

# Ronald P De Vries

## List of Publications by Year in descending order

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261  
papers

21,706  
citations

16791

66  
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12272

138  
g-index

266  
all docs

266  
docs citations

266  
times ranked

17439  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Paleozoic Origin of Enzymatic Lignin Decomposition Reconstructed from 31 Fungal Genomes. <i>Science</i> , 2012, 336, 1715-1719.	6.0	1,424
2	Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101.	13.7	1,113
3	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	9.4	1,047
4	Genomic Analysis of the Necrotrophic Fungal Pathogens <i>Sclerotinia sclerotiorum</i> and <i>Botrytis cinerea</i> . <i>PLoS Genetics</i> , 2011, 7, e1002230.	1.5	902
5	<i>Aspergillus</i> Enzymes Involved in Degradation of Plant Cell Wall Polysaccharides. <i>Microbiology and Molecular Biology Reviews</i> , 2001, 65, 497-522.	2.9	822
6	Fungal enzyme sets for plant polysaccharide degradation. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1477-1492.	1.7	563
7	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispensome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	1.5	532
8	The Plant Cell Wall "Decomposing Machinery Underlies the Functional Diversity of Forest Fungi. <i>Science</i> , 2011, 333, 762-765.	6.0	512
9	Genome sequence of the model mushroom <i>Schizophyllum commune</i> . <i>Nature Biotechnology</i> , 2010, 28, 957-963.	9.4	490
10	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	9.4	428
11	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
12	Genome sequence of the necrotrophic plant pathogen <i>Pythium ultimum</i> reveals original pathogenicity mechanisms and effector repertoire. <i>Genome Biology</i> , 2010, 11, R73.	13.9	391
13	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	3.3	359
14	Plant-Polysaccharide-Degrading Enzymes from Basidiomycetes. <i>Microbiology and Molecular Biology Reviews</i> , 2014, 78, 614-649.	2.9	340
15	The Transcriptional Activator XlnR Regulates Both Xylanolytic and Endoglucanase Gene Expression in <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 1998, 64, 3615-3619.	1.4	326
16	The Amsterdam Declaration on Fungal Nomenclature. <i>IMA Fungus</i> , 2011, 2, 105-111.	1.7	320
17	The genome sequence of the model ascomycete fungus <i>Podospira anserina</i> . <i>Genome Biology</i> , 2008, 9, R77.	13.9	301
18	Comparative genomics of <i>Ceriporiopsis subvermispora</i> and <i>Phanerochaete chrysosporium</i> provide insight into selective ligninolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 5458-5463.	3.3	259

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19	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
20	Synergy between enzymes from <i>Aspergillus</i> involved in the degradation of plant cell wall polysaccharides. Carbohydrate Research, 2000, 327, 401-410.	1.1	229
21	Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7, 5.	2.5	228
22	The Genomes of the Fungal Plant Pathogens <i>Cladosporium fulvum</i> and <i>Dothistroma septosporum</i> Reveal Adaptation to Different Hosts and Lifestyles But Also Signatures of Common Ancestry. PLoS Genetics, 2012, 8, e1003088.	1.5	226
23	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. New Phytologist, 2012, 194, 1001-1013.	3.5	210
24	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
25	Regulators of plant biomass degradation in ascomycetous fungi. Biotechnology for Biofuels, 2017, 10, 152.	6.2	202
26	Trehalose is required for the acquisition of tolerance to a variety of stresses in the filamentous fungus <i>Aspergillus nidulans</i> The GenBank accession number for the sequence reported in this paper is AF043230.. Microbiology (United Kingdom), 2001, 147, 1851-1862.	0.7	187
27	Modern Taxonomy of Biotechnologically Important <i>Aspergillus</i> and <i>Penicillium</i> Species. Advances in Applied Microbiology, 2014, 86, 199-249.	1.3	186
28	CreA modulates the XlnR-induced expression on xylose of <i>Aspergillus niger</i> genes involved in xylan degradation. Research in Microbiology, 1999, 150, 281-285.	1.0	178
29	Resolving the polyphyletic nature of <i>Pyricularia</i> ( <i>Pyriculariaceae</i> ). Studies in Mycology, 2014, 79, 85-120.	4.5	175
30	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. Current Biology, 2016, 26, 1577-1584.	1.8	175
31	Mannitol Is Required for Stress Tolerance in <i>Aspergillus niger</i> Conidiospores. Eukaryotic Cell, 2003, 2, 690-698.	3.4	174
32	The secretome of the maize pathogen <i>Ustilago maydis</i> . Fungal Genetics and Biology, 2008, 45, S63-S70.	0.9	162
33	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . Nature Genetics, 2018, 50, 1688-1695.	9.4	160
34	A New Black <i>Aspergillus</i> Species, <i>A. vadensis</i> , Is a Promising Host for Homologous and Heterologous Protein Production. Applied and Environmental Microbiology, 2004, 70, 3954-3959.	1.4	154
35	The <i>Aspergillus niger</i> <i>faeB</i> 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
36	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. Biotechnology Letters, 2008, 30, 387-396.	1.1	136

