Arthur F J Ram

List of Publications by Year
in descending order

131 papers	9,357 citations	47006 47 h-index	43889 91 g-index
135 all docs	135 docs citations	135 times ranked	7556 citing authors

#	Article	IF	Citations
1	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	17.5	1,047
2	Agrobacterium-mediated transformation as a tool for functional genomics in fungi. Current Genetics, 2005, 48, 1-17.	1.7	445
3	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
4	Large Scale Identification of Genes Involved in Cell Surface Biosynthesis and Architecture in <i>Saccharomyces cerevisiae</i>. Genetics, 1997, 147, 435-450.	2.9	350
5	Identification of fungal cell wall mutants using susceptibility assays based on Calcofluor white and Congo red. Nature Protocols, 2006, 1, 2253-2256.	12.0	339
6	A new approach for isolating cell wall mutants inSaccharomyces cerevisiae by screening for hypersensitivity to calcofluor white. Yeast, 1994, 10, 1019-1030.	1.7	311
7	In silicio identification of glycosyl-phosphatidylinositol-anchored plasma-membrane and cell wall proteins ofSaccharomyces cerevisiae. , 1997, 13, 1477-1489.		299
8	Highly efficient gene targeting in the Aspergillus niger kusA mutant. Journal of Biotechnology, 2007, 128, 770-775.	3.8	259
9	Novel Aspects of Tomato Root Colonization and Infection by Fusarium oxysporum f. sp. radicis-lycopersici Revealed by Confocal Laser Scanning Microscopic Analysis Using the Green Fluorescent Protein as a Marker. Molecular Plant-Microbe Interactions, 2002, 15, 172-179.	2.6	248
10	Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7, 5.	5.1	228
11	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
12	Loss of the Plasma Membrane-Bound Protein Gas1p in <i>Saccharomyces cerevisiae</i> Results in the Release of Î²1,3-Glucan into the Medium and Induces a Compensation Mechanism To Ensure Cell Wall Integrity. Journal of Bacteriology, 1998, 180, 1418-1424.	2.2	184
13	Agrobacterium-mediated transformation of the filamentous fungus Aspergillus awamori. Nature Protocols, 2008, 3, 1671-1678.	12.0	174
14	Fungal Gene Expression on Demand: an Inducible, Tunable, and Metabolism-Independent Expression System for Aspergillus niger. Applied and Environmental Microbiology, 2011, 77, 2975-2983.	3.1	154
15	Expanding the ku70 toolbox for filamentous fungi: establishment of complementation vectors and recipient strains for advanced gene analyses. Applied Microbiology and Biotechnology, 2010, 87, 1463-1473.	3.6	148
16	Aspergillus as a multi-purpose cell factory: current status and perspectives. Biotechnology Letters, 2011, 33, 469-476.	2.2	145
17	Galactofuranose in eukaryotes: aspects of biosynthesis and functional impact. Glycobiology, 2012, 22, 456-469.	2.5	126
18	Glucoamylase::green fluorescent protein fusions to monitor protein secretion in Aspergillus niger. Microbiology (United Kingdom), 2000, 146, 415-426.	1.8	118

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19	Functional characterization of Rho GTPases in <i>Aspergillus niger</i> uncovers conserved and diverged roles of Rho proteins within filamentous fungi. Molecular Microbiology, 2011, 79, 1151-1167.	2.5	117
20	The cell wall stress response in Aspergillus niger involves increased expression of the glutamine : fructose-6-phosphate amidotransferase-encoding gene (gfaA) and increased deposition of chitin in the cell wall. Microbiology (United Kingdom), 2004, 150, 3315-3326.	1.8	116
21	The molecular and genetic basis of conidial pigmentation in Aspergillus niger. Fungal Genetics and Biology, 2011, 48, 544-553.	2.1	111
22	The carbon starvation response of Aspergillus niger during submerged cultivation: Insights from the transcriptome and secretome. BMC Genomics, 2012, 13, 380.	2.8	108
23	Aspergillus niger genome-wide analysis reveals a large number of novel alpha-glucan acting enzymes with unexpected expression profiles. Molecular Genetics and Genomics, 2008, 279, 545-561.	2.1	100
