## Ronald P De Vries

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Xylitol production from plant biomass by Aspergillus niger through metabolic engineering. Bioresource Technology, 2022, 344, 126199.	9.6	20
2	Fungal xylanolytic enzymes: Diversity and applications. Bioresource Technology, 2022, 344, 126290.	9.6	33
3	Comparative characterization of nine novel GH51, GH54 and GH62 αâ€∢scp>lâ€arabinofuranosidases from <i>Penicillium subrubescens</i> . FEBS Letters, 2022, 596, 360-368.	2.8	8
4	Glycoside Hydrolase family 30 harbors fungal subfamilies with distinct polysaccharide specificities. New Biotechnology, 2022, 67, 32-41.	4.4	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.	4.1	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.	2.1	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.	2.8	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.	4.2	4
9	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus Aspergillus niger. IScience, 2022, 25, 104065.	4.1	5
10	Carbohydrate esterase family 16 contains fungal hemicellulose acetyl esterases (HAEs) with varying specificity. New Biotechnology, 2022, 70, 28-38.	4.4	9
11	Potential Fungi Isolated From Anti-biodegradable Chinese Medicine Residue to Degrade Lignocellulose. Frontiers in Microbiology, 2022, 13, .	3.5	2
12	GH10 and GH11 endoxylanases in Penicillium subrubescens: Comparative characterization and synergy with GH51, GH54, GH62 α-L-arabinofuranosidases from the same fungus. New Biotechnology, 2022, 70, 84-92.	4.4	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.	2.4	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, .	3.1	17
18	Genetic barcodes allow traceability of CRISPR/Cas9-derived Aspergillus niger strains without affecting their fitness. Current Genetics, 2021, 67, 673-684.	1.7	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.	4.1	4
20	Revisiting a â€~simple' fungal metabolic pathway reveals redundancy, complexity and diversity. Microbial Biotechnology, 2021, 14, 2525-2537.	4.2	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.	4.1	14
22	Characterization of d-xylose reductase, XyrB, from Aspergillus niger. Biotechnology Reports (Amsterdam, Netherlands), 2021, 30, e00610.	4.4	5
23	Blocking utilization of major plant biomass polysaccharides leads <i>Aspergillusniger</i> towards utilization of minor components. Microbial Biotechnology, 2021, 14, 1683-1698.	4.2	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.	3.6	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.	4.0	14
26	From lignocellulose to plastics: Knowledge transfer on the degradation approaches by fungi. Biotechnology Advances, 2021, 50, 107770.	11.7	33
27	The Cultivation Method Affects the Transcriptomic Response of Aspergillus niger to Growth on Sugar Beet Pulp. Microbiology Spectrum, 2021, 9, e0106421.	3.0	6
28	Carbon utilization and growth-inhibition of citrus-colonizing Phyllosticta species. Fungal Biology, 2021, 125, 815-825.	2.5	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.	3.0	16
30	Machine learning prediction of novel pectinolytic enzymes in Aspergillus niger through integrating heterogeneous (post-) genomics data. Microbial Genomics, 2021, 7, .	2.0	2
31	Recombinant production and characterization of six novel GH27 and GH36 α-galactosidases from Penicillium subrubescens and their synergism with a commercial mannanase during the hydrolysis of lignocellulosic biomass. Bioresource Technology, 2020, 295, 122258.	9.6	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.	3.2	34
33	Evolutionary adaptation of <i>Aspergillus niger</i> for increased ferulic acid tolerance. Journal of Applied Microbiology, 2020, 128, 735-746.	3.1	10
34	Macroalgae Derived Fungi Have High Abilities to Degrade Algal Polymers. Microorganisms, 2020, 8, 52.	3.6	24
35	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus Dichomitus squalens. Journal of Biotechnology, 2020, 308, 35-39.	3.8	7
36	Colonies of the fungus Aspergillus niger are highly differentiated to adapt to local carbon source variation. Environmental Microbiology, 2020, 22, 1154-1166.	3.8	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.	4.1	17
38	Feruloyl Esterases for Biorefineries: Subfamily Classified Specificity for Natural Substrates. Frontiers in Bioengineering and Biotechnology, 2020, 8, 332.	4.1	39
39	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . DNA Research, 2020, 27, .	3.4	32
40	A comparative genomics study of 23 Aspergillus species from section Flavi. Nature Communications, 2020, 11, 1106.	12.8	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.	5.3	11
42	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. Trends in Microbiology, 2020, 28, 487-499.	7.7	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.	5.1	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.	9.6	15
47	Engineering of primary carbon metabolism in filamentous fungi. Biotechnology Advances, 2020, 43, 107551.	11.7	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.	3.2	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.	4.1	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.	6.7	25