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37	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	0.9	133
38	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. <i>Biotechnology for Biofuels</i> , 2016, 9, 231.	6.2	133
39	Comparative genomics of the white-rot fungi, <i>Phanerochaete carnos</i> a and <i>P. chrysosporium</i> , to elucidate the genetic basis of the distinct wood types they colonize. <i>BMC Genomics</i> , 2012, 13, 444.	1.2	125
40	A comparative genomics study of 23 <i>Aspergillus</i> species from section Flavi. <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
41	Analysis of regulation of pentose utilisation in <i>Aspergillus niger</i> reveals evolutionary adaptations in Eurotiales. <i>Studies in Mycology</i> , 2011, 69, 31-38.	4.5	123
42	Transcriptome analysis of <i>Aspergillus niger</i> grown on sugarcane bagasse. <i>Biotechnology for Biofuels</i> , 2011, 4, 40.	6.2	122
43	Prevalence of transcription factors in ascomycete and basidiomycete fungi. <i>BMC Genomics</i> , 2014, 15, 214.	1.2	114
44	<sc><i>B</i></sc><i>acillus subtilis</i> attachment to <sc><i>A</i></sc><i>spergillus niger</i> hyphae results in mutually altered metabolism. <i>Environmental Microbiology</i> , 2015, 17, 2099-2113.	1.8	112
45	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015, 8, 107.	6.2	111
46	Spatial Differentiation in the Vegetative Mycelium of <i>Aspergillus niger</i>. <i>Eukaryotic Cell</i> , 2007, 6, 2311-2322.	3.4	106
47	Establishment of compatibility in the <i>Ustilago maydis</i> /maize pathosystem. <i>Journal of Plant Physiology</i> , 2008, 165, 29-40.	1.6	106
48	Carbohydrate-active enzymes from the zygomycete fungus <i>Rhizopus oryzae</i> : a highly specialized approach to carbohydrate degradation depicted at genome level. <i>BMC Genomics</i> , 2011, 12, 38.	1.2	105
49	Improved enzyme production by co-cultivation of <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> and with other fungi. <i>International Biodeterioration and Biodegradation</i> , 2011, 65, 248-252.	1.9	105
50	Construction of a cellulase hyper-expression system in <i>Trichoderma reesei</i> by promoter and enzyme engineering. <i>Microbial Cell Factories</i> , 2012, 11, 21.	1.9	105
51	Expression profiling of pectinolytic genes from <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2002, 530, 41-47.	1.3	102
52	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	0.9	99
53	Generic names in Magnaporthales. <i>IMA Fungus</i> , 2016, 7, 155-159.	1.7	98
54	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