24	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	2.1	99
25	Regulation of cell wallÎ²-glucan assembly:PTC1 Negatively affectsPBS2 Action in a pathway that includes modulation ofEXG1 transcription. Molecular Genetics and Genomics, 1995, 248, 260-269.	2.4	97
26	Comprehensive genomic analysis of cell wall genes in Aspergillus nidulans. Fungal Genetics and Biology, 2009, 46, S72-S81.	2.1	97
27	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.	2.8	91
28	Using Non-homologous End-Joining-Deficient Strains for Functional Gene Analyses in Filamentous Fungi. Methods in Molecular Biology, 2012, 835, 133-150.	0.9	86
29	<i>Aspergillus fumigatus</i>MADS-Box Transcription Factor<i>rlmA</i>Is Required for Regulation of the Cell Wall Integrity and Virulence. G3: Genes, Genomes, Genetics, 2016, 6, 2983-3002.	1.8	83
30	Expression of agsA, one of five 1,3-Î±-d-glucan synthase-encoding genes in Aspergillus niger, is induced in response to cell wall stress. Fungal Genetics and Biology, 2005, 42, 165-177.	2.1	81
31	A Novel Screening Method for Cell Wall Mutants in <i>Aspergillus niger</i> Identifies UDP-Galactopyranose Mutase as an Important Protein in Fungal Cell Wall Biosynthesis. Genetics, 2008, 178, 873-881.	2.9	81
32	The Aspergillus niger MADS-box transcription factor RlmA is required for cell wall reinforcement in response to cell wall stress. Molecular Microbiology, 2005, 58, 305-319.	2.5	79
33	Carbohydrate Binding Modules: Diversity of Domain Architecture in Amylases and Cellulases From Filamentous Microorganisms. Frontiers in Bioengineering and Biotechnology, 2020, 8, 871.	4.1	78
34	Effective lead selection for improved protein production in Aspergillus niger based on integrated genomics. Fungal Genetics and Biology, 2009, 46, S141-S152.	2.1	77
35	A one-step method to convert vectors into binary vectors suited for Agrobacterium-mediated transformation. Current Genetics, 2004, 45, 242-248.	1.7	76
36	Transcriptomic comparison of Aspergillus niger growing on two different sugars reveals coordinated regulation of the secretory pathway. BMC Genomics, 2009, 10, 44.	2.8	76

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37	Expanding the chemical space for natural products by Aspergillus-Streptomyces co-cultivation and biotransformation. Scientific Reports, 2015, 5, 10868.	3.3	74
38	Survival in the Presence of Antifungals. Journal of Biological Chemistry, 2007, 282, 32935-32948.	3.4	72
39	Identification of a Classical Mutant in the Industrial Host<i>Aspergillus niger</i>by Systems Genetics: LaeA Is Required for Citric Acid Production and Regulates the Formation of Some Secondary Metabolites. G3: Genes, Genomes, Genetics, 2016, 6, 193-204.	1.8	65
40	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
41	Database mining and transcriptional analysis of genes encoding inulin-modifying enzymes of Aspergillus niger. Microbiology (United Kingdom), 2006, 152, 3061-3073.	1.8	63
42	Identification of InuR, a new Zn(II)2Cys6 transcriptional activator involved in the regulation of inulinolytic genes in Aspergillus niger. Molecular Genetics and Genomics, 2008, 279, 11-26.	2.1	60
43	Identification and characterization of a family of secretion-related small GTPase-encoding genes from the filamentous fungus Aspergillus niger : a putative SEC4 homologue is not essential for growth. Molecular Microbiology, 2001, 41, 513-525.	2.5	57
44	Efficient marker free CRISPR/Cas9 genome editing for functional analysis of gene families in filamentous fungi. Fungal Biology and Biotechnology, 2019, 6, 13.	5.1	57
45	Galactofuranose-Coated Gold Nanoparticles Elicit a Pro-inflammatory Response in Human Monocyte-Derived Dendritic Cells and Are Recognized by DC-SIGN. ACS Chemical Biology, 2014, 9, 383-389.	3.4	56
