Merja Penttil

List of Publications by Year in Descending Order

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

 220
 15,092
 72
 115

 papers
 citations
 h-index
 g-index

 221
 16,535
 5.6
 6.21

 ext. papers
 ext. citations
 avg, IF
 L-index

#	Paper	IF	Citations
220	NordAqua, a Nordic Center of Excellence to develop an algae-based photosynthetic production platform. <i>Physiologia Plantarum</i> , 2021 , 173, 507-513	4.6	2
219	Bioinspired Functionally Graded Composite Assembled Using Cellulose Nanocrystals and Genetically Engineered Proteins with Controlled Biomineralization. <i>Advanced Materials</i> , 2021 , 33, e2102	2 65 8	5
218	Controllable coacervation of recombinantly produced spider silk protein using kosmotropic salts. Journal of Colloid and Interface Science, 2020, 560, 149-160	9.3	4
217	Evaluation of synthetic formaldehyde and methanol assimilation pathways in. <i>Fungal Biology and Biotechnology</i> , 2019 , 6, 27	7.5	9
216	Coacervation of resilin fusion proteins containing terminal functionalities. <i>Colloids and Surfaces B: Biointerfaces</i> , 2018 , 171, 590-596	6	6
215	A universal gene expression system for fungi. Nucleic Acids Research, 2018, 46, e111	20.1	41
214	Phase transitions as intermediate steps in the formation of molecularly engineered protein fibers. <i>Communications Biology</i> , 2018 , 1, 86	6.7	31
213	Yeast as a tool to express sugar acid transporters with biotechnological interest. <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	9
212	Elastic and pH-Responsive Hybrid Interfaces Created with Engineered Resilin and Nanocellulose. <i>Biomacromolecules</i> , 2017 , 18, 1866-1873	6.9	15
211	The Crystal Structure of a Bacterial l-Arabinonate Dehydratase Contains a [2Fe-2S] Cluster. <i>ACS Chemical Biology</i> , 2017 , 12, 1919-1927	4.9	19
21 0	Production of ethylene glycol or glycolic acid from D-xylose in Saccharomyces cerevisiae. <i>Applied Microbiology and Biotechnology</i> , 2017 , 101, 8151-8163	5.7	43
209	Single-Molecule Force Spectroscopy Study on Modular Resilin Fusion Protein. ACS Omega, 2017, 2, 6906	6- <u>6</u> 915	8
208	A design-build-test cycle using modeling and experiments reveals interdependencies between upper glycolysis and xylose uptake in recombinant and improves predictive capabilities of large-scale kinetic models. <i>Biotechnology for Biofuels</i> , 2017 , 10, 166	7.8	22
207	Xylose-induced dynamic effects on metabolism and gene expression in engineered Saccharomyces cerevisiae in anaerobic glucose-xylose cultures. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 969-	-85 ⁷	21
206	Production and applications of carbohydrate-derived sugar acids as generic biobased chemicals. <i>Critical Reviews in Biotechnology</i> , 2016 , 36, 904-16	9.4	53
205	Characterization of a unique Caulobacter crescentus aldose-aldose oxidoreductase having dual activities. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 673-85	5.7	3
204	Synthetic Transcription Amplifier System for Orthogonal Control of Gene Expression in Saccharomyces cerevisiae. <i>PLoS ONE</i> , 2016 , 11, e0148320	3.7	25