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55	Differential Expression of Three $\beta$ -Galactosidase Genes and a Single $\beta$ -Galactosidase Gene from <i>Aspergillus niger</i> . Applied and Environmental Microbiology, 1999, 65, 2453-2460.	1.4	97
56	Cloning and characterization of <i>Aspergillus niger</i> genes encoding an $\beta$ -galactosidase and a $\beta$ -mannosidase involved in galactomannan degradation. FEBS Journal, 2001, 268, 2982-2990.	0.2	92
57	The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. BMC Genomics, 2014, 15, 486.	1.2	91
58	Plant biomass degradation by fungi. Fungal Genetics and Biology, 2014, 72, 2-9.	0.9	91
59	Genomics, Lifestyles and Future Prospects of Wood-Decay and Litter-Decomposing Basidiomycota. Advances in Botanical Research, 2014, 70, 329-370.	0.5	87
60	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
61	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
62	The <i>Aspergillus niger</i> <i>faeB</i> 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
63	Identification of genes encoding microbial glucuronoyl esterases. FEBS Letters, 2007, 581, 4029-4035.	1.3	83
64	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. Biotechnology Advances, 2019, 37, 107396.	6.0	83
65	Genomic and transcriptomic analysis of <i>Laccaria bicolor</i> CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. Fungal Genetics and Biology, 2014, 72, 168-181.	0.9	81
66	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
67	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
68	<i>aguA</i> , the Gene Encoding an Extracellular $\beta$ -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
69	Regulation of pentose utilisation by AraR, but not XlnR, differs in <i>Aspergillus nidulans</i> and <i>Aspergillus niger</i> . Applied Microbiology and Biotechnology, 2011, 91, 387-397.	1.7	67
70	A broader role for AmyR in <i>Aspergillus niger</i> : 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
71	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
72	Selective Cleavage of Lignin $\beta$ -O-4 Aryl Ether Bond by $\beta$ -Etherase of the White-Rot Fungus <i>Dichomitus squalens</i> . ACS Sustainable Chemistry and Engineering, 2018, 6, 2878-2882.	3.2	66

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73	The transcriptional activator GaaR of <i>Aspergillus niger</i> is required for release and utilization of galacturonic acid from pectin. <i>FEBS Letters</i> , 2016, 590, 1804-1815.	1.3	64
74	Combinatorial control of gene expression in <i>Aspergillus niger</i> grown on sugar beet pectin. <i>Scientific Reports</i> , 2017, 7, 12356.	1.6	64
75	The influence of <i>Aspergillus niger</i> transcription factors AraR and XlnR in the gene expression during growth in d-xylose, l-arabinose and steam-exploded sugarcane bagasse. <i>Fungal Genetics and Biology</i> , 2013, 60, 29-45.	0.9	63
76	Horizontal gene transfer and gene dosage drives adaptation to wood colonization in a tree pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3451-3456.	3.3	63
77	Glycerol dehydrogenase, encoded by <i>gldB</i> is essential for osmotolerance in <i>Aspergillus nidulans</i> . <i>Molecular Microbiology</i> , 2003, 49, 131-141.	1.2	62
78	Nutritional physiology of a rock-inhabiting, model microcolonial fungus from an ancestral lineage of the Chaetothyriales (Ascomycetes). <i>Fungal Genetics and Biology</i> , 2013, 56, 54-66.	0.9	62
79	The gold-standard genome of <i>Aspergillus niger</i> NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. <i>Studies in Mycology</i> , 2018, 91, 61-78.	4.5	62
80	Carbohydrate-related enzymes of important Phytophthora plant pathogens. <i>Fungal Genetics and Biology</i> , 2014, 72, 192-200.	0.9	61
81	The <i>Aspergillus niger</i> xylulose kinase gene is co-expressed with genes encoding arabinan degrading enzymes, and is essential for growth on d-xylose and l-arabinose. <i>FEBS Journal</i> , 2001, 268, 5414-5423.	0.2	60
82	Growth and hydrolase profiles can be used as characteristics to distinguish <i>Aspergillus niger</i> and other black aspergilli. <i>Studies in Mycology</i> , 2011, 69, 19-30.	4.5	60
83	Phylogeny of the industrial relevant, thermophilic genera <i>Myceliophthora</i> and <i>Coryascus</i> . <i>Fungal Diversity</i> , 2012, 52, 197-207.	4.7	59
84	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
85	<i>Aspergillus vadensis</i> , a new species of the group of black Aspergilli. <i>Antonie Van Leeuwenhoek</i> , 2005, 87, 195-203.	0.7	58
86	Heterogenic expression of genes encoding secreted proteins at the periphery of <i>Aspergillus niger</i> colonies. <i>Environmental Microbiology</i> , 2011, 13, 216-225.	1.8	58
87	<i>Aspergillus niger</i> RhaR, a regulator involved in l-rhamnose release and catabolism. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 5531-40.	1.7	56
88	The molecular response of the white rot fungus <i>Dicellaea sp.</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
89	Expression-based clustering of CAZyme-encoding genes of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2017, 18, 900.	1.2	54
90	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

