

Ronald P De Vries

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

251
papers

16,275
citations

62
h-index

123
g-index

266
ext. papers

19,740
ext. citations

6.9
avg, IF

6.32
L-index

#	Paper	IF	Citations
251	Fungal glycoside hydrolase family 44 xyloglucanases are restricted to the phylum Basidiomycota and show a distinct xyloglucan cleavage pattern.. <i>IScience</i> , 2022 , 25, 103666	6.1	0
250	Detailed analysis of the D-galactose catabolic pathways in <i>Aspergillus niger</i> reveals complexity at both metabolic and regulatory level.. <i>Fungal Genetics and Biology</i> , 2022 , 159, 103670	3.9	0
249	Fungal xylanolytic enzymes: Diversity and applications. <i>Bioresource Technology</i> , 2022 , 344, 126290	11	3
248	Comparative characterization of nine novel GH51, GH54 and GH62 β -arabinofuranosidases from <i>Penicillium subrubescens</i> .. <i>FEBS Letters</i> , 2022 ,	3.8	1
247	Xylitol production from plant biomass by <i>Aspergillus niger</i> through metabolic engineering. <i>Bioresource Technology</i> , 2022 , 344, 126199	11	2
246	Unraveling the regulation of sugar beet pulp utilization in the industrially relevant fungus .. <i>IScience</i> , 2022 , 25, 104065	6.1	1
245	GH10 and GH11 endoxylanases in <i>Penicillium subrubescens</i> : Comparative characterization and synergy with GH51, GH54, GH62 β -arabinofuranosidases from the same fungus. <i>New Biotechnology</i> , 2022 , 70, 84-92	6.4	1
244	Glycoside Hydrolase family 30 harbors fungal subfamilies with distinct polysaccharide specificities.. <i>New Biotechnology</i> , 2021 , 67, 32-41	6.4	1
243	Genetic barcodes allow traceability of CRISPR/Cas9-derived <i>Aspergillus niger</i> strains without affecting their fitness. <i>Current Genetics</i> , 2021 , 67, 673-684	2.9	1
242	Re-routing of Sugar Catabolism Provides a Better Insight Into Fungal Flexibility in Using Plant Biomass-Derived Monomers as Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021 , 9, 644216	5.8	1
241	Revisiting a 'simple' fungal metabolic pathway reveals redundancy, complexity and diversity. <i>Microbial Biotechnology</i> , 2021 , 14, 2525-2537	6.3	5
240	Production of Protocatechuic Acid from -Hydroxyphenyl (H) Units and Related Aromatic Compounds Using an <i>Aspergillus niger</i> Cell Factory. <i>MBio</i> , 2021 , 12, e0039121	7.8	6
239	Characterization of d-xylose reductase, XyrB, from. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2021 , 30, e00610	5.3	2
238	Blocking utilization of major plant biomass polysaccharides leads <i>Aspergillus niger</i> towards utilization of minor components. <i>Microbial Biotechnology</i> , 2021 , 14, 1683-1698	6.3	4
237	Genetic Engineering for Strain Improvement in Filamentous Fungi 2021 , 489-504		2
236	Molecular engineering to improve lignocellulosic biomass based applications using filamentous fungi. <i>Advances in Applied Microbiology</i> , 2021 , 114, 73-109	4.9	5
235	Degradation of Homocyclic Aromatic Compounds by Fungi 2021 , 477-488		