46	Isolation of two laccase genes from the white-rot fungus Pleurotus eryngii and heterologous expression of the pel3 encoded protein. Journal of Biotechnology, 2008, 134, 9-19.	3.8	53
47	Molecular and Biochemical Characterization of a Novel Intracellular Invertase from Aspergillus niger with Transfructosylating Activity. Eukaryotic Cell, 2007, 6, 674-681.	3.4	52
48	Effects of a defective ERAD pathway on growth and heterologous protein production in Aspergillus niger. Applied Microbiology and Biotechnology, 2011, 89, 357-373.	3.6	51
49	Identification of SPT14/CWH6 as the yeast homologue of hPIG-A, a gene involved in the biosynthesis of GPI anchors. Biochimica Et Biophysica Acta - General Subjects, 1995, 1243, 549-551.	2.4	49
50	Green fluorescent protein-cell wall fusion proteins are covalently incorporated into the cell wall ofSaccharomyces cerevisiae. FEMS Microbiology Letters, 1998, 162, 249-255.	1.8	49
51	Deletion of <i>flbA</i> Results in Increased Secretome Complexity and Reduced Secretion Heterogeneity in Colonies of <i>Aspergillus niger</i>. Journal of Proteome Research, 2013, 12, 1808-1819.	3.7	49
52	Genome-wide expression analysis upon constitutive activation of the HacA bZIP transcription factor in Aspergillus niger reveals a coordinated cellular response to counteract ER stress. BMC Genomics, 2012, 13, 350.	2.8	46
53	The transcriptomic fingerprint of glucoamylase over-expression in Aspergillus niger. BMC Genomics, 2012, 13, 701.	2.8	46
54	Role of Pigmentation in Protecting <i>Aspergillus niger</i> Conidiospores Against Pulsed Light Radiation. Photochemistry and Photobiology, 2013, 89, 758-761.	2.5	45

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55	Reconstruction of Signaling Networks Regulating Fungal Morphogenesis by Transcriptomics. Eukaryotic Cell, 2009, 8, 1677-1691.	3.4	42
56	Autophagy promotes survival in aging submerged cultures of the filamentous fungus Aspergillus niger. Applied Microbiology and Biotechnology, 2013, 97, 8205-8218.	3.6	42
57	Characterizing MttA as a mitochondrial cis-aconitic acid transporter by metabolic engineering. Metabolic Engineering, 2016, 35, 95-104.	7.0	42
58	An Evolutionarily Conserved Transcriptional Activator-Repressor Module Controls Expression of Genes for D-Galacturonic Acid Utilization in<i>Aspergillus niger</i>. Genetics, 2017, 205, 169-183.	2.9	42
59	Heme biosynthesis and its regulation: towards understanding and improvement of heme biosynthesis in filamentous fungi. Applied Microbiology and Biotechnology, 2011, 91, 447-460.	3.6	41
60	Characterisation of CwpA, a putative glycosylphosphatidylinositol-anchored cell wall mannoprotein in the filamentous fungus Aspergillus niger. Fungal Genetics and Biology, 2005, 42, 873-885.	2.1	37
61	Inducer-independent production of pectinases in Aspergillus niger by overexpression of the D-galacturonic acid-responsive transcription factor gaaR. Applied Microbiology and Biotechnology, 2018, 102, 2723-2736.	3.6	37
62	Genome mining and functional genomics for siderophore production in Aspergillus niger. Briefings in Functional Genomics, 2014, 13, 482-492.	2.7	36
63	Dynamic and Functional Profiling of Xylan-Degrading Enzymes in <i>Aspergillus</i> Secretomes Using Activity-Based Probes. ACS Central Science, 2019, 5, 1067-1078.	11.3	34
64	Modulating Transcriptional Regulation of Plant Biomass Degrading Enzyme Networks for Rational Design of Industrial Fungal Strains. Frontiers in Bioengineering and Biotechnology, 2018, 6, 133.	4.1	33
65	Rational Design of Mechanism-Based Inhibitors and Activity-Based Probes for the Identification of Retaining Î±-<scp>l</scp>-Arabinofuranosidases. Journal of the American Chemical Society, 2020, 142, 4648-4662.	13.7	33
66	The Saccharomyces cerevisiae CWH8 gene is required for full levels of dolichol-linked oligosaccharides in the endoplasmic reticulum and for efficient N-glycosylation. Glycobiology, 1999, 9, 243-253.	2.5	32