51	The quest for fungal strains and their co-culture potential to improve enzymatic degradation of Chinese distillers' grain and other agricultural wastes. International Biodeterioration and Biodegradation, 2019, 144, 104765.	3.9	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.	11.7	83
54	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus Dichomitus squalens. Microbiology Resource Announcements, 2019, 8, .	0.6	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.	4.4	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.	11.7	46
58	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus <i>Dichomitus squalens</i> . Applied and Environmental Microbiology, 2019, 85, .	3.1	21
59	Transcriptome analysis of Aspergillus niger xInR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. BMC Genomics, 2019, 20, 853.	2.8	5
60	Enzymatic Adaptation of Podospora anserina to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. Biotechnology Journal, 2019, 14, 1800185.	3.5	11
61	l-Arabinose induces d-galactose catabolism via the Leloir pathway in Aspergillus nidulans. Fungal Genetics and Biology, 2019, 123, 53-59.	2.1	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.	1.9	13
63	Temporal microbiota and biochemical profiles during production and ripening of Divle Cave cheese. International Journal of Dairy Technology, 2018, 71, 99-106.	2.8	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.	2.1	0
66	A senescence-delaying pre-culture medium for transcriptomics of Podospora anserina. Journal of Microbiological Methods, 2018, 146, 33-36.	1.6	5
67	Selective Cleavage of Lignin β- <i>O</i> -4 Aryl Ether Bond by β-Etherase of the White-Rot Fungus <i>Dichomitus squalens</i> . ACS Sustainable Chemistry and Engineering, 2018, 6, 2878-2882.	6.7	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.	2.1	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.	2.8	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.	3.3	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, .	3.1	31

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73	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. New Biotechnology, 2018, 40, 282-287.	4.4	29
74	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. New Biotechnology, 2018, 41, 9-14.	4.4	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.	2.1	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.	2.1	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.	7.2	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.	7.2	21
79	Genomic and exoproteomic diversity in plant biomass degradation approaches among Aspergilli. Studies in Mycology, 2018, 91, 79-99.	7.2	24
80	Fungal Stress Database (FSD)––a repository of fungal stress physiological data. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	13
81	Genomic and Genetic Insights Into a Cosmopolitan Fungus, Paecilomyces variotii (Eurotiales). Frontiers in Microbiology, 2018, 9, 3058.	3.5	35
82	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. Environmental Microbiology, 2018, 20, 4141-4156.	3.8	36
83	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	5.1	20
84	The obligate alkalophilic soda″ake fungus Sodiomyces alkalinus has shifted to a protein diet. Molecular Ecology, 2018, 27, 4808-4819.	3.9	20
85	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. Nature Genetics, 2018, 50, 1688-1695.	21.4	160
86	Improved Hemicellulase Production by Genetic Modification of Carbon Catabolite Repression and Xylanolitic Activation in Aspergillus niger. Current Biotechnology, 2018, 7, 10-18.	0.4	7
87	Physiological background of the remarkably high Cd <sup>2+</sup> tolerance of the <i>Aspergillus fumigatus</i> Af293 strain. Journal of Basic Microbiology, 2018, 58, 957-967.	3.3	10
88	On the origin of vanillyl alcohol oxidases. Fungal Genetics and Biology, 2018, 116, 24-32.	2.1	28
89	In Silico Analysis of Putative Sugar Transporter Genes in Aspergillus niger Using Phylogeny and Comparative Transcriptomics. Frontiers in Microbiology, 2018, 9, 1045.	3.5	47
90	The Synthetic Potential of Fungal Feruloyl Esterases: A Correlation with Current Classification Systems and Predicted Structural Properties. Catalysts, 2018, 8, 242.	3.5	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.	2.8	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.	4.2	36
93	Introduction: Overview of Fungal Genomics. Methods in Molecular Biology, 2018, 1775, 1-7.	0.9	Ο
94	Evolutionary Adaptation to Generate Mutants. Methods in Molecular Biology, 2018, 1775, 133-137.	0.9	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.	4.2	23
97	Mixed colonies of Aspergillus niger and Aspergillus oryzae cooperatively degrading wheat bran. Fungal Genetics and Biology, 2017, 102, 31-37.	2.1	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.	3.8	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.	8.8	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.	4.4	22
102	Characterisation of three fungal glucuronoyl esterases on glucuronic acid ester model compounds. Applied Microbiology and Biotechnology, 2017, 101, 5301-5311.	3.6	23
103	The pathway intermediate 2â€ketoâ€3â€deoxy‣â€galactonate mediates the induction of genes involved in Dâ€galacturonic acid utilization in <i>Aspergillus niger</i> . FEBS Letters, 2017, 591, 1408-1418.	2.8	25
