affects secretion in colonies of Aspergillus niger. Antonie Van Leeuwenhoek, 2015, 107, 225-240.	0.7	14
152	Genetic Interaction of Aspergillus nidulans galR, xlnR and araR in Regulating D-Galactose and L-Arabinose Release and Catabolism Gene Expression. PLoS ONE, 2015, 10, e0143200.	1.1	41
153	Oxalate-Metabolising Genes of the White-Rot Fungus Dichomitus squalens Are Differentially Induced on Wood and at High Proton Concentration. PLoS ONE, 2014, 9, e87959.	1.1	29
154	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. Microbiology and Molecular Biology Reviews, 2014, 78, 614-649.	2.9	340
155	Synergistic effect of <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> enzyme sets on the saccharification of wheat straw and sugarcane bagasse. Biotechnology Journal, 2014, 9, 1329-1338.	1.8	38
156	8 Degradation and Modification of Plant Biomass by Fungi. , 2014, , 175-208.		26
157	Aspergillus niger RhaR, a regulator involved in l-rhamnose release and catabolism. Applied Microbiology and Biotechnology, 2014, 98, 5531-40.	1.7	56
158	Modern Taxonomy of Biotechnologically Important Aspergillus and Penicillium Species. Advances in Applied Microbiology, 2014, 86, 199-249.	1.3	186
159	Overexpression, purification and characterisation of homologous <i>Î±</i>-<scp>l</scp>-arabinofuranosidase and <i>endo</i>-1,4-<i>Î²</i>-<scp>d</scp>-glucanase in <i>Aspergillus vadensis</i>. Journal of Industrial Microbiology and Biotechnology, 2014, 41, 1697-1708.	1.4	6
160	Resolving the polyphyletic nature of<i>Pyricularia</i>(<i>Pyriculariaceae</i>). Studies in Mycology, 2014, 79, 85-120.	4.5	175
161	Similar is not the same: Differences in the function of the (hemi-)cellulolytic regulator XlnR (Xlr1/Xyr1) in filamentous fungi. Fungal Genetics and Biology, 2014, 72, 73-81.	0.9	80
162	Genomic and transcriptomic analysis of Laccaria bicolor CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. Fungal Genetics and Biology, 2014, 72, 168-181.	0.9	81

#	ARTICLE	IF	CITATIONS
163	Genomics, Lifestyles and Future Prospects of Wood-Decay and Litter-Decomposing Basidiomycota. Advances in Botanical Research, 2014, 70, 329-370.	0.5	87
164	(Post-)Genomics approaches in fungal research. Briefings in Functional Genomics, 2014, 13, 424-439.	1.3	16
165	Regulation of Plant Biomass Utilization in Aspergillus. Advances in Applied Microbiology, 2014, 88, 31-56.	1.3	48
166	The genome of the white-rot fungus Pycnoporus cinnabarinus: a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	1.2	91
167	A genomic survey of proteases in Aspergilli. BMC Genomics, 2014, 15, 523.	1.2	36
168	Complementary symbiont contributions to plant decomposition in a fungus-farming termite. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14500-14505.	3.3	243
169	Plant biomass degradation by fungi. Fungal Genetics and Biology, 2014, 72, 1.	0.9	3
170	An improved and reproducible protocol for the extraction of high quality fungal RNA from plant biomass substrates. Fungal Genetics and Biology, 2014, 72, 201-206.	0.9	20
171	Carbohydrate-related enzymes of important Phytophthora plant pathogens. Fungal Genetics and Biology, 2014, 72, 192-200.	0.9	61
172	Prevalence of transcription factors in ascomycete and basidiomycete fungi. BMC Genomics, 2014, 15, 214.	1.2	114
173	Plant biomass degradation by fungi. Fungal Genetics and Biology, 2014, 72, 2-9.	0.9	91
174	The transcriptional activators AraR and XlnR from Aspergillus niger regulate expression of pentose catabolic and pentose phosphate pathway genes. Research in Microbiology, 2014, 165, 531-540.	1.0	34
