Arthur F J Ram

List of Publications by Year in descending order

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131 papers	9,357 citations	46918 47 h-index	91 g-index
135	135	135	7556
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Natural Variation and the Role of Zn2Cys6 Transcription Factors SdrA, WarA and WarB in Sorbic Acid Resistance of Aspergillus niger. Microorganisms, 2022, 10, 221.	1.6	3
2	Toward Microbial Recycling and Upcycling of Plastics: Prospects and Challenges. Frontiers in Microbiology, 2022, 13, 821629.	1.5	20
3	Intraspecific variability in heat resistance of fungal conidia. Food Research International, 2022, 156, 111302.	2.9	3
4	High sorbic acid resistance of Penicillium roqueforti is mediated by the SORBUS gene cluster. PLoS Genetics, 2022, 18, e1010086.	1.5	4
5	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.	1.1	4
6	Genetic Characterization of Mutations Related to Conidiophore Stalk Length Development in Aspergillus niger Laboratory Strain N402. Frontiers in Genetics, 2021, 12, 666684.	1.1	6
7	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.	2.5	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 Aspergillus niger. Frontiers in Fungal Biology, 2021, 2, .	0.9	7
9	Genome sequencing of the neotype strain CBS 554.65 reveals the MAT1–2 locus of Aspergillus niger. BMC Genomics, 2021, 22, 679.	1.2	5
10	Functional analysis of three putative galactofuranosyltransferases with redundant functions in galactofuranosylation in Aspergillus niger. Archives of Microbiology, 2020, 202, 197-203.	1.0	11
11	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.	0.9	14
12	Subpopulations of hyphae secrete proteins or resist heat stress in <i>Aspergillus oryzae</i> colonies. Environmental Microbiology, 2020, 22, 447-455.	1.8	13
13	Glycosylated cyclophellitol-derived activity-based probes and inhibitors for cellulases. RSC Chemical Biology, 2020, 1, 148-155.	2.0	13
14	Carbohydrate Binding Modules: Diversity of Domain Architecture in Amylases and Cellulases From Filamentous Microorganisms. Frontiers in Bioengineering and Biotechnology, 2020, 8, 871.	2.0	78
15	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.	1.6	5
16	Conserved white-rot enzymatic mechanism for wood decay in the Basidiomycota genus <i>Pycnoporus </i> DNA Research, 2020, 27, .	1.5	32
17	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
18	Rational Design of Mechanism-Based Inhibitors and Activity-Based Probes for the Identification of Retaining α- <scp>I</scp> -Arabinofuranosidases. Journal of the American Chemical Society, 2020, 142, 4648-4662.	6.6	33