67	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i>. DNA Research, 2020, 27, .	3.4	32
68	The Transcriptomic Signature of RacA Activation and Inactivation Provides New Insights into the Morphogenetic Network of Aspergillus niger. PLoS ONE, 2013, 8, e68946.	2.5	32
69	The polarisome component SpaA localises to hyphal tips of Aspergillus niger and is important for polar growth. Fungal Genetics and Biology, 2008, 45, 152-164.	2.1	29
70	Molecular genetic analysis of vesicular transport in Aspergillus niger reveals partial conservation of the molecular mechanism of exocytosis in fungi. Microbiology (United Kingdom), 2014, 160, 316-329.	1.8	29
71	Velvet domain protein VosA represses the zinc cluster transcription factor SclB regulatory network for Aspergillus nidulans asexual development, oxidative stress response and secondary metabolism. PLoS Genetics, 2018, 14, e1007511.	3.5	29
72	Saccharomyces cerevisiae YCRO17c/CWH43encodes a putative sensor/transporter protein upstream of theBCK2branch of the PKC1-dependent cell wall integrity pathway. Yeast, 2001, 18, 827-840.	1.7	28

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73	Agrobacterium -Mediated Transformation of Aspergillus awamori in the Absence of Full-Length VirD2, VirC2, or VirE2 Leads to Insertion of Aberrant T-DNA Structures. Journal of Bacteriology, 2004, 186, 2038-2045.	2.2	28
74	New resources for functional analysis of omics data for the genus Aspergillus. BMC Genomics, 2011, 12, 486.	2.8	28
75	Improving cellulase production by Aspergillus niger using adaptive evolution. Biotechnology Letters, 2016, 38, 969-974.	2.2	28
76	Transcriptomic and molecular genetic analysis of the cell wall salvage response of<i>Aspergillus niger</i>to the absence of galactofuranose synthesis. Cellular Microbiology, 2016, 18, 1268-1284.	2.1	27
77	Activity of Quinones from Teak (Tectona grandis) on Fungal Cell Wall Stress. Planta Medica, 2006, 72, 943-944.	1.3	26
78	Genetics, Genetic Manipulation, and Approaches to Strain Improvement of Filamentous Fungi. , 2014, , 318-329.		26
79	Efficient Generation of Aspergillus niger Knock Out Strains by Combining NHEJ Mutants and a Split Marker Approach. Fungal Biology, 2015, , 263-272.	0.6	26
80	A new vector for efficient gene targeting to the pyrG locus in Aspergillus niger. Fungal Biology and Biotechnology, 2015, 2, 2.	5.1	26
81	A set of isogenic auxotrophic strains for constructing multiple gene deletion mutants and parasexual crossings in Aspergillus niger. Archives of Microbiology, 2016, 198, 861-868.	2.2	26
82	The pathway intermediate 2â€ketoâ€3â€deoxyâ€Lâ€galactonate mediates the induction of genes involved in Dâ€galacturonic acid utilization in <i>Aspergillus niger</i>. FEBS Letters, 2017, 591, 1408-1418.	2.8	25
83	A new method for screening and isolation of hypersecretion mutants in Aspergillus niger. Applied Microbiology and Biotechnology, 2006, 69, 711-717.	3.6	24
84	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
85	The FlbA-regulated predicted transcription factor Fum21 of Aspergillus niger is involved in fumonisin production. Antonie Van Leeuwenhoek, 2018, 111, 311-322.	1.7	24
86	Systems Approaches to Predict the Functions of Glycoside Hydrolases during the Life Cycle of Aspergillus niger Using Developmental Mutants â^†brlA and â^†flbA. PLoS ONE, 2015, 10, e0116269.	2.5	22
87	I-SceI-mediated double-strand DNA breaks stimulate efficient gene targeting in the industrial fungus Trichoderma reesei. Applied Microbiology and Biotechnology, 2015, 99, 10083-10095.	3.6	22
88	Vacuolar H+-ATPase plays a key role in cell wall biosynthesis of Aspergillus niger. Fungal Genetics and Biology, 2012, 49, 284-293.	2.1	20
89	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	5.1	20
90	Toward Microbial Recycling and Upcycling of Plastics: Prospects and Challenges. Frontiers in Microbiology, 2022, 13, 821629.	3.5	20