203	Machine Learning of Protein Interactions in Fungal Secretory Pathways. <i>PLoS ONE</i> , 2016 , 11, e0159302	3.7	4
202	Genome wide analysis of protein production load in Trichoderma reesei. <i>Biotechnology for Biofuels</i> , 2016 , 9, 132	7.8	16
201	Whole-genome metabolic model of built by comparative reconstruction. <i>Biotechnology for Biofuels</i> , 2016 , 9, 252	7.8	13
200	Characterization and mutagenesis of two novel iron-sulphur cluster pentonate dehydratases. <i>Applied Microbiology and Biotechnology</i> , 2016 , 100, 7549-63	5.7	22
199	Swollenin from Trichoderma reesei exhibits hydrolytic activity against cellulosic substrates with features of both endoglucanases and cellobiohydrolases. <i>Bioresource Technology</i> , 2015 , 181, 105-13	11	60
198	Overexpression of PAD1 and FDC1 results in significant cinnamic acid decarboxylase activity in Saccharomyces cerevisiae. <i>AMB Express</i> , 2015 , 5, 12	4.1	38
197	The use of carbohydrate binding modules (CBMs) to monitor changes in fragmentation and cellulose fiber surface morphology during cellulase- and Swollenin-induced deconstruction of lignocellulosic substrates. <i>Journal of Biological Chemistry</i> , 2015 , 290, 2938-45	5.4	33
196	Metabolic engineering of the fungal D-galacturonate pathway for L-ascorbic acid production. <i>Microbial Cell Factories</i> , 2015 , 14, 2	6.4	33
195	A novel aldose-aldose oxidoreductase for co-production of D-xylonate and xylitol from D-xylose with Saccharomyces cerevisiae. <i>Applied Microbiology and Biotechnology</i> , 2015 , 99, 9439-47	5.7	15
194	Capillary electrophoresis with laser-induced fluorescence detection for studying amino acid uptake by yeast during beer fermentation. <i>Talanta</i> , 2015 , 131, 366-71	6.2	26
193	Structure and function of Caulobacter crescentus aldose-aldose oxidoreductase. <i>Biochemical Journal</i> , 2015 , 472, 297-307	3.8	9
192	Enabling Low Cost Biopharmaceuticals: A Systematic Approach to Delete Proteases from a Well-Known Protein Production Host Trichoderma reesei. <i>PLoS ONE</i> , 2015 , 10, e0134723	3.7	45
191	Integration of transcription and flux data reveals molecular paths associated with differences in oxygen-dependent phenotypes of Saccharomyces cerevisiae. <i>BMC Systems Biology</i> , 2014 , 8, 16	3.5	2
190	Screening of candidate regulators for cellulase and hemicellulase production in Trichoderma reesei and identification of a factor essential for cellulase production. <i>Biotechnology for Biofuels</i> , 2014 , 7, 14	7.8	158
189	Molecular and functional characterization of an invertase secreted by Ashbya gossypii. <i>Molecular Biotechnology</i> , 2014 , 56, 524-34	3	15
188	Single cell and in vivo analyses elucidate the effect of xylC lactonase during production of D-xylonate in Saccharomyces cerevisiae. <i>Metabolic Engineering</i> , 2014 , 25, 238-47	9.7	21
187	Intracellular pH responses in the industrially important fungus Trichoderma reesei. <i>Fungal Genetics and Biology</i> , 2014 , 70, 86-93	3.9	7
186	L-lactic acid production from D-xylose with Candida sonorensis expressing a heterologous lactate dehydrogenase encoding gene. <i>Microbial Cell Factories</i> , 2014 , 13, 107	6.4	19