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19	Identification of SclB, a Zn(II)2Cys6 transcription factor involved in sclerotium formation in Aspergillus niger. Fungal Genetics and Biology, 2020, 139, 103377.	0.9	10
20	A seven-membered cell wall related transglycosylase gene family in Aspergillus niger is relevant for cell wall integrity in cell wall mutants with reduced $\hat{l}\pm$ -glucan or galactomannan. Cell Surface, 2020, 6, 100039.	1.5	15
21	Growing a circular economy with fungal biotechnology: a white paper. Fungal Biology and Biotechnology, 2020, 7, 5.	2.5	228
22	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
23	Aspergillus fumigatus establishes infection in zebrafish by germination of phagocytized conidia, while Aspergillus niger relies on extracellular germination. Scientific Reports, 2019, 9, 12791.	1.6	19
24	Efficient marker free CRISPR/Cas9 genome editing for functional analysis of gene families in filamentous fungi. Fungal Biology and Biotechnology, 2019, 6, 13.	2.5	57
25	Dynamic and Functional Profiling of Xylan-Degrading Enzymes in <i>Aspergillus</i> Secretomes Using Activity-Based Probes. ACS Central Science, 2019, 5, 1067-1078.	5.3	34
26	Mutations in AraR leading to constitutive of arabinolytic genes in Aspergillus niger under derepressing conditions. Applied Microbiology and Biotechnology, 2019, 103, 4125-4136.	1.7	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. Applied and Environmental Microbiology, 2019, 85, .	1.4	9
28	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.	1.2	12
29	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.	1.7	37
30	The FlbA-regulated predicted transcription factor Fum21 of Aspergillus niger is involved in fumonisin production. Antonie Van Leeuwenhoek, 2018, 111, 311-322.	0.7	24
31	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	2.5	20
32	Modulating Transcriptional Regulation of Plant Biomass Degrading Enzyme Networks for Rational Design of Industrial Fungal Strains. Frontiers in Bioengineering and Biotechnology, 2018, 6, 133.	2.0	33
33	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.	1.5	29
34	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.	0.4	6
35	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
36	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.	1.3	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> . Genetics, 2017, 205, 169-183.	1.2	42
38	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.	1.1	27
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.	0.8	65
40	<i>Aspergillus fumigatus</i> MADS-Box Transcription Factor <i>rlmA</i> Is Required for Regulation of the Cell Wall Integrity and Virulence. G3: Genes, Genomes, Genetics, 2016, 6, 2983-3002.	0.8	83
41	Highly active promoters and native secretion signals for protein production during extremely low growth rates in Aspergillus niger. Microbial Cell Factories, 2016, 15, 145.	1.9	19
42	Autophagy is dispensable to overcome <scp>ER</scp> stress in the filamentous fungus <i>Aspergillus niger</i> MicrobiologyOpen, 2016, 5, 647-658.	1.2	7
43	Current challenges of research on filamentous fungi in relation to human welfare and a sustainable bio-economy: a white paper. Fungal Biology and Biotechnology, 2016, 3, 6.	2.5	208
44	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.	1.0	26
45	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.	0.7	17
46	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.	1.3	64
47	Characterizing MttA as a mitochondrial cis-aconitic acid transporter by metabolic engineering. Metabolic Engineering, 2016, 35, 95-104.	3.6	42
48	Improving cellulase production by Aspergillus niger using adaptive evolution. Biotechnology Letters, 2016, 38, 969-974.	1.1	28
49	I-Scel enzyme mediated integration (SEMI) for fast and efficient gene targeting in Trichoderma reesei. Journal of Biotechnology, 2016, 222, 25-28.	1.9	14
50	Identification and functional analysis of two Golgi-localized UDP-galactofuranose transporters with overlapping functions in Aspergillus niger. BMC Microbiology, 2015, 15, 253.	1.3	15
51	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.	1.1	22
52	Efficient Generation of Aspergillus niger Knock Out Strains by Combining NHEJ Mutants and a Split Marker Approach. Fungal Biology, 2015, , 263-272.	0.3	26
53	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.	0.9	24
54	Expanding the chemical space for natural products by Aspergillus-Streptomyces co-cultivation and biotransformation. Scientific Reports, 2015, 5, 10868.	1.6	74

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55	A new vector for efficient gene targeting to the pyrG locus in Aspergillus niger. Fungal Biology and Biotechnology, 2015, 2, 2.	2.5	26
56	I-Scel-mediated double-strand DNA breaks stimulate efficient gene targeting in the industrial fungus Trichoderma reesei. Applied Microbiology and Biotechnology, 2015, 99, 10083-10095.	1.7	22
57	Identification of the UDP-glucose-4-epimerase required for galactofuranose biosynthesis and galactose metabolism in A. niger. Fungal Biology and Biotechnology, 2014, 1, 6.	2.5	19
58	Genome mining and functional genomics for siderophore production in Aspergillus niger. Briefings in Functional Genomics, 2014, 13, 482-492.	1.3	36
59	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.	2.5	15
60	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.	1.2	91
61	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.	0.7	29
62	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.	1.6	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 Aspergillus niger. Applied Microbiology and Biotechnology, 2013, 97, 8205-8218.	1.7	42
65	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.	1.8	49
66	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.	1.7	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. Photochemistry and Photobiology, 2013, 89, 758-761.	1.3	45
69	The Transcriptomic Signature of RacA Activation and Inactivation Provides New Insights into the Morphogenetic Network of Aspergillus niger. PLoS ONE, 2013, 8, e68946.	1.1	32
70	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.	1.1	19
71	Galactofuranose in eukaryotes: aspects of biosynthesis and functional impact. Glycobiology, 2012, 22, 456-469.	1.3	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. FEMS Microbiology Letters, 2012, 335, 104-112.	0.7	9

