

Jack Jack T Pronk

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.

263
papers

17,043
citations

71
h-index

121
g-index

270
ext. papers

19,317
ext. citations

5.2
avg, IF

6.47
L-index

#	Paper	IF	Citations
263	Pathway engineering strategies for improved product yield in yeast-based industrial ethanol production.. <i>Synthetic and Systems Biotechnology</i> , 2022 , 7, 554-566	4.2	2
262	Class-II dihydroorotate dehydrogenases from three phylogenetically distant fungi support anaerobic pyrimidine biosynthesis. <i>Fungal Biology and Biotechnology</i> , 2021 , 8, 10	7.5	0
261	Engineering heterologous molybdenum-cofactor-biosynthesis and nitrate-assimilation pathways enables nitrate utilization by <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021 , 65, 11-29	9.7	3
260	Critical parameters and procedures for anaerobic cultivation of yeasts in bioreactors and anaerobic chambers. <i>FEMS Yeast Research</i> , 2021 , 21,	3.1	3
259	Identification of Oxygen-Independent Pathways for Pyridine Nucleotide and Coenzyme A Synthesis in Anaerobic Fungi by Expression of Candidate Genes in Yeast. <i>MBio</i> , 2021 , 12, e0096721	7.8	2
258	Uncoupling growth and succinic acid production in an industrial <i>Saccharomyces cerevisiae</i> strain. <i>Biotechnology and Bioengineering</i> , 2021 , 118, 1576-1586	4.9	4
257	A squalene-hopene cyclase in represents a eukaryotic adaptation to sterol-limited anaerobic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	2
256	Engineering the thermotolerant industrial yeast <i>Kluyveromyces marxianus</i> for anaerobic growth. <i>Metabolic Engineering</i> , 2021 , 67, 347-364	9.7	5
255	Engineering oxygen-independent biotin biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021 , 67, 88-103	9.7	1
254	Elimination of aromatic fusel alcohols as by-products of strains engineered for phenylpropanoid production by 2-oxo-acid decarboxylase replacement. <i>Metabolic Engineering Communications</i> , 2021 , 13, e00183	6.5	
253	Squalene-Tetrahymanol Cyclase Expression Enables Sterol-Independent Growth of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	7
252	Contribution of Complex I NADH Dehydrogenase to Respiratory Energy Coupling in Glucose-Grown Cultures of. <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	3
251	Improving Industrially Relevant Phenotypic Traits by Engineering Chromosome Copy Number in. <i>Frontiers in Genetics</i> , 2020 , 11, 518	4.5	5
250	" <i>Galacturonibacter soehngengii</i> " Shows Acetogenic Catabolism of Galacturonic Acid but Lacks a Canonical Carbon Monoxide Dehydrogenase/Acetyl-CoA Synthase Complex. <i>Frontiers in Microbiology</i> , 2020 , 11, 63	5.7	5
249	Vitamin requirements and biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020 , 37, 283-304	3.4	33
248	Exploiting the Diversity of <i>Saccharomycotina</i> Yeasts To Engineer Biotin-Independent Growth of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	7
247	Physiological responses of <i>Saccharomyces cerevisiae</i> to industrially relevant conditions: Slow growth, low pH, and high CO levels. <i>Biotechnology and Bioengineering</i> , 2020 , 117, 721-735	4.9	9

