

Arthur F J Ram

List of Publications by Year in descending order

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131
papers

9,357
citations

47006

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135
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docs citations

135
times ranked

7556
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Natural Variation and the Role of Zn2Cys6 Transcription Factors SdrA, WarA and WarB in Sorbic Acid Resistance of <i>Aspergillus niger</i> . <i>Microorganisms</i> , 2022, 10, 221. | 3.6 | 3 |
| 2 | Toward Microbial Recycling and Upcycling of Plastics: Prospects and Challenges. <i>Frontiers in Microbiology</i> , 2022, 13, 821629. | 3.5 | 20 |
| 3 | Intraspecific variability in heat resistance of fungal conidia. <i>Food Research International</i> , 2022, 156, 111302. | 6.2 | 3 |
| 4 | High sorbic acid resistance of <i>Penicillium roqueforti</i> is mediated by the SORBUS gene cluster. <i>PLoS Genetics</i> , 2022, 18, e1010086. | 3.5 | 4 |
| 5 | Loss of function of the carbon catabolite repressor CreA leads to low but inducer-independent expression from the feruloyl esterase B promoter in <i>Aspergillus niger</i> . <i>Biotechnology Letters</i> , 2021, 43, 1323-1336. | 2.2 | 4 |
| 6 | Genetic Characterization of Mutations Related to Conidiophore Stalk Length Development in <i>Aspergillus niger</i> Laboratory Strain N402. <i>Frontiers in Genetics</i> , 2021, 12, 666684. | 2.3 | 6 |
| 7 | Preservation stress resistance of melanin deficient conidia from <i>Paecilomyces variotii</i> and <i>Penicillium roqueforti</i> mutants generated via CRISPR/Cas9 genome editing. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 4. | 5.1 | 19 |
| 8 | Identification of a Conserved Transcriptional Activator-Repressor Module Controlling the Expression of Genes Involved in Tannic Acid Degradation and Gallic Acid Utilization in <i>Aspergillus niger</i> . <i>Frontiers in Fungal Biology</i> , 2021, 2, . | 2.0 | 7 |
| 9 | Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1-2 locus of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2021, 22, 679. | 2.8 | 5 |
| 10 | Functional analysis of three putative galactofuranosyltransferases with redundant functions in galactofuranosylation in <i>Aspergillus niger</i> . <i>Archives of Microbiology</i> , 2020, 202, 197-203. | 2.2 | 11 |
| 11 | Rab GDP-dissociation inhibitor gdiA is an essential gene required for cell wall chitin deposition in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2020, 136, 103319. | 2.1 | 14 |
| 12 | Subpopulations of hyphae secrete proteins or resist heat stress in <i>Aspergillus oryzae</i> colonies. <i>Environmental Microbiology</i> , 2020, 22, 447-455. | 3.8 | 13 |
| 13 | Glycosylated cyclophellitol-derived activity-based probes and inhibitors for cellulases. <i>RSC Chemical Biology</i> , 2020, 1, 148-155. | 4.1 | 13 |
| 14 | Carbohydrate Binding Modules: Diversity of Domain Architecture in Amylases and Cellulases From Filamentous Microorganisms. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 871. | 4.1 | 78 |
| 15 | Deletion of the <i>Aspergillus niger</i> Pro-Protein Processing Protease Gene <i>kexB</i> Results in a pH-Dependent Morphological Transition during Submerged Cultivations and Increases Cell Wall Chitin Content. <i>Microorganisms</i> , 2020, 8, 1918. | 3.6 | 5 |
| 16 | Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus</i> . <i>DNA Research</i> , 2020, 27, . | 3.4 | 32 |
| 17 | Interrogation of the cell wall integrity pathway in <i>Aspergillus niger</i> identifies a putative negative regulator of transcription involved in chitin deposition. <i>Gene</i> , 2020, 763, 100028. | 2.3 | 5 |
| 18 | Rational Design of Mechanism-Based Inhibitors and Activity-Based Probes for the Identification of Retaining β -Arabinofuranosidases. <i>Journal of the American Chemical Society</i> , 2020, 142, 4648-4662. | 13.7 | 33 |