234	Bioinformatics Approaches for Fungal Biotechnology 2021 , 536-554		
233	Discovery and Functional Analysis of a Salicylic Acid Hydroxylase from <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2021 , 87,	4.8	8
232	The chimeric GaaR-XlnR transcription factor induces pectinolytic activities in the presence of D-xylose in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 5553-5564	5.7	2
231	Vanillic acid and methoxyhydroquinone production from guaiacyl units and related aromatic compounds using <i>Aspergillus niger</i> cell factories. <i>Microbial Cell Factories</i> , 2021 , 20, 151	6.4	1
230	From lignocellulose to plastics: Knowledge transfer on the degradation approaches by fungi. <i>Biotechnology Advances</i> , 2021 , 50, 107770	17.8	5
229	The Cultivation Method Affects the Transcriptomic Response of <i>Aspergillus niger</i> to Growth on Sugar Beet Pulp. <i>Microbiology Spectrum</i> , 2021 , 9, e0106421	8.9	2
228	Carbon utilization and growth-inhibition of citrus-colonizing <i>Phyllosticta</i> species. <i>Fungal Biology</i> , 2021 , 125, 815-825	2.8	0
227	CreA-mediated repression of gene expression occurs at low monosaccharide levels during fungal plant biomass conversion in a time and substrate dependent manner. <i>Cell Surface</i> , 2021 , 7, 100050	4.8	5
226	Machine learning prediction of novel pectinolytic enzymes in through integrating heterogeneous (post-) genomics data. <i>Microbial Genomics</i> , 2021 , 7,	4.4	1
225	Feruloyl Esterases for Biorefineries: Subfamily Classified Specificity for Natural Substrates. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 332	5.8	15
224	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020 , 27,	4.5	13
223	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020 , 11, 1106	17.4	54
222	Identification of a gene encoding the last step of the L-rhamnose catabolic pathway in <i>Aspergillus niger</i> revealed the inducer of the pathway regulator. <i>Microbiological Research</i> , 2020 , 234, 126426	5.3	6
221	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. <i>Trends in Microbiology</i> , 2020 , 28, 487-499	12.4	12
220	The Current Biotechnological Status and Potential of Plant and Algal Biomass Degrading/Modifying Enzymes from Ascomycete Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020 , 81-120	2.4	9
219	<i>Penicillium subrubescens</i> adapts its enzyme production to the composition of plant biomass. <i>Bioresource Technology</i> , 2020 , 311, 123477	11	10
218	Engineering of primary carbon metabolism in filamentous fungi. <i>Biotechnology Advances</i> , 2020 , 43, 107554	5.8	11
217	CRISPR/Cas9 facilitates rapid generation of constitutive forms of transcription factors in <i>Aspergillus niger</i> through specific on-site genomic mutations resulting in increased saccharification of plant biomass. <i>Enzyme and Microbial Technology</i> , 2020 , 136, 109508	3.8	16

216	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	3.8	20
215	Evolutionary adaptation of <i>Aspergillus niger</i> for increased ferulic acid tolerance. <i>Journal of Applied Microbiology</i> , 2020 , 128, 735-746	4.7	5
214	Mixtures of aromatic compounds induce ligninolytic gene expression in the wood-rotting fungus <i>Dichomitus squalens</i> . <i>Journal of Biotechnology</i> , 2020 , 308, 35-39	3.7	4
213	Colonies of the fungus <i>Aspergillus niger</i> are highly differentiated to adapt to local carbon source variation. <i>Environmental Microbiology</i> , 2020 , 22, 1154-1166	5.2	7
212	Functional Validation of Two Fungal Subfamilies in Carbohydrate Esterase Family 1 by Biochemical Characterization of Esterases From Uncharacterized Branches. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020 , 8, 694	5.8	10
211	Recombinant production and characterization of six novel GH27 and GH36 β -galactosidases from <i>Penicillium subrubescens</i> and their synergism with a commercial mannanase during the hydrolysis of lignocellulosic biomass. <i>Bioresource Technology</i> , 2020 , 295, 122258	11	12
210	Evidence for ligninolytic activity of the ascomycete fungus. <i>Biotechnology for Biofuels</i> , 2020 , 13, 75	7.8	16
209	Growing a circular economy with fungal biotechnology: a white paper. <i>Fungal Biology and Biotechnology</i> , 2020 , 7, 5	7.5	97
208	Xyr1 is predominantly involved in xylan degradation and xylose catabolism. <i>Biotechnology for Biofuels</i> , 2019 , 12, 220	7.8	5
207	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. <i>Biotechnology Advances</i> , 2019 , 37, 107396	17.8	37
206	Draft Genome Sequences of Three Monokaryotic Isolates of the White-Rot Basidiomycete Fungus <i>Dichomitus squalens</i> . <i>Microbiology Resource Announcements</i> , 2019 , 8,	1.3	8
205	Deletion of either the regulatory gene or metabolic gene in leads to increased CAZyme gene expression on crude plant biomass. <i>Biotechnology for Biofuels</i> , 2019 , 12, 81	7.8	7
204	The presence of trace components significantly broadens the molecular response of <i>Aspergillus niger</i> to guar gum. <i>New Biotechnology</i> , 2019 , 51, 57-66	6.4	6
203	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019 , 7, 249	5.8	13
202	Discovery of Novel p-Hydroxybenzoate-m-hydroxylase, Protocatechuate 3,4 Ring-Cleavage Dioxygenase, and Hydroxyquinol 1,2 Ring-Cleavage Dioxygenase from the Filamentous Fungus <i>Aspergillus niger</i> . <i>ACS Sustainable Chemistry and Engineering</i> , 2019 , 7, 19081-19089	8.3	15
201	The quest for fungal strains and their co-culture potential to improve enzymatic degradation of Chinese distillers' grain and other agricultural wastes. <i>International Biodeterioration and Biodegradation</i> , 2019 , 144, 104765	4.8	8
200	Macroalgae Derived Fungi Have High Abilities to Degrade Algal Polymers. <i>Microorganisms</i> , 2019 , 8,	4.9	8
199	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	17.8	26