185	Engineering chimeric thermostable GH7 cellobiohydrolases in Saccharomyces cerevisiae. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 2991-3001	5.7	30
184	Categorisation of sugar acid dehydratases in Aspergillus niger. Fungal Genetics and Biology, 2014 , 64, 67-72	3.9	11
183	Structure and function of a decarboxylating Agrobacterium tumefaciens keto-deoxy-d-galactarate dehydratase. <i>Biochemistry</i> , 2014 , 53, 8052-60	3.2	8
182	Comparative genome-scale reconstruction of gapless metabolic networks for present and ancestral species. <i>PLoS Computational Biology</i> , 2014 , 10, e1003465	5	59
181	The diverse role of Pdr12 in resistance to weak organic acids. <i>Yeast</i> , 2014 , 31, 219-32	3.4	30
180	L-arabinose/D-galactose 1-dehydrogenase of Rhizobium leguminosarum bv. trifolii characterised and applied for bioconversion of L-arabinose to L-arabonate with Saccharomyces cerevisiae. <i>Applied Microbiology and Biotechnology</i> , 2014 , 98, 9653-65	5.7	11
179	Investigation of protein secretion and secretion stress in Ashbya gossypii. BMC Genomics, 2014, 15, 113	74.5	8
178	Transcriptome of Saccharomyces cerevisiae during production of D-xylonate. <i>BMC Genomics</i> , 2014 , 15, 763	4.5	4
177	Anaerobic Carbon Metabolism of Saccharomyces cerevisiae 2014 , 57-82		3
176	Production of L-lactic acid by the yeast Candida sonorensis expressing heterologous bacterial and fungal lactate dehydrogenases. <i>Microbial Cell Factories</i> , 2013 , 12, 53	6.4	36
175	Glycolic acid production in the engineered yeasts Saccharomyces cerevisiae and Kluyveromyces lactis. <i>Microbial Cell Factories</i> , 2013 , 12, 82	6.4	84
174	Online capillary electrophoresis for monitoring carboxylic acid production by yeast during bioreactor cultivations. <i>Analytical Chemistry</i> , 2013 , 85, 9705-12	7.8	14
173	Low pH D-xylonate production with Pichia kudriavzevii. <i>Bioresource Technology</i> , 2013 , 133, 555-62	11	57
172	Characterization of the Ashbya gossypii secreted N-glycome and genomic insights into its N-glycosylation pathway. <i>Carbohydrate Research</i> , 2013 , 381, 19-27	2.9	12
171	Swollenin aids in the amorphogenesis step during the enzymatic hydrolysis of pretreated biomass. <i>Bioresource Technology</i> , 2013 , 142, 498-503	11	83
170	Xylanase XYN IV from Trichoderma reesei showing exo- and endo-xylanase activity. <i>FEBS Journal</i> , 2013 , 280, 285-301	5.7	58
169	Capillary electrophoresis for the monitoring of phenolic compounds in bioprocesses. <i>Journal of Chromatography A</i> , 2013 , 1278, 175-80	4.5	12
168	Single-cell measurements of enzyme levels as a predictive tool for cellular fates during organic acid production. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 7569-82	4.8	5

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167	Yeast oligo-mediated genome engineering (YOGE). ACS Synthetic Biology, 2013, 2, 741-9	5.7	116
166	Noninvasive high-throughput single-cell analysis of the intracellular pH of Saccharomyces cerevisiae by ratiometric flow cytometry. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 7179-87	4.8	28
165	Random and direct mutagenesis to enhance protein secretion in Ashbya gossypii. <i>Bioengineered</i> , 2013 , 4, 322-31	5.7	19
164	Dynamic flux balance analysis of the metabolism of Saccharomyces cerevisiae during the shift from fully respirative or respirofermentative metabolic states to anaerobiosis. <i>FEBS Journal</i> , 2012 , 279, 3338	-5:4	23
163	Metabolic engineering of Saccharomyces cerevisiae for bioconversion of D-xylose to D-xylonate. <i>Metabolic Engineering</i> , 2012 , 14, 427-36	9.7	65
162	Visualization of cellobiohydrolase I from Trichoderma reesei moving on crystalline cellulose using high-speed atomic force microscopy. <i>Methods in Enzymology</i> , 2012 , 510, 169-82	1.7	20
161	Identification of the galactitol dehydrogenase, LadB, that is part of the oxido-reductive D-galactose catabolic pathway in Aspergillus niger. <i>Fungal Genetics and Biology</i> , 2012 , 49, 152-9	3.9	23
160	Characterisation of the gene cluster for l-rhamnose catabolism in the yeast Scheffersomyces (Pichia) stipitis. <i>Gene</i> , 2012 , 492, 177-85	3.8	25
159	Lipid production in batch and fed-batch cultures of Rhodosporidium toruloides from 5 and 6 carbon carbohydrates. <i>BMC Biotechnology</i> , 2012 , 12, 26	3.5	96
158	Re-annotation of the CAZy genes of Trichoderma reesei and transcription in the presence of lignocellulosic substrates. <i>Microbial Cell Factories</i> , 2012 , 11, 134	6.4	124
157	Challenges in enzymatic hydrolysis and fermentation of pretreated Arundo donax revealed by a comparison between SHF and SSF. <i>Process Biochemistry</i> , 2012 , 47, 1452-1459	4.8	73
156	Microbial D-xylonate production. Applied Microbiology and Biotechnology, 2012, 96, 1-8	5.7	71
155	Nutritional requirements and strain heterogeneity in Ashbya gossypii. <i>Journal of Basic Microbiology</i> , 2012 , 52, 582-9	2.7	13
154	Sorbitol dehydrogenase of Aspergillus niger, SdhA, is part of the oxido-reductive D-galactose pathway and essential for D-sorbitol catabolism. <i>FEBS Letters</i> , 2012 , 586, 378-83	3.8	21
153	Engineering filamentous fungi for conversion of D-galacturonic acid to L-galactonic acid. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 8676-83	4.8	42
152	Characterization of a novel Agrobacterium tumefaciens galactarolactone cycloisomerase enzyme for direct conversion of D-galactarolactone to 3-deoxy-2-keto-L-threo-hexarate. <i>Journal of Biological Chemistry</i> , 2012 , 287, 17662-17671	5.4	25
151	High level secretion of cellobiohydrolases by Saccharomyces cerevisiae. <i>Biotechnology for Biofuels</i> , 2011 , 4, 30	7.8	119
150	Traffic jams reduce hydrolytic efficiency of cellulase on cellulose surface. <i>Science</i> , 2011 , 333, 1279-82	33.3	439