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|----|--|------|-----------|
| 19 | Identification of SclB, a Zn(II)2Cys6 transcription factor involved in sclerotium formation in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2020, 139, 103377. | 2.1 | 10 |
| 20 | A seven-membered cell wall related transglycosylase gene family in <i>Aspergillus niger</i> is relevant for cell wall integrity in cell wall mutants with reduced 1 α -glucan or galactomannan. <i>Cell Surface</i> , 2020, 6, 100039. | 3.0 | 15 |
| 21 | Growing a circular economy with fungal biotechnology: a white paper. <i>Fungal Biology and Biotechnology</i> , 2020, 7, 5. | 5.1 | 228 |
| 22 | Meeting a Challenge: A View on Studying Transcriptional Control of Genes Involved in Plant Biomass Degradation in <i>Aspergillus niger</i> . <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 211-235. | 2.4 | 1 |
| 23 | <i>Aspergillus fumigatus</i> establishes infection in zebrafish by germination of phagocytized conidia, while <i>Aspergillus niger</i> relies on extracellular germination. <i>Scientific Reports</i> , 2019, 9, 12791. | 3.3 | 19 |
| 24 | Efficient marker free CRISPR/Cas9 genome editing for functional analysis of gene families in filamentous fungi. <i>Fungal Biology and Biotechnology</i> , 2019, 6, 13. | 5.1 | 57 |
| 25 | Dynamic and Functional Profiling of Xylan-Degrading Enzymes in <i>Aspergillus</i> Secretomes Using Activity-Based Probes. <i>ACS Central Science</i> , 2019, 5, 1067-1078. | 11.3 | 34 |
| 26 | Mutations in AraR leading to constitutive of arabinolytic genes in <i>Aspergillus niger</i> under derepressing conditions. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 4125-4136. | 3.6 | 5 |
| 27 | FlbA-Regulated Gene <i>rpnR</i> Is Involved in Stress Resistance and Impacts Protein Secretion when <i>Aspergillus niger</i> Is Grown on Xylose. <i>Applied and Environmental Microbiology</i> , 2019, 85, . | 3.1 | 9 |
| 28 | W361R mutation in GaaR, the regulator of D-galacturonic acid-responsive genes, leads to constitutive production of pectinases in <i>Aspergillus niger</i> . <i>MicrobiologyOpen</i> , 2019, 8, e00732. | 3.0 | 12 |
| 29 | Inducer-independent production of pectinases in <i>Aspergillus niger</i> by overexpression of the D-galacturonic acid-responsive transcription factor gaaR. <i>Applied Microbiology and Biotechnology</i> , 2018, 102, 2723-2736. | 3.6 | 37 |
| 30 | The FlbA-regulated predicted transcription factor Fum21 of <i>Aspergillus niger</i> is involved in fumonisin production. <i>Antonie Van Leeuwenhoek</i> , 2018, 111, 311-322. | 1.7 | 24 |
| 31 | A community-driven reconstruction of the <i>Aspergillus niger</i> metabolic network. <i>Fungal Biology and Biotechnology</i> , 2018, 5, 16. | 5.1 | 20 |
| 32 | Modulating Transcriptional Regulation of Plant Biomass Degrading Enzyme Networks for Rational Design of Industrial Fungal Strains. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 133. | 4.1 | 33 |
| 33 | Velvet domain protein VosA represses the zinc cluster transcription factor SclB regulatory network for <i>Aspergillus nidulans</i> asexual development, oxidative stress response and secondary metabolism. <i>PLoS Genetics</i> , 2018, 14, e1007511. | 3.5 | 29 |
| 34 | Parasexual Crossings for Bulk Segregant Analysis in <i>Aspergillus niger</i> to Facilitate Mutant Identification Via Whole Genome Sequencing. <i>Methods in Molecular Biology</i> , 2018, 1775, 277-287. | 0.9 | 6 |
| 35 | 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. | 8.8 | 417 |
| 36 | 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. | 2.8 | 25 |