198	Glucose-Mediated Repression of Plant Biomass Utilization in the White-Rot Fungus. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	10
197	Transcriptome analysis of <i>Aspergillus niger</i> xlnR and xkiA mutants grown on corn Stover and soybean hulls reveals a highly complex regulatory network. <i>BMC Genomics</i> , 2019 , 20, 853	4.5	4
196	Enzymatic Adaptation of <i>Podospora anserina</i> to Different Plant Biomass Provides Leads to Optimized Commercial Enzyme Cocktails. <i>Biotechnology Journal</i> , 2019 , 14, e1800185	5.6	8
195	l-Arabinose induces d-galactose catabolism via the Leloir pathway in <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2019 , 123, 53-59	3.9	2
194	<i>Talaromyces borbonicus</i> , sp. nov., a novel fungus from biodegraded <i>Arundo donax</i> with potential abilities in lignocellulose conversion. <i>Mycologia</i> , 2018 , 110, 316-324	2.4	8
193	Temporal microbiota and biochemical profiles during production and ripening of Divle Cave cheese. <i>International Journal of Dairy Technology</i> , 2018 , 71, 99-106	3.7	
192	Draft Genome Sequence of the Basidiomycete White-Rot Fungus <i>Phlebia centrifuga</i> . <i>Genome Announcements</i> , 2018 , 6,		4
191	A senescence-delaying pre-culture medium for transcriptomics of <i>Podospora anserina</i> . <i>Journal of Microbiological Methods</i> , 2018 , 146, 33-36	2.8	4
190	Selective Cleavage of Lignin β -4 Aryl Ether Bond by β Etherase of the White-Rot Fungus. <i>ACS Sustainable Chemistry and Engineering</i> , 2018 , 6, 2878-2882	8.3	43
189	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. <i>Fungal Genetics and Biology</i> , 2018 , 112, 12-20	3.9	7
188	ARA1 regulates not only l-arabinose but also d-galactose catabolism in <i>Trichoderma reesei</i> . <i>FEBS Letters</i> , 2018 , 592, 60-70	3.8	18
187	Draft Genome Sequence of. <i>Genome Announcements</i> , 2018 , 6,		1
186	The fungus <i>Aspergillus niger</i> consumes sugars in a sequential manner that is not mediated by the carbon catabolite repressor CreA. <i>Scientific Reports</i> , 2018 , 8, 6655	4.9	14
185	Induction of Genes Encoding Plant Cell Wall-Degrading Carbohydrate-Active Enzymes by Lignocellulose-Derived Monosaccharides and Cellobiose in the White-Rot Fungus <i>Dichomitus squalens</i> . <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	16
184	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. <i>New Biotechnology</i> , 2018 , 40, 282-287	6.4	24
183	Analysis of Putative Sugar Transporter Genes in Using Phylogeny and Comparative Transcriptomics. <i>Frontiers in Microbiology</i> , 2018 , 9, 1045	5.7	22
182	The Synthetic Potential of Fungal Feruloyl Esterases: A Correlation with Current Classification Systems and Predicted Structural Properties. <i>Catalysts</i> , 2018 , 8, 242	4	9
181	Blocking hexose entry into glycolysis activates alternative metabolic conversion of these sugars and upregulates pentose metabolism in <i>Aspergillus nidulans</i> . <i>BMC Genomics</i> , 2018 , 19, 214	4.5	10