175	The distinctive regulatory roles of PrtT in the cell metabolism of Penicillium oxalicum. Fungal Genetics and Biology, 2014, 63, 42-54.	0.9	32
176	The influence of Aspergillus niger transcription factors AraR and XlnR in the gene expression during growth in d-xylose, l-arabinose and steam-exploded sugarcane bagasse. Fungal Genetics and Biology, 2013, 60, 29-45.	0.9	63
177	Xlr1 is involved in the transcriptional control of the pentose catabolic pathway, but not hemi-cellulolytic enzymes in Magnaporthe oryzae. Fungal Genetics and Biology, 2013, 57, 76-84.	0.9	32
178	The pentose catabolic pathway of the rice-blast fungus Magnaporthe oryzae involves a novel pentose reductase restricted to few fungal species. FEBS Letters, 2013, 587, 1346-1352.	1.3	16
179	Preface to Agaricus bisporus â€“ Beyond the genome Special Issue. Fungal Genetics and Biology, 2013, 55, 1.	0.9	0
180	Aspergillus: Genomics of a Cosmopolitan Fungus. Soil Biology, 2013, , 89-126.	0.6	4

#	ARTICLE	IF	CITATIONS
181	Carbohydrate utilization and metabolism is highly differentiated in Agaricus bisporus. BMC Genomics, 2013, 14, 663.	1.2	35
182	Phylogenetic analysis and substrate specificity of GH2 Î²â€mannosidases from <i>Aspergillus</i> species. FEBS Letters, 2013, 587, 3444-3449.	1.3	15
183	Nutritional physiology of a rock-inhabiting, model microcolonial fungus from an ancestral lineage of the Chaetothyriales (Ascomycetes). Fungal Genetics and Biology, 2013, 56, 54-66.	0.9	62
184	Occurrence of Aspergillus allahabadii on sandstone at Bayon temple, Angkor Thom, Cambodia. International Biodeterioration and Biodegradation, 2013, 76, 112-117.	1.9	44
185	Physiological and molecular aspects of degradation of plant polysaccharides by fungi: What have we learned from <i>Aspergillus</i>?. Biotechnology Journal, 2013, 8, 884-894.	1.8	67
186	Efficient Plant Biomass Degradation by Thermophilic Fungus Myceliophthora heterothallica. Applied and Environmental Microbiology, 2013, 79, 1316-1324.	1.4	47
187	Disruption of the <scp>L</scp>â€arabitol dehydrogenase encoding gene in <i>Aspergillus tubingensis</i> results in increased xylanase production. Biotechnology Journal, 2013, 8, 905-911.	1.8	7
188	The Genomes of the Fungal Plant Pathogens Cladosporium fulvum and Dothistroma septosporum Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	1.5	226
189	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 17501-17506.	3.3	359
190	GalX regulates the <scp>d</scp>â€galactose oxidoâ€reductive pathway in <i>Aspergillus niger</i>. FEBS Letters, 2012, 586, 3980-3985.	1.3	39
191	Insight into tradeâ€off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	3.5	210
192	Mapping the polysaccharide degradation potential of Aspergillus niger. BMC Genomics, 2012, 13, 313.	1.2	35
193	Degradation of different pectins by fungi: correlations and contrasts between the pectinolytic enzyme sets identified in genomes and the growth on pectins of different origin. BMC Genomics, 2012, 13, 321.	1.2	86
194	Comparative genomics of the white-rot fungi, Phanerochaete carnosa and P. chrysosporium, to elucidate the genetic basis of the distinct wood types they colonize. BMC Genomics, 2012, 13, 444.	1.2	125
195	Construction of a cellulase hyper-expression system in Trichoderma reesei by promoter and enzyme engineering. Microbial Cell Factories, 2012, 11, 21.	1.9	105
196	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 5458-5463.	3.3	259