149	Cloning of two genes (LAT1,2) encoding specific L: -arabinose transporters of the L: -arabinose fermenting yeast Ambrosiozyma monospora. <i>Applied Biochemistry and Biotechnology</i> , 2011 , 164, 604-1	1 ^{3.2}	25
148	The effects of disruption of phosphoglucose isomerase gene on carbon utilisation and cellulase production in Trichoderma reesei Rut-C30. <i>Microbial Cell Factories</i> , 2011 , 10, 40	6.4	12
147	Correlation of gene expression and protein production rate - a system wide study. <i>BMC Genomics</i> , 2011 , 12, 616	4.5	54
146	Influence of growth temperature on the production of antibody Fab fragments in different microbes: a host comparative analysis. <i>Biotechnology Progress</i> , 2011 , 27, 38-46	2.8	37
145	Transcriptional responses of Saccharomyces cerevisiae to shift from respiratory and respirofermentative to fully fermentative metabolism. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 461-76	3.8	22
144	Transformation system for Hypocrea jecorina (Trichoderma reesei) that favors homologous integration and employs reusable bidirectionally selectable markers. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 114-21	4.8	119
143	Bioconversion of d-xylose to d-xylonate with Kluyveromyces lactis. <i>Metabolic Engineering</i> , 2011 , 13, 38	3- 9 .†⁄	248
142	Crystal structure of uronate dehydrogenase from Agrobacterium tumefaciens. <i>Journal of Biological Chemistry</i> , 2011 , 286, 27294-300	5.4	25
141	Metabolic engineering of fungal strains for conversion of D-galacturonate to meso-galactarate. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 169-75	4.8	58
140	Identification of an L-arabinose reductase gene in Aspergillus niger and its role in L-arabinose catabolism. <i>Journal of Biological Chemistry</i> , 2010 , 285, 23622-8	5.4	36
139	Detecting novel genes with sparse arrays. <i>Gene</i> , 2010 , 467, 41-51	3.8	11
138	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010 , 1, 145	17.4	78
137	Enhancing the flux of D-glucose to the pentose phosphate pathway in Saccharomyces cerevisiae for the production of D-ribose and ribitol. <i>Applied Microbiology and Biotechnology</i> , 2010 , 85, 731-9	5.7	19
136	Identification in Agrobacterium tumefaciens of the D-galacturonic acid dehydrogenase gene. <i>Applied Microbiology and Biotechnology</i> , 2010 , 86, 901-9	5.7	39
135	Expression of Trichoderma reesei cellulases CBHI and EGI in Ashbya gossypii. <i>Applied Microbiology and Biotechnology</i> , 2010 , 87, 1437-46	5.7	31
134	Saccharomyces cerevisiae engineered to produce D-xylonate. <i>Applied Microbiology and Biotechnology</i> , 2010 , 88, 751-60	5.7	252
133	Array comparative genomic hybridization analysis of Trichoderma reesei strains with enhanced cellulase production properties. <i>BMC Genomics</i> , 2010 , 11, 441	4.5	68
132	The T rueTL-xylulose reductase of filamentous fungi identified in Aspergillus niger. <i>FEBS Letters</i> , 2010 , 584, 3540-4	3.8	24