180	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	6.3	25
179	Introduction: Overview of Fungal Genomics. <i>Methods in Molecular Biology</i> , 2018 , 1775, 1-7	1.4	
178	Evolutionary Adaptation to Generate Mutants. <i>Methods in Molecular Biology</i> , 2018 , 1775, 133-137	1.4	1
177	Role of Microbial Cultures and Enzymes During Cheese Production and Ripening. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> , 2018 , 182-203	0.3	2
176	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. <i>New Biotechnology</i> , 2018 , 41, 9-14	6.4	20
175	Temporal transcriptome analysis of the white-rot fungus <i>Obba rivulosa</i> shows expression of a constitutive set of plant cell wall degradation targeted genes during growth on solid spruce wood. <i>Fungal Genetics and Biology</i> , 2018 , 112, 47-54	3.9	14
174	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	3.9	30
173	The gold-standard genome of NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. <i>Studies in Mycology</i> , 2018 , 91, 61-78	22.2	33
172	Duplications and losses of genes encoding known elements of the stress defence system of the <i>Aspergilli</i> contribute to the evolution of these filamentous fungi but do not directly influence their environmental stress tolerance. <i>Studies in Mycology</i> , 2018 , 91, 23-36	22.2	8
171	Genomic and exoproteomic diversity in plant biomass degradation approaches among <i>Aspergilli</i> . <i>Studies in Mycology</i> , 2018 , 91, 79-99	22.2	12
170	Fungal Stress Database (FSD)--a repository of fungal stress physiological data. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018,	5	9
169	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). <i>Frontiers in Microbiology</i> , 2018 , 9, 3058	5.7	23
168	<i>Dichomitus squalens</i> partially tailors its molecular responses to the composition of solid wood. <i>Environmental Microbiology</i> , 2018 , 20, 4141-4156	5.2	19
167	A community-driven reconstruction of the metabolic network. <i>Fungal Biology and Biotechnology</i> , 2018 , 5, 16	7.5	12
166	The obligate alkalophilic soda-lake fungus <i>Sodiomyces alkalinus</i> has shifted to a protein diet. <i>Molecular Ecology</i> , 2018 , 27, 4808-4819	5.7	10
165	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018 , 50, 1688-1695	36.3	100
164	Improved Hemicellulase Production by Genetic Modification of Carbon Catabolite Repression and Xylanolytic Activation in <i>Aspergillus niger</i> . <i>Current Biotechnology</i> , 2018 , 7, 10-18	0.6	6
163	Physiological background of the remarkably high Cd tolerance of the <i>Aspergillus fumigatus</i> Af293 strain. <i>Journal of Basic Microbiology</i> , 2018 , 58, 957-967	2.7	6