197	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. Science, 2012, 336, 1715-1719.	6.0	1,424
198	d-Galactose uptake is nonfunctional in the conidiospores of Aspergillus niger. FEMS Microbiology Letters, 2012, 329, 198-203.	0.7	16

#	ARTICLE	IF	CITATIONS
199	Phylogeny of the industrial relevant, thermophilic genera Myceliophthora and Corynascus. Fungal Diversity, 2012, 52, 197-207.	4.7	59
200	A broader role for AmyR in Aspergillus niger: regulation of the utilisation of d-glucose or d-galactose containing oligo- and polysaccharides. Applied Microbiology and Biotechnology, 2012, 93, 285-293.	1.7	67
201	Analysis of regulation of pentose utilisation in Aspergillus niger reveals evolutionary adaptations in Eurotiales. Studies in Mycology, 2011, 69, 31-38.	4.5	123
202	Growth and hydrolase profiles can be used as characteristics to distinguish Aspergillus niger and other black aspergilli. Studies in Mycology, 2011, 69, 19-30.	4.5	60
203	Genomic Analysis of the Necrotrophic Fungal Pathogens Sclerotinia sclerotiorum and Botrytis cinerea. PLoS Genetics, 2011, 7, e1002230.	1.5	902
204	Comparative genomic analysis of the thermophilic biomass-degrading fungi Myceliophthora thermophila and Thielavia terrestris. Nature Biotechnology, 2011, 29, 922-927.	9.4	428
205	Heterogenic expression of genes encoding secreted proteins at the periphery of <i>Aspergillus niger</i> colonies. Environmental Microbiology, 2011, 13, 216-225.	1.8	58
206	The Î±-glucuronidase Agu1 from Schizophyllum commune is a member of a novel glycoside hydrolase family (GH115). Applied Microbiology and Biotechnology, 2011, 90, 1323-1332.	1.7	39
207	Regulation of pentose utilisation by AraR, but not XlnR, differs in Aspergillus nidulans and Aspergillus niger. Applied Microbiology and Biotechnology, 2011, 91, 387-397.	1.7	67
208	Fungal enzyme sets for plant polysaccharide degradation. Applied Microbiology and Biotechnology, 2011, 91, 1477-1492.	1.7	563
209	Transcriptome analysis of Aspergillus niger grown on sugarcane bagasse. Biotechnology for Biofuels, 2011, 4, 40.	6.2	122
210	Carbohydrate-active enzymes from the zygomycete fungus Rhizopus oryzae: a highly specialized approach to carbohydrate degradation depicted at genome level. BMC Genomics, 2011, 12, 38.	1.2	105
211	Improved enzyme production by co-cultivation of Aspergillus niger and Aspergillus oryzae and with other fungi. International Biodeterioration and Biodegradation, 2011, 65, 248-252.	1.9	105
212	Post-genomic approaches to understanding interactions between fungi and their environment. IMA Fungus, 2011, 2, 81-86.	1.7	11
213	The Plant Cell Wallâ€"Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. Science, 2011, 333, 762-765.	6.0	512
214	Finished Genome of the Fungal Wheat Pathogen Mycosphaerella graminicola Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. PLoS Genetics, 2011, 7, e1002070.	1.5	532
215	Unique Regulatory Mechanism for d-Galactose Utilization in Aspergillus nidulans. Applied and Environmental Microbiology, 2011, 77, 7084-7087.	1.4	48
216	The Amsterdam Declaration on Fungal Nomenclature. IMA Fungus, 2011, 2, 105-111.	1.7	320

#	Article	IF	Citations
217	(Hemi-)Cellulose Degrading Enzymes and Their Encoding Genes from Aspergillus and Trichoderma. , 2011, , 341-355.		2
218	Fungal Degradation of Plant Bacterial Strategies for Plant. , 2011, , .		0
219	Genome sequence of the model mushroom Schizophyllum commune. Nature Biotechnology, 2010, 28, 957-963.	9.4	490