104	Occurrence and function of enzymes for lignocellulose degradation in commercial Agaricus bisporus cultivation. Applied Microbiology and Biotechnology, 2017, 101, 4363-4369.	3.6	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.	2.2	20
107	Microbial Interactions. Fungal Genetics and Biology, 2017, 102, 1-3.	2.1	0
108	Expanding the feruloyl esterase gene family of Aspergillus niger by characterization of a feruloyl esterase, FaeC. New Biotechnology, 2017, 37, 200-209.	4.4	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.	3.8	55
110	Combinatorial control of gene expression in Aspergillus niger grown on sugar beet pectin. Scientific Reports, 2017, 7, 12356.	3.3	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.	1.6	12
112	High resolution visualization and exoâ€proteomics reveal the physiological role of XInR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i> . Environmental Microbiology, 2017, 19, 4587-4598.	3.8	6
113	N -acetylglucosamine, the building block of chitin, inhibits growth of Neurospora crassa. Fungal Genetics and Biology, 2017, 107, 1-11.	2.1	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.	3.3	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.	2.8	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.	3.8	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.	2.8	22
120	Fungal Ligninolytic Enzymes and Their Applications. Microbiology Spectrum, 2016, 4, .	3.0	19
121	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	3.9	175
122	Characterization and biotechnological application of recombinant xylanases from Aspergillus nidulans. International Journal of Biological Macromolecules, 2016, 91, 60-67.	7.5	35
123	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. Fungal Biology, 2016, , 119-160.	0.6	2
124	Volatile compound profiling of Turkish Divle Cave cheese during production and ripening. Journal of Dairy Science, 2016, 99, 5120-5131.	3.4	37
125	Penicillium subrubescens is a promising alternative for Aspergillus niger in enzymatic plant biomass saccharification. New Biotechnology, 2016, 33, 834-841.	4.4	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.	4.7	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.	3.8	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.	5.1	208
131	Cooperation of <i>Aspergillus nidulans</i> enzymes increases plant polysaccharide saccharification. Biotechnology Journal, 2016, 11, 988-992.	3.5	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.	2.8	64
134	Enhancing saccharification of wheat straw by mixing enzymes from genetically-modified Trichoderma reesei and Aspergillus niger. Biotechnology Letters, 2016, 38, 65-70.	2.2	24
135	Improving cellulase production by Aspergillus niger using adaptive evolution. Biotechnology Letters, 2016, 38, 969-974.	2.2	28
136	The diversity and evolution of microbiota in traditional Turkish Divle Cave cheese during ripening. International Dairy Journal, 2016, 58, 50-53.	3.0	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.	3.3	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.	3.8	49
141	Compost Grown Agaricus bisporus Lacks the Ability to Degrade and Consume Highly Substituted Xylan Fragments. PLoS ONE, 2015, 10, e0134169.	2.5	19
142	Disruption of photoautotrophic intertidal mats by filamentous fungi. Environmental Microbiology, 2015, 17, 2910-2921.	3.8	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.	2.4	97
144	Sugar Catabolism in Aspergillus and Other Fungi Related to the Utilization of Plant Biomass. Advances in Applied Microbiology, 2015, 90, 1-28.	2.4	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.	7.1	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.	2.1	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.	10.2	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.	9.6	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.	3.8	112
151	FluG affects secretion in colonies of Aspergillus niger. Antonie Van Leeuwenhoek, 2015, 107, 225-240.	1.7	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.	2.5	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.	2.5	29
154	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. Microbiology and Molecular Biology Reviews, 2014, 78, 614-649.	6.6	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.	3.5	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.	3.6	56
158	Modern Taxonomy of Biotechnologically Important Aspergillus and Penicillium Species. Advances in Applied Microbiology, 2014, 86, 199-249.	2.4	186
159	Overexpression, purification and characterisation of homologous <i>α</i> - <scp>l</scp> -arabinofuranosidase and <i>endo</i> -1,4- <i>β</i> - <scp>d</scp> -glucanase in <i>Aspergillus vadensis</i> . Journal of Industrial Microbiology and Biotechnology, 2014, 41, 1697-1708.	3.0	6
160	Resolving the polyphyletic nature of <i>Pyricularia</i> ( <i>Pyriculariaceae</i> ). Studies in Mycology, 2014, 79, 85-120.	7.2	175
161	Similar is not the same: Differences in the function of the (hemi-)cellulolytic regulator XInR (XIr1/Xyr1) in filamentous fungi. Fungal Genetics and Biology, 2014, 72, 73-81.	2.1	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.	2.1	81

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