162	On the origin of vanillyl alcohol oxidases. <i>Fungal Genetics and Biology</i> , 2018 , 116, 24-32	3.9	10
161	Secretion of small proteins is species-specific within <i>Aspergillus</i> sp. <i>Microbial Biotechnology</i> , 2017 , 10, 323-329	6.3	11
160	Mixed colonies of <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> cooperatively degrading wheat bran. <i>Fungal Genetics and Biology</i> , 2017 , 102, 31-37	3.9	16
159	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	3.7	21
158	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	18.3	261
157	Genome Sequence of the Basidiomycete White-Rot Fungus FBCC735. <i>Genome Announcements</i> , 2017 , 5,		4
156	Cultivation of <i>Podospora anserina</i> on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. <i>New Biotechnology</i> , 2017 , 37, 162-171	6.4	19
155	Characterisation of three fungal glucuronoyl esterases on glucuronic acid ester model compounds. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 5301-5311	5.7	16
154	The pathway intermediate 2-keto-3-deoxy-L-galactonate mediates the induction of genes involved in D-galacturonic acid utilization in <i>Aspergillus niger</i> . <i>FEBS Letters</i> , 2017 , 591, 1408-1418	3.8	20
153	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	5.7	38
152	Regulators of plant biomass degradation in ascomycetous fungi. <i>Biotechnology for Biofuels</i> , 2017 , 10, 152	7.8	111
151	Hydrolytic potential of five fungal supernatants to enhance a commercial enzyme cocktail. <i>Biotechnology Letters</i> , 2017 , 39, 1403-1411	3	13
150	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	6.4	35
149	The molecular response of the white-rot fungus <i>Dichomitus squalens</i> to wood and non-woody biomass as examined by transcriptome and exoproteome analyses. <i>Environmental Microbiology</i> , 2017 , 19, 1237-1250	5.2	34
148	Combinatorial control of gene expression in <i>Aspergillus niger</i> grown on sugar beet pectin. <i>Scientific Reports</i> , 2017 , 7, 12356	4.9	37
147	Genetic transformation of the white-rot fungus <i>Dichomitus squalens</i> using a new commercial protoplasting cocktail. <i>Journal of Microbiological Methods</i> , 2017 , 143, 38-43	2.8	7
146	High resolution visualization and exo-proteomics reveal the physiological role of XlnR and AraR in plant biomass colonization and degradation by <i>Aspergillus niger</i> . <i>Environmental Microbiology</i> , 2017 , 19, 4587-4598	5.2	5
145	Functional diversity in monokaryons. <i>IMA Fungus</i> , 2017 , 8, 17-25	6.8	12

144	N-acetylglucosamine, the building block of chitin, inhibits growth of <i>Neurospora crassa</i> . <i>Fungal Genetics and Biology</i> , 2017 , 107, 1-11	3.9	9
143	In vivo functional analysis of L-rhamnose metabolic pathway in <i>Aspergillus niger</i> : a tool to identify the potential inducer of RhaR. <i>BMC Microbiology</i> , 2017 , 17, 214	4.5	16
142	Fungal Ligninolytic Enzymes and Their Applications 2017 , 1049-1061		2
141	Expression-based clustering of CAZyme-encoding genes of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2017 , 18, 900	4.5	36
140	Mold-Ripened and Raw Milk Cheeses: Production, Risks, and Benefits to Human Health 2017 , 353-361		1
139	Protease and lipase activities of fungal and bacterial strains derived from an artisanal raw ewe's milk cheese. <i>International Journal of Food Microbiology</i> , 2016 , 237, 17-27	5.8	48
138	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. <i>Biotechnology for Biofuels</i> , 2016 , 9, 231	7.8	92
137	Draft Genome Sequence of the White-Rot Fungus <i>Obba rivulosa</i> 3A-2. <i>Genome Announcements</i> , 2016 , 4,		9
136	Generic names in Magnaporthales. <i>IMA Fungus</i> , 2016 , 7, 155-9	6.8	66
135	Cooperation of <i>Aspergillus nidulans</i> enzymes increases plant polysaccharide saccharification. <i>Biotechnology Journal</i> , 2016 , 11, 988-92	5.6	5
134	Sexual crossing of thermophilic fungus <i>Myceliophthora heterothallica</i> improved enzymatic degradation of sugar beet pulp. <i>Biotechnology for Biofuels</i> , 2016 , 9, 41	7.8	5
133	The transcriptional activator GaaR of <i>Aspergillus niger</i> is required for release and utilization of d-galacturonic acid from pectin. <i>FEBS Letters</i> , 2016 , 590, 1804-15	3.8	44
132	Enhancing saccharification of wheat straw by mixing enzymes from genetically-modified <i>Trichoderma reesei</i> and <i>Aspergillus niger</i> . <i>Biotechnology Letters</i> , 2016 , 38, 65-70	3	22
131	Improving cellulase production by <i>Aspergillus niger</i> using adaptive evolution. <i>Biotechnology Letters</i> , 2016 , 38, 969-74	3	21
130	The diversity and evolution of microbiota in traditional Turkish Divle Cave cheese during ripening. <i>International Dairy Journal</i> , 2016 , 58, 50-53	3.5	28
129	Evolutionary Adaptation as a Tool to Generate Targeted Mutant Strains as Evidence by Increased Inulinase Production in <i>Aspergillus oryzae</i> 2016 , 189-196		2
128	A novel L-arabinose-responsive regulator discovered in the rice-blast fungus <i>Pyricularia oryzae</i> (<i>Magnaporthe oryzae</i>). <i>FEBS Letters</i> , 2016 , 590, 550-8	3.8	15
127	Fungal Ligninolytic Enzymes and Their Applications. <i>Microbiology Spectrum</i> , 2016 , 4,	8.9	17