(2007-2010)

131	Capillary electrophoresis for the monitoring of carboxylic acid production by Gluconobacter oxydans. <i>Journal of Chromatography A</i> , 2010 , 1217, 1537-42	4.5	31
130	Bioconversion of D-galacturonate to keto-deoxy-L-galactonate (3-deoxy-L-threo-hex-2-ulosonate) using filamentous fungi. <i>BMC Biotechnology</i> , 2010 , 10, 63	3.5	19
129	Genetic modification of carbon catabolite repression in Trichoderma reesei for improved protein production. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 4853-60	4.8	145
128	High speed atomic force microscopy visualizes processive movement of Trichoderma reesei cellobiohydrolase I on crystalline cellulose. <i>Journal of Biological Chemistry</i> , 2009 , 284, 36186-36190	5.4	214
127	Low oxygen levels as a trigger for enhancement of respiratory metabolism in Saccharomyces cerevisiae. <i>BMC Genomics</i> , 2009 , 10, 461	4.5	43
126	13C-metabolic flux ratio and novel carbon path analyses confirmed that Trichoderma reesei uses primarily the respirative pathway also on the preferred carbon source glucose. <i>BMC Systems Biology</i> , 2009 , 3, 104	3.5	18
125	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008 , 26, 1155-60	44.5	471
124	Transcription of hexose transporters of Saccharomyces cerevisiae is affected by change in oxygen provision. <i>BMC Microbiology</i> , 2008 , 8, 53	4.5	24
123	Oxygen dependence of metabolic fluxes and energy generation of Saccharomyces cerevisiae CEN.PK113-1A. <i>BMC Systems Biology</i> , 2008 , 2, 60	3.5	91
122	Regulation of xylose metabolism in recombinant Saccharomyces cerevisiae. <i>Microbial Cell Factories</i> , 2008 , 7, 18	6.4	74
121	Role of Ace2 (Activator of Cellulases 2) within the xyn2 transcriptosome of Hypocrea jecorina. <i>Fungal Genetics and Biology</i> , 2008 , 45, 436-45	3.9	56
120	Central carbon metabolism of Saccharomyces cerevisiae in anaerobic, oxygen-limited and fully aerobic steady-state conditions and following a shift to anaerobic conditions. <i>FEMS Yeast Research</i> , 2008 , 8, 140-54	3.1	59
119	Identification in the yeast Pichia stipitis of the first L-rhamnose-1-dehydrogenase gene. <i>FEBS Journal</i> , 2008 , 275, 2482-8	5.7	17
118	Physiological evaluation of the filamentous fungus Trichoderma reesei in production processes by marker gene expression analysis. <i>BMC Biotechnology</i> , 2007 , 7, 28	3.5	11
117	The ORF YNL274c (GOR1) codes for glyoxylate reductase in Saccharomyces cerevisiae. <i>Yeast</i> , 2007 , 24, 129-36	3.4	13
116	Identification in the mould Hypocrea jecorina of a gene encoding an NADP(+): d-xylose dehydrogenase. <i>FEMS Microbiology Letters</i> , 2007 , 277, 249-53	2.9	230
115	Direct identification of hydrophobins and their processing in Trichoderma using intact-cell MALDI-TOF MS. <i>FEBS Journal</i> , 2007 , 274, 841-52	5.7	45
114	Monitoring of transcriptional regulation in Pichia pastoris under protein production conditions. <i>BMC Genomics</i> , 2007 , 8, 179	4.5	96

