Ronald P De Vries

List of Publications by Citations

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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	The Paleozoic origin of enzymatic lignin decomposition reconstructed from 31 fungal genomes. *Science*, **2012**, 336, 1715-9	33.3	1129
250	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. *Nature Biotechnology*, **2007**, 25, 221-31	44.5	889
249	Insights from the genome of the biotrophic fungal plant pathogen Ustilago maydis. *Nature*, **2006**, 444, 97-101	50.4	867
248	Aspergillus enzymes involved in degradation of plant cell wall polysaccharides. *Microbiology and Molecular Biology Reviews*, **2001**, 65, 497-522, table of contents	13.2	679
247	Genomic analysis of the necrotrophic fungal pathogens Sclerotinia sclerotiorum and Botrytis cinerea. *PLoS Genetics*, **2011**, 7, e1002230	6	659
246	The plant cell wall-decomposing machinery underlies the functional diversity of forest fungi. *Science*, **2011**, 333, 762-5	33.3	417
245	Finished genome of the fungal wheat pathogen Mycosphaerella graminicola reveals dispensome structure, chromosome plasticity, and stealth pathogenesis. *PLoS Genetics*, **2011**, 7, e1002070	6	401
244	Fungal enzyme sets for plant polysaccharide degradation. *Applied Microbiology and Biotechnology*, **2011**, 91, 1477-92	5.7	398
243	Genome sequence of the model mushroom Schizophyllum commune. *Nature Biotechnology*, **2010**, 28, 957-63	44.5	381
242	Comparative genomic analysis of the thermophilic biomass-degrading fungi Myceliophthora thermophila and Thielavia terrestris. *Nature Biotechnology*, **2011**, 29, 922-7	44.5	324
241	The transcriptional activator XlnR regulates both xylanolytic and endoglucanase gene expression in Aspergillus niger. *Applied and Environmental Microbiology*, **1998**, 64, 3615-9	4.8	289
240	Genome sequence of the necrotrophic plant pathogen Pythium ultimum reveals original pathogenicity mechanisms and effector repertoire. *Genome Biology*, **2010**, 11, R73	18.3	280
239	Genome sequence of the button mushroom Agaricus bisporus 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, 17501-6	11.5	277
238	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. *Genome Biology*, **2017**, 18, 28	18.3	261
237	The amsterdam declaration on fungal nomenclature. *IMA Fungus*, **2011**, 2, 105-12	6.8	260
236	Plant-polysaccharide-degrading enzymes from Basidiomycetes. *Microbiology and Molecular Biology Reviews*, **2014**, 78, 614-49	13.2	242
235	The genome sequence of the model ascomycete fungus Podospora anserina. *Genome Biology*, **2008** , 9, R77	18.3	237

234	Comparative genomics of Ceriporiopsis subvermispora and Phanerochaete chrysosporium provide insight into selective ligninolysis. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 5458-63	11.5	225
233	Synergy between enzymes from Aspergillus involved in the degradation of plant cell wall polysaccharides. *Carbohydrate Research*, **2000**, 327, 401-10	2.9	211
232	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	6	189
231	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. *New Phytologist*, **2012**, 194, 1001-1013	9.8	168
230	Trehalose is required for the acquisition of tolerance to a variety of stresses in the filamentous fungus Aspergillus nidulans. *Microbiology (United Kingdom)*, **2001**, 147, 1851-1862	2.9	167
229	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, 14500-5	11.5	163
228	Mannitol is required for stress tolerance in Aspergillus niger conidiospores. *Eukaryotic Cell*, **2003**, 2, 690-8		162
227	The secretome of the maize pathogen Ustilago maydis. *Fungal Genetics and Biology*, **2008**, 45 Suppl 1, S63-70	3.9	142
226	CreA modulates the XlnR-induced expression on xylose of Aspergillus niger genes involved in xylan degradation. *Research in Microbiology*, **1999**, 150, 281-5	4	139
225	Resolving the polyphyletic nature of Pyricularia (Pyriculariaceae). *Studies in Mycology*, **2014**, 79, 85-120	22.2	131
224	A new black Aspergillus species, A. vadensis, is a promising host for homologous and heterologous protein production. *Applied and Environmental Microbiology*, **2004**, 70, 3954-9	4.8	127
223	Modern taxonomy of biotechnologically important Aspergillus and Penicillium species. *Advances in Applied Microbiology*, **2014**, 86, 199-249	4.9	125
222	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	3.8	122
221	Biotechnological applications and potential of fungal feruloyl esterases based on prevalence, classification and biochemical diversity. *Biotechnology Letters*, **2008**, 30, 387-96	3	119
220	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. *Current Biology*, **2016**, 26, 1577-1584	6.3	119
219	Regulators of plant biomass degradation in ascomycetous fungi. *Biotechnology for Biofuels*, **2017**, 10, 152	7.8	111
218	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 Suppl 1, S161-S169	3.9	106
217	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. *Nature Genetics*, **2018**, 50, 1688-1695	36.3	100