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|----|---|-----|-----------|
| 37 | An Evolutionarily Conserved Transcriptional Activator-Repressor Module Controls Expression of Genes for D-Galacturonic Acid Utilization in <i>Aspergillus niger</i> . <i>Genetics</i> , 2017, 205, 169-183. | 2.9 | 42 |
| 38 | Transcriptomic and molecular genetic analysis of the cell wall salvage response of <i>Aspergillus niger</i> to the absence of galactofuranose synthesis. <i>Cellular Microbiology</i> , 2016, 18, 1268-1284. | 2.1 | 27 |
| 39 | Identification of a Classical Mutant in the Industrial Host <i>Aspergillus niger</i> by Systems Genetics: <i>LaeA</i> Is Required for Citric Acid Production and Regulates the Formation of Some Secondary Metabolites. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 193-204. | 1.8 | 65 |
| 40 | <i>Aspergillus fumigatus</i> MADS-Box Transcription Factor <i>rlmA</i> Is Required for Regulation of the Cell Wall Integrity and Virulence. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2983-3002. | 1.8 | 83 |
| 41 | Highly active promoters and native secretion signals for protein production during extremely low growth rates in <i>Aspergillus niger</i> . <i>Microbial Cell Factories</i> , 2016, 15, 145. | 4.0 | 19 |
| 42 | Autophagy is dispensable to overcome ER stress in the filamentous fungus <i>Aspergillus niger</i> . <i>MicrobiologyOpen</i> , 2016, 5, 647-658. | 3.0 | 7 |
| 43 | Current challenges of research on filamentous fungi in relation to human welfare and a sustainable bio-economy: a white paper. <i>Fungal Biology and Biotechnology</i> , 2016, 3, 6. | 5.1 | 208 |
| 44 | A set of isogenic auxotrophic strains for constructing multiple gene deletion mutants and parasexual crossings in <i>Aspergillus niger</i> . <i>Archives of Microbiology</i> , 2016, 198, 861-868. | 2.2 | 26 |
| 45 | The unconventional secretion of PepN is independent of a functional autophagy machinery in the filamentous fungus <i>Aspergillus niger</i> . <i>FEMS Microbiology Letters</i> , 2016, 363, fnw152. | 1.8 | 17 |
| 46 | 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. | 2.8 | 64 |
| 47 | Characterizing MttA as a mitochondrial cis-aconitic acid transporter by metabolic engineering. <i>Metabolic Engineering</i> , 2016, 35, 95-104. | 7.0 | 42 |
| 48 | Improving cellulase production by <i>Aspergillus niger</i> using adaptive evolution. <i>Biotechnology Letters</i> , 2016, 38, 969-974. | 2.2 | 28 |
| 49 | I-SceI enzyme mediated integration (SEMI) for fast and efficient gene targeting in <i>Trichoderma reesei</i> . <i>Journal of Biotechnology</i> , 2016, 222, 25-28. | 3.8 | 14 |
| 50 | Identification and functional analysis of two Golgi-localized UDP-galactofuranose transporters with overlapping functions in <i>Aspergillus niger</i> . <i>BMC Microbiology</i> , 2015, 15, 253. | 3.3 | 15 |
| 51 | Systems Approaches to Predict the Functions of Glycoside Hydrolases during the Life Cycle of <i>Aspergillus niger</i> Using Developmental Mutants Δ trIA and Δ trbA. <i>PLoS ONE</i> , 2015, 10, e0116269. | 2.5 | 22 |
| 52 | Efficient Generation of <i>Aspergillus niger</i> Knock Out Strains by Combining NHEJ Mutants and a Split Marker Approach. <i>Fungal Biology</i> , 2015, , 263-272. | 0.6 | 26 |
| 53 | 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. | 2.1 | 24 |
| 54 | Expanding the chemical space for natural products by <i>Aspergillus-Streptomyces</i> co-cultivation and biotransformation. <i>Scientific Reports</i> , 2015, 5, 10868. | 3.3 | 74 |