126	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016 , 26, 1577-1584	6.3	119
125	Characterization and biotechnological application of recombinant xylanases from <i>Aspergillus nidulans</i> . <i>International Journal of Biological Macromolecules</i> , 2016 , 91, 60-7	7.9	29
124	Homologous and Heterologous Expression of Basidiomycete Genes Related to Plant Biomass Degradation. <i>Fungal Biology</i> , 2016 , 119-160	2.3	2
123	Volatile compound profiling of Turkish Divle Cave cheese during production and ripening. <i>Journal of Dairy Science</i> , 2016 , 99, 5120-5131	4	24
122	<i>Penicillium subrubescens</i> is a promising alternative for <i>Aspergillus niger</i> in enzymatic plant biomass saccharification. <i>New Biotechnology</i> , 2016 , 33, 834-841	6.4	23
121	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, 3451-6	11.5	47
120	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	3.9	21
119	Accumulation of recalcitrant xylan in mushroom-compost is due to a lack of xylan substituent removing enzyme activities of <i>Agaricus bisporus</i> . <i>Carbohydrate Polymers</i> , 2015 , 132, 359-68	10.3	5
118	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, 670-6	11	33
117	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. <i>Biotechnology for Biofuels</i> , 2015 , 8, 107	7.8	74
116	<i>Bacillus subtilis</i> attachment to <i>Aspergillus niger</i> hyphae results in mutually altered metabolism. <i>Environmental Microbiology</i> , 2015 , 17, 2099-113	5.2	77
115	FluG affects secretion in colonies of <i>Aspergillus niger</i> . <i>Antonie Van Leeuwenhoek</i> , 2015 , 107, 225-40	2.1	9
114	Spatial differentiation of gene expression in <i>Aspergillus niger</i> colony grown for sugar beet pulp utilization. <i>Scientific Reports</i> , 2015 , 5, 13592	4.9	12
113	Uncovering the abilities of <i>Agaricus bisporus</i> to degrade plant biomass throughout its life cycle. <i>Environmental Microbiology</i> , 2015 , 17, 3098-109	5.2	37
112	Compost Grown <i>Agaricus bisporus</i> Lacks the Ability to Degrade and Consume Highly Substituted Xylan Fragments. <i>PLoS ONE</i> , 2015 , 10, e0134169	3.7	16
111	Disruption of photoautotrophic intertidal mats by filamentous fungi. <i>Environmental Microbiology</i> , 2015 , 17, 2910-21	5.2	11
110	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	4.9	70
109	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	4.9	34

108	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	3.7	31
107	<i>Aspergillus niger</i> RhaR, a regulator involved in L-rhamnose release and catabolism. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 5531-40	5.7	50
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93	Prevalence of transcription factors in ascomycete and basidiomycete fungi. <i>BMC Genomics</i> , 2014 , 15, 214	4.5	75
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