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91	Identification of the UDP-glucose-4-epimerase required for galactofuranose biosynthesis and galactose metabolism in A. niger. Fungal Biology and Biotechnology, 2014, 1, 6.	5.1	19
92	Highly active promoters and native secretion signals for protein production during extremely low growth rates in Aspergillus niger. Microbial Cell Factories, 2016, 15, 145.	4.0	19
93	Aspergillus fumigatus establishes infection in zebrafish by germination of phagocytized conidia, while Aspergillus niger relies on extracellular germination. Scientific Reports, 2019, 9, 12791.	3.3	19
94	Preservation stress resistance of melanin deficient conidia from Paecilomyces variotii and Penicillium roqueforti mutants generated via CRISPR/Cas9 genome editing. Fungal Biology and Biotechnology, 2021, 8, 4.	5.1	19
95	The Transcriptional Repressor TupA in Aspergillus niger Is Involved in Controlling Gene Expression Related to Cell Wall Biosynthesis, Development, and Nitrogen Source Availability. PLoS ONE, 2013, 8, e78102.	2.5	19
96	The unconventional secretion of PepN is independent of a functional autophagy machinery in the filamentous fungus<i>Aspergillus niger</i>. FEMS Microbiology Letters, 2016, 363, fnw152.	1.8	17
97	Functional YFP-tagging of the essential GDP-mannose transporter reveals an important role for the secretion related small GTPase SrgC protein in maintenance of Golgi bodies in Aspergillus niger. Fungal Biology, 2011, 115, 253-264.	2.5	15
98	The capacity of Aspergillus niger to sense and respond to cell wall stress requires at least three transcription factors: RlmA, MsnA and CrzA. Fungal Biology and Biotechnology, 2014, 1, 5.	5.1	15
99	Identification and functional analysis of two Golgi-localized UDP-galactofuranose transporters with overlapping functions in Aspergillus niger. BMC Microbiology, 2015, 15, 253.	3.3	15
100	A seven-membered cell wall related transglycosylase gene family in Aspergillus niger is relevant for cell wall integrity in cell wall mutants with reduced Î±-glucan or galactomannan. Cell Surface, 2020, 6, 100039.	3.0	15
101	The protein kinase Kic1 affects 1,6-Î²-glucan levels in the cell wall of Saccharomyces cerevisiae. Microbiology (United Kingdom), 2002, 148, 4035-4048.	1.8	15
102	Methods for Investigating the UPR in Filamentous Fungi. Methods in Enzymology, 2011, 490, 1-29.	1.0	14
103	Fungal Î±-arabinofuranosidases of glycosyl hydrolase families 51 and 54 show a dual arabinofuranosyl- and galactofuranosyl-hydrolyzing activity. Biological Chemistry, 2012, 393, 767-775.	2.5	14
104	The role of coproporphyrinogen III oxidase and ferrochelatase genes in heme biosynthesis and regulation in Aspergillus niger. Applied Microbiology and Biotechnology, 2013, 97, 9773-9785.	3.6	14
105	I-SceI enzyme mediated integration (SEMI) for fast and efficient gene targeting in Trichoderma reesei. Journal of Biotechnology, 2016, 222, 25-28.	3.8	14
106	Rab GDP-dissociation inhibitor gdiA is an essential gene required for cell wall chitin deposition in Aspergillus niger. Fungal Genetics and Biology, 2020, 136, 103319.	2.1	14
107	Subpopulations of hyphae secrete proteins or resist heat stress in <i>Aspergillus oryzae</i> colonies. Environmental Microbiology, 2020, 22, 447-455.	3.8	13
108	Glycosylated cyclophellitol-derived activity-based probes and inhibitors for cellulases. RSC Chemical Biology, 2020, 1, 148-155.	4.1	13

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109	W361R mutation in GaaR, the regulator of Dâ€galacturonic acidâ€responsive genes, leads to constitutive production of pectinases in <i>Aspergillus niger</i>. MicrobiologyOpen, 2019, 8, e00732.	3.0	12
110	Functional analysis of three putative galactofuranosyltransferases with redundant functions in galactofuranosylation in Aspergillus niger. Archives of Microbiology, 2020, 202, 197-203.	2.2	11