216	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	4.5	97
215	Growing a circular economy with fungal biotechnology: a white paper. *Fungal Biology and Biotechnology*, **2020**, 7, 5	7.5	97
214	Spatial differentiation in the vegetative mycelium of Aspergillus niger. *Eukaryotic Cell*, **2007**, 6, 2311-22		94
213	Diversity of fungal feruloyl esterases: updated phylogenetic classification, properties, and industrial applications. *Biotechnology for Biofuels*, **2016**, 9, 231	7.8	92
212	Construction of a cellulase hyper-expression system in Trichoderma reesei by promoter and enzyme engineering. *Microbial Cell Factories*, **2012**, 11, 21	6.4	92
211	Establishment of compatibility in the Ustilago maydis/maize pathosystem. *Journal of Plant Physiology*, **2008**, 165, 29-40	3.6	89
210	Transcriptome analysis of Aspergillus niger grown on sugarcane bagasse. *Biotechnology for Biofuels* , **2011**, 4, 40	7.8	88
209	Improved enzyme production by co-cultivation of Aspergillus niger and Aspergillus oryzae and with other fungi. *International Biodeterioration and Biodegradation*, **2011**, 65, 248-252	4.8	88
208	Analysis of regulation of pentose utilisation in Aspergillus niger reveals evolutionary adaptations in Eurotiales. *Studies in Mycology*, **2011**, 69, 31-8	22.2	87
207	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	4.5	86
206	Cloning and characterization of Aspergillus niger genes encoding an alpha-galactosidase and a beta-mannosidase involved in galactomannan degradation. *FEBS Journal*, **2001**, 268, 2982-90		83
205	Regulation of the feruloyl esterase (faeA) gene from Aspergillus niger. *Applied and Environmental Microbiology*, **1999**, 65, 5500-3	4.8	83
204	The 2008 update of the Aspergillus nidulans genome annotation: a community effort. *Fungal Genetics and Biology*, **2009**, 46 Suppl 1, S2-13	3.9	82
203	Differential expression of three alpha-galactosidase genes and a single beta-galactosidase gene from Aspergillus niger. *Applied and Environmental Microbiology*, **1999**, 65, 2453-60	4.8	80
202	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, 377-86	3.8	78
201	Bacillus subtilis attachment to Aspergillus niger hyphae results in mutually altered metabolism. *Environmental Microbiology*, **2015**, 17, 2099-113	5.2	77
200	Expression profiling of pectinolytic genes from Aspergillus niger. *FEBS Letters*, **2002**, 530, 41-7	3.8	76
199	Prevalence of transcription factors in ascomycete and basidiomycete fungi. *BMC Genomics*, **2014**, 15, 214	4.5	75