220	Spatial and Developmental Differentiation of Mannitol Dehydrogenase and Mannitol-1-Phosphate Dehydrogenase in Aspergillus niger. Eukaryotic Cell, 2010, 9, 1398-1402.	3.4	20
221	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. Genome Biology, 2010, 11, R73.	13.9	391
222	A single amino acid change (Y318F) in the L-arabitol dehydrogenase (LadA) from Aspergillus niger results in a significant increase in affinity for D-sorbitol. BMC Microbiology, 2009, 9, 166.	1.3	6
223	Characterization of oxylipins and dioxygenase genes in the asexual fungus Aspergillus niger. BMC Microbiology, 2009, 9, 59.	1.3	30
224	The <i>Hypocrea jecorina</i> (syn. <i>Trichoderma reesei</i>) <i>lxr1</i> gene encodes a <scp>d</scp>â€mannitol dehydrogenase and is not involved in <scp>l</scp>â€arabinose catabolism. FEBS Letters, 2009, 583, 1309-1313.	1.3	24
225	Two glucuronoyl esterases of Phanerochaete chrysosporium. Archives of Microbiology, 2009, 191, 133-140.	1.0	51
226	Technical advance in fungal biotechnology: development of a miniaturized culture method and an automated high-throughput screening. Letters in Applied Microbiology, 2009, 49, 278-282.	1.0	27
227	Post-genomic insights into the plant polysaccharide degradation potential of Aspergillus nidulans and comparison to Aspergillus niger and Aspergillus oryzae. Fungal Genetics and Biology, 2009, 46, S161-S169.	0.9	133
228	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99
229	Control and possible applications of a novel carrot-spoilage basidiomycete, FibulorhizoctoniaÂ psychrophila. Antonie Van Leeuwenhoek, 2008, 93, 407-413.	0.7	10
230	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. Biotechnology Letters, 2008, 30, 387-396.	1.1	136
231	The genome sequence of the model ascomycete fungus Podospora anserina. Genome Biology, 2008, 9, R77.	13.9	301
232	Establishment of compatibility in the Ustilago maydis/maize pathosystem. Journal of Plant Physiology, 2008, 165, 29-40.	1.6	106
233	The secretome of the maize pathogen Ustilago maydis. Fungal Genetics and Biology, 2008, 45, S63-S70.	0.9	162
234	Spatial Differentiation in the Vegetative Mycelium of <i>Aspergillus niger</i>. Eukaryotic Cell, 2007, 6, 2311-2322.	3.4	106

#	ARTICLE	IF	CITATIONS
235	Localization of protein secretion in fungal colonies using a novel culturing technique; the ring-plate system. Journal of Microbiological Methods, 2007, 69, 399-401.	0.7	27
236	Identification of genes encoding microbial glucuronoyl esterases. FEBS Letters, 2007, 581, 4029-4035.	1.3	83
237	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	9.4	1,047
238	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. Nature, 2006, 444, 97-101.	13.7	1,113
239	Aspergillus vadensis, a new species of the group of black Aspergilli. Antonie Van Leeuwenhoek, 2005, 87, 195-203.	0.7	58
240	The Value of Genome Sequences in the Rapid Identification of Novel Genes Encoding Specific Plant Cell Wall Degrading Enzymes. Current Genomics, 2005, 6, 157-187.	0.7	22
241	A New Black Aspergillus Species, A. vadensis , Is a Promising Host for Homologous and Heterologous Protein Production. Applied and Environmental Microbiology, 2004, 70, 3954-3959.	1.4	154
242	Glycerol dehydrogenase, encoded by gldB is essential for osmotolerance in Aspergillus nidulans. Molecular Microbiology, 2003, 49, 131-141.	1.2	62
243	Mannitol Is Required for Stress Tolerance in Aspergillus niger Conidiospores. Eukaryotic Cell, 2003, 2, 690-698.	3.4	174