246	Adaptive Laboratory Evolution and Reverse Engineering of Single-Vitamin Prototrophies in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020 , 86,	4.8	11
245	Connecting central carbon and aromatic amino acid metabolisms to improve de novo 2-phenylethanol production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019 , 56, 165-180	9.7	37
244	Lager-brewing yeasts in the era of modern genetics. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	16
243	Functional expression of a bacterial α -ketoglutarate dehydrogenase in the cytosol of <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019 , 56, 190-197	9.7	3
242	Phenotype-Independent Isolation of Interspecies Hybrids by Dual-Dye Fluorescent Staining and Fluorescence-Activated Cell Sorting. <i>Frontiers in Microbiology</i> , 2019 , 10, 871	5.7	4
241	Laboratory Evolution of a Δ Hybrid Under Simulated Lager-Brewing Conditions. <i>Frontiers in Genetics</i> , 2019 , 10, 242	4.5	17
240	In vivo recombination of <i>Saccharomyces eubayanus</i> maltose-transporter genes yields a chimeric transporter that enables maltotriose fermentation. <i>PLoS Genetics</i> , 2019 , 15, e1007853	6	20
239	A Novel D-Galacturonate Fermentation Pathway in Links Initial Reactions of the Galacturonate-Isomerase Route With the Phosphoketolase Pathway. <i>Frontiers in Microbiology</i> , 2019 , 10, 3027	5.7	5
238	Anaerobic growth of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D does not depend on synthesis or supplementation of unsaturated fatty acids. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	12
237	Quantitative Physiology of Non-Energy-Limited Retentostat Cultures of <i>Saccharomyces cerevisiae</i> at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	6
236	Himalayan Genome Sequences Reveal Genetic Markers Explaining Heterotic Maltotriose Consumption by <i>Saccharomyces pastorianus</i> Hybrids. <i>Applied and Environmental Microbiology</i> , 2019 , 85,	4.8	12
235	Allele-specific genome editing using CRISPR-Cas9 is associated with loss of heterozygosity in diploid yeast. <i>Nucleic Acids Research</i> , 2019 , 47, 1362-1372	20.1	18
234	A toolkit for rapid CRISPR-SpCas9 assisted construction of hexose-transport-deficient <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	18
233	Reassessment of requirements for anaerobic xylose fermentation by engineered, non-evolved <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2019 , 19,	3.1	6
232	Genome editing in <i>Kluyveromyces</i> and <i>Ogataea</i> yeasts using a broad-host-range Cas9/gRNA co-expression plasmid. <i>FEMS Yeast Research</i> , 2018 , 18,	3.1	45
231	The transporter AraT enables high-affinity, glucose-insensitive l-arabinose transport in. <i>Biotechnology for Biofuels</i> , 2018 , 11, 63	7.8	17
230	Galacturonate Metabolism in Anaerobic Chemostat Enrichment Cultures: Combined Fermentation and Acetogenesis by the Dominant sp. nov. "Candidatus Galacturonibacter soehngengii". <i>Applied and Environmental Microbiology</i> , 2018 , 84,	4.8	4
229	Structural, Physiological and Regulatory Analysis of Maltose Transporter Genes in CBS 12357. <i>Frontiers in Microbiology</i> , 2018 , 9, 1786	5.7	27

228	Fermentation of glucose-xylose-arabinose mixtures by a synthetic consortium of single-sugar-fermenting <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2018 , 18,	3.1	21
227	Optimizing anaerobic growth rate and fermentation kinetics in strains expressing Calvin-cycle enzymes for improved ethanol yield. <i>Biotechnology for Biofuels</i> , 2018 , 11, 17	7.8	29
226	Under pressure: evolutionary engineering of yeast strains for improved performance in fuels and chemicals production. <i>Current Opinion in Biotechnology</i> , 2018 , 50, 47-56	11.4	88
225	Combined engineering of disaccharide transport and phosphorolysis for enhanced ATP yield from sucrose fermentation in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2018 , 45, 121-133	9.7	17
224	Evaluation of a novel cloud-based software platform for structured experiment design and linked data analytics. <i>Scientific Data</i> , 2018 , 5, 180195	8.2	7
223	Laboratory evolution of a glucose-phosphorylation-deficient, arabinose-fermenting <i>S. cerevisiae</i> strain reveals mutations in GAL2 that enable glucose-insensitive l-arabinose uptake. <i>FEMS Yeast Research</i> , 2018 , 18,	3.1	11
222	Selection of Pof Variants for the Construction of Hybrids With Reduced 4-Vinyl Guaiacol Formation. <i>Frontiers in Microbiology</i> , 2018 , 9, 1640	5.7	18
221	Laboratory evolution and physiological analysis of <i>Saccharomyces cerevisiae</i> strains dependent on sucrose uptake via the <i>Phaseolus vulgaris</i> Suf1 transporter. <i>Yeast</i> , 2018 , 35, 639-652	3.4	3
220	Laboratory evolution for forced glucose-xylose co-consumption enables identification of mutations that improve mixed-sugar fermentation by xylose-fermenting <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2018 , 18,	3.1	29
219	Metabolic engineering strategies for optimizing acetate reduction, ethanol yield and osmotolerance in <i>S. cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2017 , 10, 107	7.8	24
218	<i>Saccharomyces cerevisiae</i> strains for second-generation ethanol production: from academic exploration to industrial implementation. <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	108
217	Laboratory Evolution of a Biotin-Requiring <i>Saccharomyces cerevisiae</i> Strain for Full Biotin Prototrophy and Identification of Causal Mutations. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	21
216	Industrial Relevance of Chromosomal Copy Number Variation in <i>Saccharomyces</i> Yeasts. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	39
215	Mutations in PMR1 stimulate xylose isomerase activity and anaerobic growth on xylose of engineered <i>Saccharomyces cerevisiae</i> by influencing manganese homeostasis. <i>Scientific Reports</i> , 2017 , 7, 46155	4.9	44
214	A Simulator-Assisted Workshop for Teaching Chemostat Cultivation in Academic Classes on Microbial Physiology. <i>Journal of Microbiology and Biology Education</i> , 2017 , 18,	1.3	2
213	Extreme calorie restriction in yeast retentostats induces uniform non-quiescent growth arrest. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2017 , 1864, 231-242	4.9	3
212	Elimination of sucrose transport and hydrolysis in <i>Saccharomyces cerevisiae</i> : a platform strain for engineering sucrose metabolism. <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	20
211	A CRISPR/Cas9-based exploration into the elusive mechanism for lactate export in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2017 , 17,	3.1	21