198	Plant biomass degradation by fungi. *Fungal Genetics and Biology*, **2014**, 72, 2-9	3.9	75
197	Identification of genes encoding microbial glucuronoyl esterases. *FEBS Letters*, **2007**, 581, 4029-35	3.8	75
196	Closely related fungi employ diverse enzymatic strategies to degrade plant biomass. *Biotechnology for Biofuels*, **2015**, 8, 107	7.8	74
195	Aromatic metabolism of filamentous fungi in relation to the presence of aromatic compounds in plant biomass. *Advances in Applied Microbiology*, **2015**, 91, 63-137	4.9	70
194	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	4.5	69
193	Generic names in Magnaporthales. *IMA Fungus*, **2016**, 7, 155-9	6.8	66
192	Genomic and transcriptomic analysis of Laccaria bicolor CAZome reveals insights into polysaccharides remodelling during symbiosis establishment. *Fungal Genetics and Biology*, **2014**, 72, 168-181	3.9	62
191	Genomics, Lifestyles and Future Prospects of Wood-Decay and Litter-Decomposing Basidiomycota. *Advances in Botanical Research*, **2014**, 70, 329-370	2.2	62
190	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	4.5	62
189	aguA, the gene encoding an extracellular alpha-glucuronidase from Aspergillus tubingensis, is specifically induced on xylose and not on glucuronic acid. *Journal of Bacteriology*, **1998**, 180, 243-9	3.5	62
188	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	3.9	58
187	Regulation of pentose utilisation by AraR, but not XlnR, differs in Aspergillus nidulans and Aspergillus niger. *Applied Microbiology and Biotechnology*, **2011**, 91, 387-97	5.7	57
186	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, 285-93	5.7	56
185	Glycerol dehydrogenase, encoded by gldB is essential for osmotolerance in Aspergillus nidulans. *Molecular Microbiology*, **2003**, 49, 131-41	4.1	56
184	The Aspergillus niger D-xylulose kinase gene is co-expressed with genes encoding arabinan degrading enzymes, and is essential for growth on D-xylose and L-arabinose. *FEBS Journal*, **2001**, 268, 5414-23		56
183	A comparative genomics study of 23 Aspergillus species from section Flavi. *Nature Communications*, **2020**, 11, 1106	17.4	54
182	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	3.9	52
181	Aspergillus vadensis, a new species of the group of black Aspergilli. *Antonie Van Leeuwenhoek*, **2005**, 87, 195-203	2.1	52

180	Aspergillus niger RhaR, a regulator involved in L-rhamnose release and catabolism. *Applied Microbiology and Biotechnology*, **2014**, 98, 5531-40	5.7	50
179	Physiological and molecular aspects of degradation of plant polysaccharides by fungi: what have we learned from Aspergillus?. *Biotechnology Journal*, **2013**, 8, 884-94	5.6	50
178	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	5.8	48
177	Heterogenic expression of genes encoding secreted proteins at the periphery of Aspergillus niger colonies. *Environmental Microbiology*, **2011**, 13, 216-225	5.2	48
176	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	2.9	48
175	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, 3451-6	11.5	47
174	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	3.9	46
173	Growth and hydrolase profiles can be used as characteristics to distinguish Aspergillus niger and other black aspergilli. *Studies in Mycology*, **2011**, 69, 19-30	22.2	46
172	Two glucuronoyl esterases of Phanerochaete chrysosporium. *Archives of Microbiology*, **2009**, 191, 133-40	3	45
171	The transcriptional activator GaaR of Aspergillus niger is required for release and utilization of d-galacturonic acid from pectin. *FEBS Letters*, **2016**, 590, 1804-15	3.8	44
170	Selective Cleavage of Lignin 4 Aryl Ether Bond by Etherase of the White-Rot Fungus. *ACS Sustainable Chemistry and Engineering*, **2018**, 6, 2878-2882	8.3	43
169	Phylogeny of the industrial relevant, thermophilic genera Myceliophthora and Corynascus. *Fungal Diversity*, **2012**, 52, 197-207	17.6	43
168	Regulation of plant biomass utilization in Aspergillus. *Advances in Applied Microbiology*, **2014**, 88, 31-56	4.9	39
167	Efficient plant biomass degradation by thermophilic fungus Myceliophthora heterothallica. *Applied and Environmental Microbiology*, **2013**, 79, 1316-24	4.8	39
166	Occurrence and function of enzymes for lignocellulose degradation in commercial Agaricus bisporus cultivation. *Applied Microbiology and Biotechnology*, **2017**, 101, 4363-4369	5.7	38
165	Unique regulatory mechanism for D-galactose utilization in Aspergillus nidulans. *Applied and Environmental Microbiology*, **2011**, 77, 7084-7	4.8	38
164	Combinatorial control of gene expression in Aspergillus niger grown on sugar beet pectin. *Scientific Reports*, **2017**, 7, 12356	4.9	37
163	A comparison between the homocyclic aromatic metabolic pathways from plant-derived compounds by bacteria and fungi. *Biotechnology Advances*, **2019**, 37, 107396	17.8	37