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91	Isolation and characterization of two specific regulatory <i>Aspergillus niger</i> mutants shows antagonistic regulation of arabinan and xylan metabolism. <i>Microbiology (United Kingdom)</i> , 2003, 149, 1183-1191.	0.7	51
92	Two glucuronoyl esterases of <i>Phanerochaete chrysosporium</i> . <i>Archives of Microbiology</i> , 2009, 191, 133-140.	1.0	51
93	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
94	The influence of pretreatment methods on saccharification of sugarcane bagasse by an enzyme extract from <i>Chrysosporthe cubensis</i> and commercial cocktails: A comparative study. <i>Bioresource Technology</i> , 2015, 192, 670-676.	4.8	49
95	Unique Regulatory Mechanism for d-Galactose Utilization in <i>Aspergillus nidulans</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 7084-7087.	1.4	48
96	Regulation of Plant Biomass Utilization in <i>Aspergillus</i> . <i>Advances in Applied Microbiology</i> , 2014, 88, 31-56.	1.3	48
97	Efficient Plant Biomass Degradation by Thermophilic Fungus <i>Myceliophthora heterothallica</i> . <i>Applied and Environmental Microbiology</i> , 2013, 79, 1316-1324.	1.4	47
98	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
99	Sugar Catabolism in <i>Aspergillus</i> and Other Fungi Related to the Utilization of Plant Biomass. <i>Advances in Applied Microbiology</i> , 2015, 90, 1-28.	1.3	46
100	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
101	Inverting character of $\beta$ -glucuronidase A from <i>Aspergillus tubingensis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2000, 1474, 360-364.	1.1	44
102	Occurrence of <i>Aspergillus allahabadii</i> on sandstone at Bayon temple, Angkor Thom, Cambodia. <i>International Biodeterioration and Biodegradation</i> , 2013, 76, 112-117.	1.9	44
103	The diversity and evolution of microbiota in traditional Turkish Divil Cave cheese during ripening. <i>International Dairy Journal</i> , 2016, 58, 50-53.	1.5	43
104	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
105	Genetic Interaction of <i>Aspergillus nidulans</i> galR, xlnR and araR in Regulating D-Galactose and L-Arabinose Release and Catabolism Gene Expression. <i>PLoS ONE</i> , 2015, 10, e0143200.	1.1	41
106	The $\beta$ -glucuronidase Agu1 from <i>Schizophyllum commune</i> is a member of a novel glycoside hydrolase family (GH115). <i>Applied Microbiology and Biotechnology</i> , 2011, 90, 1323-1332.	1.7	39
107	GalX regulates the d-galactose oxidoreductive pathway in <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2012, 586, 3980-3985.	1.3	39
108	Feruloyl Esterases for Biorefineries: Subfamily Classified Specificity for Natural Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 332.	2.0	39