111	Identification of SclB, a Zn(II)2Cys6 transcription factor involved in sclerotium formation in Aspergillus niger. Fungal Genetics and Biology, 2020, 139, 103377.	2.1	10
112	Analysis of the role of the<i>Aspergillus niger</i>aminolevulinic acid synthase (<i>hemA</i>) gene illustrates the difference between regulation of yeast and fungal haem- and sirohaem-dependent pathways. FEMS Microbiology Letters, 2012, 335, 104-112.	1.8	9
113	FlbA-Regulated Gene <i>rpnR</i> Is Involved in Stress Resistance and Impacts Protein Secretion when <i>Aspergillus niger</i> Is Grown on Xylose. Applied and Environmental Microbiology, 2019, 85, .	3.1	9
114	The Use of Open Source Bioinformatics Tools to Dissect Transcriptomic Data. Methods in Molecular Biology, 2012, 835, 311-331.	0.9	9
115	TheAspergillus nigerRmsA protein. Communicative and Integrative Biology, 2010, 3, 195-197.	1.4	8
116	Autophagy is dispensable to overcome <scp>ER</scp> stress in the filamentous fungus <i>Aspergillus niger</i>. MicrobiologyOpen, 2016, 5, 647-658.	3.0	7
117	Identification of a Conserved Transcriptional Activator-Repressor Module Controlling the Expression of Genes Involved in Tannic Acid Degradation and Gallic Acid Utilization in Aspergillus niger. Frontiers in Fungal Biology, 2021, 2, .	2.0	7
118	Parasexual Crossings for Bulk Segregant Analysis in Aspergillus niger to Facilitate Mutant Identification Via Whole Genome Sequencing. Methods in Molecular Biology, 2018, 1775, 277-287.	0.9	6
119	Genetic Characterization of Mutations Related to Conidiophore Stalk Length Development in Aspergillus niger Laboratory Strain N402. Frontiers in Genetics, 2021, 12, 666684.	2.3	6
120	Identification of a mitotic recombination hotspot on chromosome III of the asexual fungus Aspergillus niger and its possible correlation elevated basal transcription. Current Genetics, 2007, 52, 107-114.	1.7	5
121	Mutations in AraR leading to constitutive of arabinolytic genes in Aspergillus niger under derepressing conditions. Applied Microbiology and Biotechnology, 2019, 103, 4125-4136.	3.6	5
122	Deletion of the Aspergillus niger Pro-Protein Processing Protease Gene kexB Results in a pH-Dependent Morphological Transition during Submerged Cultivations and Increases Cell Wall Chitin Content. Microorganisms, 2020, 8, 1918.	3.6	5
123	Interrogation of the cell wall integrity pathway in Aspergillus niger identifies a putative negative regulator of transcription involved in chitin deposition. Gene: X, 2020, 763, 100028.	2.3	5
124	Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1â€“2 locus of Aspergillus niger. BMC Genomics, 2021, 22, 679.	2.8	5
125	Loss of function of the carbon catabolite repressor CreA leads to low but inducerâ€independent expression from the feruloyl esterase B promoter in Aspergillus niger. Biotechnology Letters, 2021, 43, 1323-1336.	2.2	4
126	Genome sequences of 24 <i>Aspergillus niger sensu stricto</i> strains to study strain diversity, heterokaryon compatibility, and sexual reproduction. G3: Genes, Genomes, Genetics, 0, , .	1.8	4

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127	High sorbic acid resistance of Penicillium roqueforti is mediated by the SORBUS gene cluster. PLoS Genetics, 2022, 18, e1010086.	3.5	4
128	Natural Variation and the Role of Zn2Cys6 Transcription Factors SdrA, WarA and WarB in Sorbic Acid Resistance of Aspergillus niger. Microorganisms, 2022, 10, 221.	3.6	3
129	Intraspecific variability in heat resistance of fungal conidia. Food Research International, 2022, 156, 111302.	6.2	3
130	Meeting a Challenge: A View on Studying Transcriptional Control of Genes Involved in Plant Biomass Degradation in Aspergillus niger. Grand Challenges in Biology and Biotechnology, 2020, , 211-235.	2.4	1
131	Screening for Compounds Exerting Antifungal Activities. , 2013, , 225-230.		0