162	Uncovering the abilities of Agaricus bisporus to degrade plant biomass throughout its life cycle. *Environmental Microbiology*, **2015**, 17, 3098-109	5.2	37
161	Expression-based clustering of CAZyme-encoding genes of Aspergillus niger. *BMC Genomics*, **2017**, 18, 900	4.5	36
160	Inverting character of alpha-glucuronidase A from Aspergillus tubingensis. *Biochimica Et Biophysica Acta - General Subjects*, **2000**, 1474, 360-4	4	36
159	Expanding the feruloyl esterase gene family of Aspergillus niger by characterization of a feruloyl esterase, FaeC. *New Biotechnology*, **2017**, 37, 200-209	6.4	35
158	The molecular response of the white-rot fungus Dichomitus squalens to wood and non-woody biomass as examined by transcriptome and exoproteome analyses. *Environmental Microbiology*, **2017**, 19, 1237-1250	5.2	34
157	Sugar catabolism in Aspergillus and other fungi related to the utilization of plant biomass. *Advances in Applied Microbiology*, **2015**, 90, 1-28	4.9	34
156	Occurrence of Aspergillus allahabadii on sandstone at Bayon temple, Angkor Thom, Cambodia. *International Biodeterioration and Biodegradation*, **2013**, 76, 112-117	4.8	34
155	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, 670-6	11	33
154	Synergistic effect of Aspergillus niger and Trichoderma reesei enzyme sets on the saccharification of wheat straw and sugarcane bagasse. *Biotechnology Journal*, **2014**, 9, 1329-38	5.6	33
153	The glucuronidase Agu1 from Schizophyllum commune is a member of a novel glycoside hydrolase family (GH115). *Applied Microbiology and Biotechnology*, **2011**, 90, 1323-32	5.7	33
152	The gold-standard genome of NRRL 3 enables a detailed view of the diversity of sugar catabolism in fungi. *Studies in Mycology*, **2018**, 91, 61-78	22.2	33
151	GalX regulates the D-galactose oxido-reductive pathway in Aspergillus niger. *FEBS Letters*, **2012**, 586, 3980-5	3.8	31
150	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	3.7	31
149	A genomic survey of proteases in Aspergilli. *BMC Genomics*, **2014**, 15, 523	4.5	30
148	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	3.9	30
147	Mapping the polysaccharide degradation potential of Aspergillus niger. *BMC Genomics*, **2012**, 13, 313	4.5	30
146	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	3.9	30
145	Characterization and biotechnological application of recombinant xylanases from Aspergillus nidulans. *International Journal of Biological Macromolecules*, **2016**, 91, 60-7	7.9	29