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73	Fungal \hat{l}_{\pm} -arabinofuranosidases of glycosyl hydrolase families 51 and 54 show a dual arabinofuranosyland galactofuranosyl-hydrolyzing activity. Biological Chemistry, 2012, 393, 767-775.	1.2	14
74	Vacuolar H+-ATPase plays a key role in cell wall biosynthesis of Aspergillus niger. Fungal Genetics and Biology, 2012, 49, 284-293.	0.9	20
75	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.	1.2	46
76	The carbon starvation response of Aspergillus niger during submerged cultivation: Insights from the transcriptome and secretome. BMC Genomics, 2012, 13, 380.	1.2	108
77	The transcriptomic fingerprint of glucoamylase over-expression in Aspergillus niger. BMC Genomics, 2012, 13, 701.	1.2	46
78	Using Non-homologous End-Joining-Deficient Strains for Functional Gene Analyses in Filamentous Fungi. Methods in Molecular Biology, 2012, 835, 133-150.	0.4	86
79	The Use of Open Source Bioinformatics Tools to Dissect Transcriptomic Data. Methods in Molecular Biology, 2012, 835, 311-331.	0.4	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 Aspergillus niger. Fungal Biology, 2011, 115, 253-264.	1.1	15
81	The molecular and genetic basis of conidial pigmentation in Aspergillus niger. Fungal Genetics and Biology, 2011, 48, 544-553.	0.9	111
82	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.	1.2	117
83	Aspergillus as a multi-purpose cell factory: current status and perspectives. Biotechnology Letters, 2011, 33, 469-476.	1.1	145
84	Effects of a defective ERAD pathway on growth and heterologous protein production in Aspergillus niger. Applied Microbiology and Biotechnology, 2011, 89, 357-373.	1.7	51
85	Heme biosynthesis and its regulation: towards understanding and improvement of heme biosynthesis in filamentous fungi. Applied Microbiology and Biotechnology, 2011, 91, 447-460.	1.7	41
86	New resources for functional analysis of omics data for the genus Aspergillus. BMC Genomics, 2011, 12, 486.	1.2	28
87	Fungal Gene Expression on Demand: an Inducible, Tunable, and Metabolism-Independent Expression System for Aspergillus niger. Applied and Environmental Microbiology, 2011, 77, 2975-2983.	1.4	154
88	Methods for Investigating the UPR in Filamentous Fungi. Methods in Enzymology, 2011, 490, 1-29.	0.4	14
89	TheAspergillus nigerRmsA protein. Communicative and Integrative Biology, 2010, 3, 195-197.	0.6	8
90	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.	1.7	148

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91	Reconstruction of Signaling Networks Regulating Fungal Morphogenesis by Transcriptomics. Eukaryotic Cell, 2009, 8, 1677-1691.	3.4	42
92	Transcriptomic comparison of Aspergillus niger growing on two different sugars reveals coordinated regulation of the secretory pathway. BMC Genomics, 2009, 10, 44.	1.2	76
93	Comprehensive genomic analysis of cell wall genes in Aspergillus nidulans. Fungal Genetics and Biology, 2009, 46, S72-S81.	0.9	97
94	Effective lead selection for improved protein production in Aspergillus niger based on integrated genomics. Fungal Genetics and Biology, 2009, 46, S141-S152.	0.9	77
95	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99
96	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.	1.0	60
97	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.	1.0	100
98	Agrobacterium-mediated transformation of the filamentous fungus Aspergillus awamori. Nature Protocols, 2008, 3, 1671-1678.	5.5	174
99	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.	0.9	29
100	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.	1.9	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. Genetics, 2008, 178, 873-881.	1.2	81
102	Molecular and Biochemical Characterization of a Novel Intracellular Invertase from Aspergillus niger with Transfructosylating Activity. Eukaryotic Cell, 2007, 6, 674-681.	3.4	52
103	Survival in the Presence of Antifungals. Journal of Biological Chemistry, 2007, 282, 32935-32948.	1.6	72
104	Highly efficient gene targeting in the Aspergillus niger kusA mutant. Journal of Biotechnology, 2007, 128, 770-775.	1.9	259
105	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	9.4	1,047
106	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.	0.8	5
107	Identification of fungal cell wall mutants using susceptibility assays based on Calcofluor white and Congo red. Nature Protocols, 2006 , 1 , 2253 - 2256 .	5 . 5	339
108	A new method for screening and isolation of hypersecretion mutants in Aspergillus niger. Applied Microbiology and Biotechnology, 2006, 69, 711-717.	1.7	24