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|----|--|-----|-----------|
| 55 | A new vector for efficient gene targeting to the pyrG locus in <i>Aspergillus niger</i> . <i>Fungal Biology and Biotechnology</i> , 2015, 2, 2. | 5.1 | 26 |
| 56 | I-SceI-mediated double-strand DNA breaks stimulate efficient gene targeting in the industrial fungus <i>Trichoderma reesei</i> . <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 10083-10095. | 3.6 | 22 |
| 57 | Identification of the UDP-glucose-4-epimerase required for galactofuranose biosynthesis and galactose metabolism in <i>A. niger</i> . <i>Fungal Biology and Biotechnology</i> , 2014, 1, 6. | 5.1 | 19 |
| 58 | Genome mining and functional genomics for siderophore production in <i>Aspergillus niger</i> . <i>Briefings in Functional Genomics</i> , 2014, 13, 482-492. | 2.7 | 36 |
| 59 | The capacity of <i>Aspergillus niger</i> to sense and respond to cell wall stress requires at least three transcription factors: RlmA, MsnA and CrzA. <i>Fungal Biology and Biotechnology</i> , 2014, 1, 5. | 5.1 | 15 |
| 60 | The genome of the white-rot fungus <i>Pycnoporus cinnabarinus</i> : a basidiomycete model with a versatile arsenal for lignocellulosic biomass breakdown. <i>BMC Genomics</i> , 2014, 15, 486. | 2.8 | 91 |
| 61 | Molecular genetic analysis of vesicular transport in <i>Aspergillus niger</i> reveals partial conservation of the molecular mechanism of exocytosis in fungi. <i>Microbiology (United Kingdom)</i> , 2014, 160, 316-329. | 1.8 | 29 |
| 62 | Galactofuranose-Coated Gold Nanoparticles Elicit a Pro-inflammatory Response in Human Monocyte-Derived Dendritic Cells and Are Recognized by DC-SIGN. <i>ACS Chemical Biology</i> , 2014, 9, 383-389. | 3.4 | 56 |
| 63 | Genetics, Genetic Manipulation, and Approaches to Strain Improvement of Filamentous Fungi. , 2014, , 318-329. | | 26 |
| 64 | Autophagy promotes survival in aging submerged cultures of the filamentous fungus <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 8205-8218. | 3.6 | 42 |
| 65 | Deletion of <i>flbA</i> Results in Increased Secretome Complexity and Reduced Secretion Heterogeneity in Colonies of <i>Aspergillus niger</i> . <i>Journal of Proteome Research</i> , 2013, 12, 1808-1819. | 3.7 | 49 |
| 66 | The role of coproporphyrinogen III oxidase and ferrochelatase genes in heme biosynthesis and regulation in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2013, 97, 9773-9785. | 3.6 | 14 |
| 67 | Screening for Compounds Exerting Antifungal Activities. , 2013, , 225-230. | | 0 |
| 68 | Role of Pigmentation in Protecting <i>Aspergillus niger</i> Conidiospores Against Pulsed Light Radiation. <i>Photochemistry and Photobiology</i> , 2013, 89, 758-761. | 2.5 | 45 |
| 69 | The Transcriptomic Signature of RacA Activation and Inactivation Provides New Insights into the Morphogenetic Network of <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2013, 8, e68946. | 2.5 | 32 |
| 70 | The Transcriptional Repressor TupA in <i>Aspergillus niger</i> Is Involved in Controlling Gene Expression Related to Cell Wall Biosynthesis, Development, and Nitrogen Source Availability. <i>PLoS ONE</i> , 2013, 8, e78102. | 2.5 | 19 |
| 71 | Galactofuranose in eukaryotes: aspects of biosynthesis and functional impact. <i>Glycobiology</i> , 2012, 22, 456-469. | 2.5 | 126 |
| 72 | 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. <i>FEMS Microbiology Letters</i> , 2012, 335, 104-112. | 1.8 | 9 |