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109	Synergistic effect of <i>Aspergillus niger</i> and <i>Trichoderma reesei</i> enzyme sets on the saccharification of wheat straw and sugarcane bagasse. <i>Biotechnology Journal</i> , 2014, 9, 1329-1338.	1.8	38
110	Volatile compound profiling of Turkish Divle Cave cheese during production and ripening. <i>Journal of Dairy Science</i> , 2016, 99, 5120-5131.	1.4	37
111	ARA1 regulates not only arabinose but also d-galactose catabolism in <i>Trichoderma reesei</i> . <i>FEBS Letters</i> , 2018, 592, 60-70.	1.3	37
112	A genomic survey of proteases in Aspergilli. <i>BMC Genomics</i> , 2014, 15, 523.	1.2	36
113	<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
114	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
115	Mapping the polysaccharide degradation potential of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2012, 13, 313.	1.2	35
116	Carbohydrate utilization and metabolism is highly differentiated in <i>Agaricus bisporus</i> . <i>BMC Genomics</i> , 2013, 14, 663.	1.2	35
117	Characterization and biotechnological application of recombinant xylanases from <i>Aspergillus nidulans</i> . <i>International Journal of Biological Macromolecules</i> , 2016, 91, 60-67.	3.6	35
118	Genomic and Genetic Insights Into a Cosmopolitan Fungus, <i>Paecilomyces variotii</i> (Eurotiales). <i>Frontiers in Microbiology</i> , 2018, 9, 3058.	1.5	35
119	The transcriptional activators AraR and XlnR from <i>Aspergillus niger</i> regulate expression of pentose catabolic and pentose phosphate pathway genes. <i>Research in Microbiology</i> , 2014, 165, 531-540.	1.0	34
120	CRISPR/Cas9 technology enables the development of the filamentous ascomycete fungus <i>Penicillium subrubescens</i> as a new industrial enzyme producer. <i>Enzyme and Microbial Technology</i> , 2020, 133, 109463.	1.6	34
121	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
122	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
123	From lignocellulose to plastics: Knowledge transfer on the degradation approaches by fungi. <i>Biotechnology Advances</i> , 2021, 50, 107770.	6.0	33
124	Fungal xylanolytic enzymes: Diversity and applications. <i>Bioresource Technology</i> , 2022, 344, 126290.	4.8	33
125	Xlr1 is involved in the transcriptional control of the pentose catabolic pathway, but not hemi-cellulolytic enzymes in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , 2013, 57, 76-84.	0.9	32
126	The distinctive regulatory roles of PrtT in the cell metabolism of <i>Penicillium oxalicum</i> . <i>Fungal Genetics and Biology</i> , 2014, 63, 42-54.	0.9	32



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127	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . DNA Research, 2020, 27, .	1.5	32
128	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> . Applied and Environmental Microbiology, 2018, 84, .	1.4	31
129	Characterization of oxylipins and dioxygenase genes in the asexual fungus <i>Aspergillus niger</i> . BMC Microbiology, 2009, 9, 59.	1.3	30
130	Oxalate-Metabolising Genes of the White-Rot Fungus <i>Dichomitus squalens</i> Are Differentially Induced on Wood and at High Proton Concentration. PLoS ONE, 2014, 9, e87959.	1.1	29
131	N -acetylglucosamine, the building block of chitin, inhibits growth of <i>Neurospora crassa</i> . Fungal Genetics and Biology, 2017, 107, 1-11.	0.9	29
132	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. New Biotechnology, 2018, 40, 282-287.	2.4	29
133	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. Enzyme and Microbial Technology, 2020, 136, 109508.	1.6	29
134	The $\beta$ -1,4-endogalactanase A gene from <i>Aspergillus niger</i> is 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
135	Improving cellulase production by <i>Aspergillus niger</i> using adaptive evolution. Biotechnology Letters, 2016, 38, 969-974.	1.1	28
136	On the origin of vanillyl alcohol oxidases. Fungal Genetics and Biology, 2018, 116, 24-32.	0.9	28
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141	8 Degradation and Modification of Plant Biomass by Fungi. , 2014, , 175-208.		26
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146	The <i>Hypocrea jecorina</i> (syn. <i>Trichoderma reesei</i> ) <i>lxr1</i> gene encodes a <i>d</i> -mannitol dehydrogenase and is not involved in <i>l</i> -arabinose catabolism. <i>FEBS Letters</i> , 2009, 583, 1309-1313.	1.3	24
147	The interaction of induction and repression mechanisms in the regulation of galacturonic acid-induced genes in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2015, 82, 32-42.	0.9	24
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150	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
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152	Secretion of small proteins is species-specific within <i>Aspergillus</i> sp. <i>Microbial Biotechnology</i> , 2017, 10, 323-329.	2.0	23
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