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109	Activity of Quinones from Teak (Tectona grandis) on Fungal Cell Wall Stress. Planta Medica, 2006, 72, 943-944.	0.7	26
110	Database mining and transcriptional analysis of genes encoding inulin-modifying enzymes of Aspergillus niger. Microbiology (United Kingdom), 2006, 152, 3061-3073.	0.7	63
111	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.	1.2	79
112	Agrobacterium-mediated transformation as a tool for functional genomics in fungi. Current Genetics, 2005, 48, 1-17.	0.8	445
113	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.	0.9	81
114	Characterisation of CwpA, a putative glycosylphosphatidylinositol-anchored cell wall mannoprotein in the filamentous fungus Aspergillus niger. Fungal Genetics and Biology, 2005, 42, 873-885.	0.9	37
115	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.	1.0	28
116	A one-step method to convert vectors into binary vectors suited for Agrobacterium-mediated transformation. Current Genetics, 2004, 45, 242-248.	0.8	76
117	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.	0.7	116
118	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.	1.4	248
119	The protein kinase Kic1 affects 1,6-β-glucan levels in the cell wall of Saccharomyces cerevisiae. Microbiology (United Kingdom), 2002, 148, 4035-4048.	0.7	15
120	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.	1.2	57
121	Saccharomyces cerevisiae YCRO17c/CWH43encodes a putative sensor/transporter protein upstream of the BCK2branch of the PKC1-dependent cell wall integrity pathway. Yeast, 2001, 18, 827-840.	0.8	28
122	Glucoamylase::green fluorescent protein fusions to monitor protein secretion in Aspergillus niger. Microbiology (United Kingdom), 2000, 146, 415-426.	0.7	118
123	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.	1.3	32
124	Green fluorescent protein-cell wall fusion proteins are covalently incorporated into the cell wall ofSaccharomyces cerevisiae. FEMS Microbiology Letters, 1998, 162, 249-255.	0.7	49
125	Loss of the Plasma Membrane-Bound Protein Gas1p in <i>Saccharomyces cerevisiae</i> Results in the Release of \hat{I}^2 1,3-Glucan into the Medium and Induces a Compensation Mechanism To Ensure Cell Wall Integrity. Journal of Bacteriology, 1998, 180, 1418-1424.	1.0	184
126	In silicio identification of glycosyl-phosphatidylinositol-anchored plasma-membrane and cell wall proteins of Saccharomyces cerevisiae., 1997, 13, 1477-1489.		299

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127	Large Scale Identification of Genes Involved in Cell Surface Biosynthesis and Architecture in <i>Saccharomyces cerevisiae</i> . Genetics, 1997, 147, 435-450.	1.2	350
128	Regulation of cell wall \hat{l}^2 -glucan assembly:PTC1 Negatively affectsPBS2 Action in a pathway that includes modulation of EXG1 transcription. Molecular Genetics and Genomics, 1995, 248, 260-269.	2.4	97
129	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.	1.1	49
130	A new approach for isolating cell wall mutants in Saccharomyces cerevisiae by screening for hypersensitivity to calcofluor white. Yeast, 1994, 10, 1019-1030.	0.8	311
131	Genome sequences of 24 <i> Aspergillus niger sensu stricto $\langle li \rangle$ strains to study strain diversity, heterokaryon compatibility, and sexual reproduction. G3: Genes, Genomes, Genetics, 0, , .</i>	0.8	4