144	The diversity and evolution of microbiota in traditional Turkish Divle Cave cheese during ripening. *International Dairy Journal*, **2016**, 58, 50-53	3.5	28
143	Carbohydrate-related enzymes of important Phytophthora plant pathogens. *Fungal Genetics and Biology*, **2014**, 72, 192-200	3.9	28
142	Carbohydrate utilization and metabolism is highly differentiated in Agaricus bisporus. *BMC Genomics*, **2013**, 14, 663	4.5	27
141	Characterization of oxylipins and dioxygenase genes in the asexual fungus Aspergillus niger. *BMC Microbiology*, **2009**, 9, 59	4.5	27
140	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	17.8	26
139	Characterization of a feruloyl esterase from Aspergillus terreus facilitates the division of fungal enzymes from Carbohydrate Esterase family 1 of the carbohydrate-active enzymes (CAZy) database. *Microbial Biotechnology*, **2018**, 11, 869-880	6.3	25
138	The transcriptional activators AraR and XlnR from Aspergillus niger regulate expression of pentose catabolic and pentose phosphate pathway genes. *Research in Microbiology*, **2014**, 165, 531-40	4	25
137	Localization of protein secretion in fungal colonies using a novel culturing technique; the ring-plate system. *Journal of Microbiological Methods*, **2007**, 69, 399-401	2.8	25
136	Fungal glucuronoyl esterases: Genome mining based enzyme discovery and biochemical characterization. *New Biotechnology*, **2018**, 40, 282-287	6.4	24
135	The beta-1,4-endogalactanase A gene from Aspergillus niger is specifically induced on arabinose and galacturonic acid and plays an important role in the degradation of pectic hairy regions. *FEBS Journal*, **2002**, 269, 4985-93		24
134	Volatile compound profiling of Turkish Divle Cave cheese during production and ripening. *Journal of Dairy Science*, **2016**, 99, 5120-5131	4	24
133	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	3.7	23
132	Penicillium subrubescens is a promising alternative for Aspergillus niger in enzymatic plant biomass saccharification. *New Biotechnology*, **2016**, 33, 834-841	6.4	23
131	Genomic and Genetic Insights Into a Cosmopolitan Fungus, (Eurotiales). *Frontiers in Microbiology*, **2018**, 9, 3058	5.7	23
130	Enhancing saccharification of wheat straw by mixing enzymes from genetically-modified Trichoderma reesei and Aspergillus niger. *Biotechnology Letters*, **2016**, 38, 65-70	3	22
129	Analysis of Putative Sugar Transporter Genes in Using Phylogeny and Comparative Transcriptomics. *Frontiers in Microbiology*, **2018**, 9, 1045	5.7	22
128	The Hypocrea jecorina (syn. Trichoderma reesei) lxr1 gene encodes a D-mannitol dehydrogenase and is not involved in L-arabinose catabolism. *FEBS Letters*, **2009**, 583, 1309-13	3.8	22
127	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	3.7	21