113	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. <i>BMC Genomics</i> , 2007 , 8, 325	4.5	38
112	Xylose transport studies with xylose-utilizing Saccharomyces cerevisiae strains expressing heterologous and homologous permeases. <i>Applied Microbiology and Biotechnology</i> , 2007 , 74, 1041-52	5.7	141
111	Overexpression of an endochitinase gene (ThEn-42) in Trichoderma atroviride for increased production of antifungal enzymes and enhanced antagonist action against pathogenic fungi. <i>Applied Biochemistry and Biotechnology</i> , 2007 , 142, 81-94	3.2	24
110	The missing link in the fungal D-galacturonate pathway: identification of the L-threo-3-deoxy-hexulosonate aldolase. <i>Journal of Biological Chemistry</i> , 2007 , 282, 26195-201	5.4	41
109	Spatially segregated SNARE protein interactions in living fungal cells. <i>Journal of Biological Chemistry</i> , 2007 , 282, 22775-85	5.4	53
108	Metabolic engineering of Saccharomyces cerevisiae for conversion of D-glucose to xylitol and other five-carbon sugars and sugar alcohols. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 5471-6	4.8	29
107	Efficient production of L-lactic acid from xylose by Pichia stipitis. <i>Applied and Environmental Microbiology</i> , 2007 , 73, 117-23	4.8	109
106	Transcriptional monitoring of steady state and effects of anaerobic phases in chemostat cultures of the filamentous fungus Trichoderma reesei. <i>BMC Genomics</i> , 2006 , 7, 247	4.5	34
105	Common features and interesting differences in transcriptional responses to secretion stress in the fungi Trichoderma reesei and Saccharomyces cerevisiae. <i>BMC Genomics</i> , 2006 , 7, 32	4.5	75
104	Transcriptional regulation of xyn1, encoding xylanase I, in Hypocrea jecorina. <i>Eukaryotic Cell</i> , 2006 , 5, 447-56		116
104		6.9	116
	5, 447-56 Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II	6.9	
103	Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II hydrophobins from Trichoderma reesei. <i>Biomacromolecules</i> , 2006 , 7, 1295-301 Rapid and multiplexed transcript analysis of microbial cultures using capillary electophoresis-detectable oligonucleotide probe pools. <i>Journal of Microbiological Methods</i> , 2006 ,		121
103	Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II hydrophobins from Trichoderma reesei. <i>Biomacromolecules</i> , 2006 , 7, 1295-301 Rapid and multiplexed transcript analysis of microbial cultures using capillary electophoresis-detectable oligonucleotide probe pools. <i>Journal of Microbiological Methods</i> , 2006 , 65, 404-16 Enzymes for the NADPH-dependent reduction of dihydroxyacetone and D-glyceraldehyde and	2.8	121 35
103 102 101	Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II hydrophobins from Trichoderma reesei. <i>Biomacromolecules</i> , 2006 , 7, 1295-301 Rapid and multiplexed transcript analysis of microbial cultures using capillary electophoresis-detectable oligonucleotide probe pools. <i>Journal of Microbiological Methods</i> , 2006 , 65, 404-16 Enzymes for the NADPH-dependent reduction of dihydroxyacetone and D-glyceraldehyde and L-glyceraldehyde in the mould Hypocrea jecorina. <i>FEBS Journal</i> , 2006 , 273, 4229-35 L-galactonate dehydratase is part of the fungal path for D-galacturonic acid catabolism. <i>Molecular</i>	2.8 5·7 4.1	121 35 33
103 102 101	Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II hydrophobins from Trichoderma reesei. <i>Biomacromolecules</i> , 2006 , 7, 1295-301 Rapid and multiplexed transcript analysis of microbial cultures using capillary electophoresis-detectable oligonucleotide probe pools. <i>Journal of Microbiological Methods</i> , 2006 , 65, 404-16 Enzymes for the NADPH-dependent reduction of dihydroxyacetone and D-glyceraldehyde and L-glyceraldehyde in the mould Hypocrea jecorina. <i>FEBS Journal</i> , 2006 , 273, 4229-35 L-galactonate dehydratase is part of the fungal path for D-galacturonic acid catabolism. <i>Molecular Microbiology</i> , 2006 , 61, 1060-8	2.8 5·7 4.1	35 33 37
10310210110099	Interaction and comparison of a class I hydrophobin from Schizophyllum commune and class II hydrophobins from Trichoderma reesei. <i>Biomacromolecules</i> , 2006 , 7, 1295-301 Rapid and multiplexed transcript analysis of microbial cultures using capillary electophoresis-detectable oligonucleotide probe pools. <i>Journal of Microbiological Methods</i> , 2006 , 65, 404-16 Enzymes for the NADPH-dependent reduction of dihydroxyacetone and D-glyceraldehyde and L-glyceraldehyde in the mould Hypocrea jecorina. <i>FEBS Journal</i> , 2006 , 273, 4229-35 L-galactonate dehydratase is part of the fungal path for D-galacturonic acid catabolism. <i>Molecular Microbiology</i> , 2006 , 61, 1060-8 Expression of Vitreoscilla hemoglobin improves the metabolism of xylose in recombinant yeast Saccharomyces cerevisiae under low oxygen conditions. <i>Enzyme and Microbial Technology</i> , 2006 , 39, 6-1	2.8 5.7 4.1 43.8	35 33 37