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|----|--|-----|-----------|
| 73 | Fungal α -arabinofuranosidases of glycosyl hydrolase families 51 and 54 show a dual arabinofuranosyl- and galactofuranosyl-hydrolyzing activity. <i>Biological Chemistry</i> , 2012, 393, 767-775. | 2.5 | 14 |
| 74 | Vacuolar H ⁺ -ATPase plays a key role in cell wall biosynthesis of <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2012, 49, 284-293. | 2.1 | 20 |
| 75 | Genome-wide expression analysis upon constitutive activation of the HacA bZIP transcription factor in <i>Aspergillus niger</i> reveals a coordinated cellular response to counteract ER stress. <i>BMC Genomics</i> , 2012, 13, 350. | 2.8 | 46 |
| 76 | The carbon starvation response of <i>Aspergillus niger</i> during submerged cultivation: Insights from the transcriptome and secretome. <i>BMC Genomics</i> , 2012, 13, 380. | 2.8 | 108 |
| 77 | The transcriptomic fingerprint of glucoamylase over-expression in <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2012, 13, 701. | 2.8 | 46 |
| 78 | Using Non-homologous End-Joining-Deficient Strains for Functional Gene Analyses in Filamentous Fungi. <i>Methods in Molecular Biology</i> , 2012, 835, 133-150. | 0.9 | 86 |
| 79 | The Use of Open Source Bioinformatics Tools to Dissect Transcriptomic Data. <i>Methods in Molecular Biology</i> , 2012, 835, 311-331. | 0.9 | 9 |
| 80 | 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 <i>Aspergillus niger</i> . <i>Fungal Biology</i> , 2011, 115, 253-264. | 2.5 | 15 |
| 81 | The molecular and genetic basis of conidial pigmentation in <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 544-553. | 2.1 | 111 |
| 82 | Functional characterization of Rho GTPases in <i>Aspergillus niger</i> uncovers conserved and diverged roles of Rho proteins within filamentous fungi. <i>Molecular Microbiology</i> , 2011, 79, 1151-1167. | 2.5 | 117 |
| 83 | <i>Aspergillus</i> as a multi-purpose cell factory: current status and perspectives. <i>Biotechnology Letters</i> , 2011, 33, 469-476. | 2.2 | 145 |
| 84 | Effects of a defective ERAD pathway on growth and heterologous protein production in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2011, 89, 357-373. | 3.6 | 51 |
| 85 | Heme biosynthesis and its regulation: towards understanding and improvement of heme biosynthesis in filamentous fungi. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 447-460. | 3.6 | 41 |
| 86 | New resources for functional analysis of omics data for the genus <i>Aspergillus</i> . <i>BMC Genomics</i> , 2011, 12, 486. | 2.8 | 28 |
| 87 | Fungal Gene Expression on Demand: an Inducible, Tunable, and Metabolism-Independent Expression System for <i>Aspergillus niger</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 2975-2983. | 3.1 | 154 |
| 88 | Methods for Investigating the UPR in Filamentous Fungi. <i>Methods in Enzymology</i> , 2011, 490, 1-29. | 1.0 | 14 |
| 89 | The <i>Aspergillus niger</i> RmsA protein. <i>Communicative and Integrative Biology</i> , 2010, 3, 195-197. | 1.4 | 8 |
| 90 | Expanding the ku70 toolbox for filamentous fungi: establishment of complementation vectors and recipient strains for advanced gene analyses. <i>Applied Microbiology and Biotechnology</i> , 2010, 87, 1463-1473. | 3.6 | 148 |