244	Isolation and characterization of two specific regulatory Aspergillus niger mutants shows antagonistic regulation of arabinan and xylan metabolism. Microbiology (United Kingdom), 2003, 149, 1183-1191.	0.7	51
245	The Aspergillus niger faeB gene encodes a second feruloyl esterase involved in pectin and xylan degradation and is specifically induced in the presence of aromatic compounds. Biochemical Journal, 2002, 363, 377-386.	1.7	141
246	The Aspergillus niger faeB gene encodes a second feruloyl esterase involved in pectin and xylan degradation and is specifically induced in the presence of aromatic compounds. Biochemical Journal, 2002, 363, 377.	1.7	84
247	Expression profiling of pectinolytic genes fromAspergillus niger. FEBS Letters, 2002, 530, 41-47.	1.3	102
248	The Î²-1,4-endogalactanase A gene fromAspergillus nigeris specifically induced on arabinose and galacturonic acid and plays an important role in the degradation of pectic hairy regions. FEBS Journal, 2002, 269, 4985-4993.	0.2	28
249	Cloning and characterization of Aspergillus niger genes encoding an Î±-galactosidase and a Î²-mannosidase involved in galactomannan degradation. FEBS Journal, 2001, 268, 2982-2990.	0.2	92
250	TheAspergillus nigerd-xylulose kinase gene is co-expressed with genes encoding arabinan degrading enzymes, and is essential for growth ond-xylose andl-arabinose. FEBS Journal, 2001, 268, 5414-5423.	0.2	60
251	Aspergillus Enzymes Involved in Degradation of Plant Cell Wall Polysaccharides. Microbiology and Molecular Biology Reviews, 2001, 65, 497-522.	2.9	822
252	Trehalose is required for the acquisition of tolerance to a variety of stresses in the filamentous fungus Aspergillus nidulans The GenBank accession number for the sequence reported in this paper is AF043230.. Microbiology (United Kingdom), 2001, 147, 1851-1862.	0.7	187

#	ARTICLE	IF	CITATIONS
253	Synergy between enzymes from Aspergillus involved in the degradation of plant cell wall polysaccharides. Carbohydrate Research, 2000, 327, 401-410.	1.1	229
254	Inverting character of Î±-glucuronidase A from Aspergillus tubingensis. Biochimica Et Biophysica Acta - General Subjects, 2000, 1474, 360-364.	1.1	44
255	Regulation of the Feruloyl Esterase (<i>faeA</i>) Gene from <i>Aspergillus niger</i>. Applied and Environmental Microbiology, 1999, 65, 5500-5503.	1.4	86
256	ThefaeA gene fromAspergillus niger encoding a feruloyl esterase with activity on xylan and pectin is subject to a complex system of regulation. Journal of the Science of Food and Agriculture, 1999, 79, 443-446.	1.7	5
257	CreA modulates the XlnR-induced expression on xylose of Aspergillus niger genes involved in xylan degradation. Research in Microbiology, 1999, 150, 281-285.	1.0	178
258	Differential Expression of Three Î±-Galactosidase Genes and a Single Î²-Galactosidase Gene from <i>Aspergillus niger</i>. Applied and Environmental Microbiology, 1999, 65, 2453-2460.	1.4	97
259	Chemical and thermal stability of ferulic acid (feruloyl) esterases from Aspergillus. Progress in Biotechnology, 1998, , 41-46.	0.2	1
260	The Transcriptional Activator XlnR Regulates Both Xylanolytic and Endoglucanase Gene Expression in <i>Aspergillus niger</i>. Applied and Environmental Microbiology, 1998, 64, 3615-3619.	1.4	326
261	<i>aguA</i> , the Gene Encoding an Extracellular Î±-Glucuronidase from <i>Aspergillus tubingensis</i> , Is Specifically Induced on Xylose and Not on Glucuronic Acid. Journal of Bacteriology, 1998, 180, 243-249.	1.0	71