210	Evolutionary Engineering in Chemostat Cultures for Improved Maltotriose Fermentation Kinetics in Lager Brewing Yeast. <i>Frontiers in Microbiology</i> , 2017 , 8, 1690	5.7	25
209	A new laboratory evolution approach to select for constitutive acetic acid tolerance in <i>Saccharomyces cerevisiae</i> and identification of causal mutations. <i>Biotechnology for Biofuels</i> , 2016 , 9, 173	7.8	88
208	<i>Pichia pastoris</i> Exhibits High Viability and a Low Maintenance Energy Requirement at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2016 , 82, 4570-4583	4.8	30
207	Replacement of the initial steps of ethanol metabolism in <i>Saccharomyces cerevisiae</i> by ATP-independent acetylating acetaldehyde dehydrogenase. <i>FEMS Yeast Research</i> , 2016 , 16, fow006	3.1	10
206	Maintenance-energy requirements and robustness of <i>Saccharomyces cerevisiae</i> at aerobic near-zero specific growth rates. <i>Microbial Cell Factories</i> , 2016 , 15, 111	6.4	26
205	Improving ethanol yield in acetate-reducing <i>Saccharomyces cerevisiae</i> by cofactor engineering of 6-phosphogluconate dehydrogenase and deletion of ALD6. <i>Microbial Cell Factories</i> , 2016 , 15, 67	6.4	33
204	Engineering cytosolic acetyl-coenzyme A supply in <i>Saccharomyces cerevisiae</i> : Pathway stoichiometry, free-energy conservation and redox-cofactor balancing. <i>Metabolic Engineering</i> , 2016 , 36, 99-115	9.7	81
203	Requirements for Carnitine Shuttle-Mediated Translocation of Mitochondrial Acetyl Moieties to the Yeast Cytosol. <i>MBio</i> , 2016 , 7,	7.8	14
202	Pathway swapping: Toward modular engineering of essential cellular processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 15060-15065	11.5	26
201	Alternative reactions at the interface of glycolysis and citric acid cycle in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2016 , 16,	3.1	23
200	How to set up collaborations between academia and industrial biotech companies. <i>Nature Biotechnology</i> , 2015 , 33, 237-40	44.5	14
199	<i>S. cerevisiae</i> \times <i>S. eubayanus</i> interspecific hybrid, the best of both worlds and beyond. <i>FEMS Yeast Research</i> , 2015 , 15,	3.1	79
198	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 5662-70	4.8	29
197	A Minimal Set of Glycolytic Genes Reveals Strong Redundancies in <i>Saccharomyces cerevisiae</i> Central Metabolism. <i>Eukaryotic Cell</i> , 2015 , 14, 804-16		24
196	Functional expression of a heterologous nickel-dependent, ATP-independent urease in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015 , 30, 130-140	9.7	13
195	The genome sequence of the popular hexose-transport-deficient <i>Saccharomyces cerevisiae</i> strain EBY.VW4000 reveals LoxP/Cre-induced translocations and gene loss. <i>FEMS Yeast Research</i> , 2015 , 15,	3.1	18
194	CRISPR/Cas9: a molecular Swiss army knife for simultaneous introduction of multiple genetic modifications in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015 , 15,	3.1	264
193	Chromosomal Copy Number Variation in <i>Saccharomyces pastorianus</i> Is Evidence for Extensive Genome Dynamics in Industrial Lager Brewing Strains. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 6253-67	4.8	50