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|-----|--|------|-----------|
| 91 | Reconstruction of Signaling Networks Regulating Fungal Morphogenesis by Transcriptomics. <i>Eukaryotic Cell</i> , 2009, 8, 1677-1691. | 3.4 | 42 |
| 92 | Transcriptomic comparison of <i>Aspergillus niger</i> growing on two different sugars reveals coordinated regulation of the secretory pathway. <i>BMC Genomics</i> , 2009, 10, 44. | 2.8 | 76 |
| 93 | Comprehensive genomic analysis of cell wall genes in <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S72-S81. | 2.1 | 97 |
| 94 | Effective lead selection for improved protein production in <i>Aspergillus niger</i> based on integrated genomics. <i>Fungal Genetics and Biology</i> , 2009, 46, S141-S152. | 2.1 | 77 |
| 95 | The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13. | 2.1 | 99 |
| 96 | Identification of InuR, a new Zn(II)2Cys6 transcriptional activator involved in the regulation of inulinolytic genes in <i>Aspergillus niger</i> . <i>Molecular Genetics and Genomics</i> , 2008, 279, 11-26. | 2.1 | 60 |
| 97 | <i>Aspergillus niger</i> genome-wide analysis reveals a large number of novel alpha-glucan acting enzymes with unexpected expression profiles. <i>Molecular Genetics and Genomics</i> , 2008, 279, 545-561. | 2.1 | 100 |
| 98 | <i>Agrobacterium</i> -mediated transformation of the filamentous fungus <i>Aspergillus awamori</i> . <i>Nature Protocols</i> , 2008, 3, 1671-1678. | 12.0 | 174 |
| 99 | The polarisome component SpaA localises to hyphal tips of <i>Aspergillus niger</i> and is important for polar growth. <i>Fungal Genetics and Biology</i> , 2008, 45, 152-164. | 2.1 | 29 |
| 100 | Isolation of two laccase genes from the white-rot fungus <i>Pleurotus eryngii</i> and heterologous expression of the pel3 encoded protein. <i>Journal of Biotechnology</i> , 2008, 134, 9-19. | 3.8 | 53 |
| 101 | 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. <i>Genetics</i> , 2008, 178, 873-881. | 2.9 | 81 |
| 102 | Molecular and Biochemical Characterization of a Novel Intracellular Invertase from <i>Aspergillus niger</i> with Transfructosylating Activity. <i>Eukaryotic Cell</i> , 2007, 6, 674-681. | 3.4 | 52 |
| 103 | Survival in the Presence of Antifungals. <i>Journal of Biological Chemistry</i> , 2007, 282, 32935-32948. | 3.4 | 72 |
| 104 | Highly efficient gene targeting in the <i>Aspergillus niger</i> kusA mutant. <i>Journal of Biotechnology</i> , 2007, 128, 770-775. | 3.8 | 259 |
| 105 | Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231. | 17.5 | 1,047 |
| 106 | Identification of a mitotic recombination hotspot on chromosome III of the asexual fungus <i>Aspergillus niger</i> and its possible correlation elevated basal transcription. <i>Current Genetics</i> , 2007, 52, 107-114. | 1.7 | 5 |
| 107 | Identification of fungal cell wall mutants using susceptibility assays based on Calcofluor white and Congo red. <i>Nature Protocols</i> , 2006, 1, 2253-2256. | 12.0 | 339 |
| 108 | A new method for screening and isolation of hypersecretion mutants in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2006, 69, 711-717. | 3.6 | 24 |