126	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	3.9	21
125	Improving cellulase production by Aspergillus niger using adaptive evolution. *Biotechnology Letters*, **2016**, 38, 969-74	3	21
124	Technical advance in fungal biotechnology: development of a miniaturized culture method and an automated high-throughput screening. *Letters in Applied Microbiology*, **2009**, 49, 278-82	2.9	21
123	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	2.6	21
122	The pathway intermediate 2-keto-3-deoxy-L-galactonate mediates the induction of genes involved in D-galacturonic acid utilization in Aspergillus niger. *FEBS Letters*, **2017**, 591, 1408-1418	3.8	20
121	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	3.8	20
120	Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies. *New Biotechnology*, **2018**, 41, 9-14	6.4	20
119	Cultivation of Podospora anserina on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. *New Biotechnology*, **2017**, 37, 162-171	6.4	19
118	Spatial and developmental differentiation of mannitol dehydrogenase and mannitol-1-phosphate dehydrogenase in Aspergillus niger. *Eukaryotic Cell*, **2010**, 9, 1398-402		19
117	Dichomitus squalens partially tailors its molecular responses to the composition of solid wood. *Environmental Microbiology*, **2018**, 20, 4141-4156	5.2	19
116	ARA1 regulates not only l-arabinose but also d-galactose catabolism in Trichoderma reesei. *FEBS Letters*, **2018**, 592, 60-70	3.8	18
115	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	3.9	17
114	Fungal Ligninolytic Enzymes and Their Applications. *Microbiology Spectrum*, **2016**, 4,	8.9	17
113	Mixed colonies of Aspergillus niger and Aspergillus oryzae cooperatively degrading wheat bran. *Fungal Genetics and Biology*, **2017**, 102, 31-37	3.9	16
112	Characterisation of three fungal glucuronoyl esterases on glucuronic acid ester model compounds. *Applied Microbiology and Biotechnology*, **2017**, 101, 5301-5311	5.7	16
111	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,	4.8	16
110	The distinctive regulatory roles of PrtT in the cell metabolism of Penicillium oxalicum. *Fungal Genetics and Biology*, **2014**, 63, 42-54	3.9	16
109	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	4.5	16

108	Compost Grown Agaricus bisporus Lacks the Ability to Degrade and Consume Highly Substituted Xylan Fragments. *PLoS ONE*, **2015**, 10, e0134169	3.7	16
107	8 Degradation and Modification of Plant Biomass by Fungi **2014**, 175-208		16
106	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	3.8	16
105	Evidence for ligninolytic activity of the ascomycete fungus. *Biotechnology for Biofuels*, **2020**, 13, 75	7.8	16
104	Feruloyl Esterases for Biorefineries: Subfamily Classified Specificity for Natural Substrates. *Frontiers in Bioengineering and Biotechnology*, **2020**, 8, 332	5.8	15
103	Discovery of Novel p-Hydroxybenzoate-m-hydroxylase, Protocatechuate 3,4 Ring-Cleavage Dioxygenase, and Hydroxyquinol 1,2 Ring-Cleavage Dioxygenase from the Filamentous Fungus Aspergillus niger. *ACS Sustainable Chemistry and Engineering*, **2019**, 7, 19081-19089	8.3	15
102	Phylogenetic analysis and substrate specificity of GH2 mannosidases from Aspergillus species. *FEBS Letters*, **2013**, 587, 3444-9	3.8	15
101	A novel L-arabinose-responsive regulator discovered in the rice-blast fungus Pyricularia oryzae (Magnaporthe oryzae). *FEBS Letters*, **2016**, 590, 550-8	3.8	15
100	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	4.9	14
99	(Post-)genomics approaches in fungal research. *Briefings in Functional Genomics*, **2014**, 13, 424-39	4.9	14
98	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	3.9	14
97	Hydrolytic potential of five fungal supernatants to enhance a commercial enzyme cocktail. *Biotechnology Letters*, **2017**, 39, 1403-1411	3	13
96	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus Pycnoporus. *DNA Research*, **2020**, 27,	4.5	13
95	Cinnamic Acid and Sorbic acid Conversion Are Mediated by the Same Transcriptional Regulator in. *Frontiers in Bioengineering and Biotechnology*, **2019**, 7, 249	5.8	13
94	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, 1346-52	3.8	13
93	Genomic and Postgenomic Diversity of Fungal Plant Biomass Degradation Approaches. *Trends in Microbiology*, **2020**, 28, 487-499	12.4	12
92	Functional diversity in monokaryons. *IMA Fungus*, **2017**, 8, 17-25	6.8	12
91	Spatial differentiation of gene expression in Aspergillus niger colony grown for sugar beet pulp utilization. *Scientific Reports*, **2015**, 5, 13592	4.9	12

90	D-Galactose uptake is nonfunctional in the conidiospores of Aspergillus niger. *FEMS Microbiology Letters*, **2012**, 329, 198-203	2.9	12
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