(2004-2005)

95	Identification in the mold Hypocrea jecorina of the first fungal D-galacturonic acid reductase. <i>Biochemistry</i> , 2005 , 44, 11234-40	3.2	40
94	The Trichoderma reesei hydrophobin genes hfb1 and hfb2 have diverse functions in fungal development. <i>FEMS Microbiology Letters</i> , 2005 , 253, 281-8	2.9	67
93	Transcriptional regulation of plant cell wall degradation by filamentous fungi. <i>FEMS Microbiology Reviews</i> , 2005 , 29, 719-39	15.1	374
92	Protein production and induction of the unfolded protein response in Trichoderma reesei strain Rut-C30 and its transformant expressing endoglucanase I with a hydrophobic tag. <i>Biotechnology and Bioengineering</i> , 2005 , 89, 335-44	4.9	32
91	Xylose chemostat isolates of Saccharomyces cerevisiae show altered metabolite and enzyme levels compared with xylose, glucose, and ethanol metabolism of the original strain. <i>Applied Microbiology and Biotechnology</i> , 2005 , 67, 827-37	5.7	250
90	Hydrophobins: the protein-amphiphiles of filamentous fungi. FEMS Microbiology Reviews, 2005, 29, 877-	96 .1	453
89	Optimization of cDNA-AFLP experiments using genomic sequence data. <i>Bioinformatics</i> , 2005 , 21, 2573-9	7.2	17
88	Cloning and characterization of the glucosidase II alpha subunit gene of Trichoderma reesei: a frameshift mutation results in the aberrant glycosylation profile of the hypercellulolytic strain Rut-C30. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 2910-24	4.8	57
87	The effect of specific growth rate on protein synthesis and secretion in the filamentous fungus Trichoderma reesei. <i>Microbiology (United Kingdom)</i> , 2005 , 151, 135-143	2.9	83
86	Role of the bga1-encoded extracellular {beta}-galactosidase of Hypocrea jecorina in cellulase induction by lactose. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 851-7	4.8	52
85	Characterization of secretory genes ypt1/yptA and nsf1/nsfA from two filamentous fungi: induction of secretory pathway genes of Trichoderma reesei under secretion stress conditions. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 459-67	4.8	28
84	Endogenous xylose pathway in Saccharomyces cerevisiae. <i>Applied and Environmental Microbiology</i> , 2004 , 70, 3681-6	4.8	93
83	A novel NADH-linked l-xylulose reductase in the l-arabinose catabolic pathway of yeast. <i>Journal of Biological Chemistry</i> , 2004 , 279, 14746-51	5.4	55
82	Endoplasmic reticulum stress leads to the selective transcriptional downregulation of the glucoamylase gene in Aspergillus niger. <i>Molecular Microbiology</i> , 2004 , 53, 1731-42	4.1	65
81	Large-scale separation and production of engineered proteins, designed for facilitated recovery in detergent-based aqueous two-phase extraction systems. <i>Process Biochemistry</i> , 2004 , 39, 889-896	4.8	69
80	Purification, crystallization and preliminary X-ray diffraction analysis of the Trichoderma reesei hydrophobin HFBI. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004 , 60, 1903-5		7
79	Atomic resolution structure of the HFBII hydrophobin, a self-assembling amphiphile. <i>Journal of Biological Chemistry</i> , 2004 , 279, 534-9	5.4	191
78	Expression in Trichoderma reesei and characterisation of a thermostable family 3 beta-glucosidase from the moderately thermophilic fungus Talaromyces emersonii. <i>Protein Expression and Purification</i> , 2004 , 38, 248-57	2	134

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