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|-----|---|-----|-----------|
| 109 | Activity of Quinones from Teak (<i>Tectona grandis</i>) on Fungal Cell Wall Stress. <i>Planta Medica</i> , 2006, 72, 943-944. | 1.3 | 26 |
| 110 | Database mining and transcriptional analysis of genes encoding inulin-modifying enzymes of <i>Aspergillus niger</i> . <i>Microbiology (United Kingdom)</i> , 2006, 152, 3061-3073. | 1.8 | 63 |
| 111 | The <i>Aspergillus niger</i> MADS-box transcription factor RlmA is required for cell wall reinforcement in response to cell wall stress. <i>Molecular Microbiology</i> , 2005, 58, 305-319. | 2.5 | 79 |
| 112 | <i>Agrobacterium</i> -mediated transformation as a tool for functional genomics in fungi. <i>Current Genetics</i> , 2005, 48, 1-17. | 1.7 | 445 |
| 113 | Expression of <i>agsA</i> , one of five 1,3- β -D-glucan synthase-encoding genes in <i>Aspergillus niger</i> , is induced in response to cell wall stress. <i>Fungal Genetics and Biology</i> , 2005, 42, 165-177. | 2.1 | 81 |
| 114 | Characterisation of CwpA, a putative glycosylphosphatidylinositol-anchored cell wall mannoprotein in the filamentous fungus <i>Aspergillus niger</i> . <i>Fungal Genetics and Biology</i> , 2005, 42, 873-885. | 2.1 | 37 |
| 115 | <i>Agrobacterium</i> -Mediated Transformation of <i>Aspergillus awamori</i> in the Absence of Full-Length VirD2, VirC2, or VirE2 Leads to Insertion of Aberrant T-DNA Structures. <i>Journal of Bacteriology</i> , 2004, 186, 2038-2045. | 2.2 | 28 |
| 116 | A one-step method to convert vectors into binary vectors suited for <i>Agrobacterium</i> -mediated transformation. <i>Current Genetics</i> , 2004, 45, 242-248. | 1.7 | 76 |
| 117 | The cell wall stress response in <i>Aspergillus niger</i> involves increased expression of the glutamine : fructose-6-phosphate amidotransferase-encoding gene (<i>gfaA</i>) and increased deposition of chitin in the cell wall. <i>Microbiology (United Kingdom)</i> , 2004, 150, 3315-3326. | 1.8 | 116 |
| 118 | Novel Aspects of Tomato Root Colonization and Infection by <i>Fusarium oxysporum</i> f. sp. <i>radicis-lycopersici</i> Revealed by Confocal Laser Scanning Microscopic Analysis Using the Green Fluorescent Protein as a Marker. <i>Molecular Plant-Microbe Interactions</i> , 2002, 15, 172-179. | 2.6 | 248 |
| 119 | The protein kinase Kic1 affects 1,6- β -glucan levels in the cell wall of <i>Saccharomyces cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 2002, 148, 4035-4048. | 1.8 | 15 |
| 120 | Identification and characterization of a family of secretion-related small GTPase-encoding genes from the filamentous fungus <i>Aspergillus niger</i> : a putative SEC4 homologue is not essential for growth. <i>Molecular Microbiology</i> , 2001, 41, 513-525. | 2.5 | 57 |
| 121 | <i>Saccharomyces cerevisiae</i> YCRO17c/CWH43 encodes a putative sensor/transporter protein upstream of the BCK2 branch of the PKC1-dependent cell wall integrity pathway. <i>Yeast</i> , 2001, 18, 827-840. | 1.7 | 28 |
| 122 | Glucoamylase::green fluorescent protein fusions to monitor protein secretion in <i>Aspergillus niger</i> . <i>Microbiology (United Kingdom)</i> , 2000, 146, 415-426. | 1.8 | 118 |
| 123 | The <i>Saccharomyces cerevisiae</i> CWH8 gene is required for full levels of dolichol-linked oligosaccharides in the endoplasmic reticulum and for efficient N-glycosylation. <i>Glycobiology</i> , 1999, 9, 243-253. | 2.5 | 32 |
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