192	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015 , 32, 1-7	11.4	51
191	Deletion of the <i>Saccharomyces cerevisiae</i> ARO8 gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2015 , 32, 29-45	3.4	25
190	Growth-rate dependency of de novo resveratrol production in chemostat cultures of an engineered <i>Saccharomyces cerevisiae</i> strain. <i>Microbial Cell Factories</i> , 2015 , 14, 133	6.4	22
189	Oxygen availability strongly affects chronological lifespan and thermotolerance in batch cultures of. <i>Microbial Cell</i> , 2015 , 2, 429-444	3.9	18
188	To divide or not to divide: a key role of Rim15 in calorie-restricted yeast cultures. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014 , 1843, 1020-30	4.9	19
187	Efficient simultaneous excision of multiple selectable marker cassettes using I-SceI-induced double-strand DNA breaks in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014 , 14, 741-54	3.1	24
186	Engineering acetyl coenzyme A supply: functional expression of a bacterial pyruvate dehydrogenase complex in the cytosol of <i>Saccharomyces cerevisiae</i> . <i>MBio</i> , 2014 , 5, e01696-14	7.8	70
185	Proteome adaptation of <i>Saccharomyces cerevisiae</i> to severe calorie restriction in Retentostat cultures. <i>Journal of Proteome Research</i> , 2014 , 13, 3542-53	5.6	14
184	Physiology of the fuel ethanol strain <i>Saccharomyces cerevisiae</i> PE-2 at low pH indicates a context-dependent performance relevant for industrial applications. <i>FEMS Yeast Research</i> , 2014 , 14, 1196-205	3.1	36
183	Physiological and transcriptional responses of anaerobic chemostat cultures of <i>Saccharomyces cerevisiae</i> subjected to diurnal temperature cycles. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 4433-49	4.8	5
182	Evolutionary engineering of a glycerol-3-phosphate dehydrogenase-negative, acetate-reducing <i>Saccharomyces cerevisiae</i> strain enables anaerobic growth at high glucose concentrations. <i>Microbial Biotechnology</i> , 2014 , 7, 44-53	6.3	30
181	Increasing ATP conservation in maltose consuming yeast, a challenge for industrial organic acid production in non-aerated reactors. <i>BMC Proceedings</i> , 2014 , 8, P185	2.3	78
180	An alternative, arginase-independent pathway for arginine metabolism in <i>Kluyveromyces lactis</i> involves guanidinobutyrase as a key enzyme. <i>Molecular Microbiology</i> , 2014 , 93, 369-89	4.1	14
179	Functional characterization of a <i>Penicillium chrysogenum</i> mutanase gene induced upon co-cultivation with <i>Bacillus subtilis</i> . <i>BMC Microbiology</i> , 2014 , 14, 114	4.5	9
178	Polycistronic expression of a β -carotene biosynthetic pathway in <i>Saccharomyces cerevisiae</i> coupled to β -ionone production. <i>Journal of Biotechnology</i> , 2014 , 192 Pt B, 383-92	3.7	75
177	Replacement of the <i>Saccharomyces cerevisiae</i> acetyl-CoA synthetases by alternative pathways for cytosolic acetyl-CoA synthesis. <i>Metabolic Engineering</i> , 2014 , 21, 46-59	9.7	82
176	Genome-scale analyses of butanol tolerance in <i>Saccharomyces cerevisiae</i> reveal an essential role of protein degradation. <i>Biotechnology for Biofuels</i> , 2013 , 6, 48	7.8	63
175	A versatile, efficient strategy for assembly of multi-fragment expression vectors in <i>Saccharomyces cerevisiae</i> using 60 bp synthetic recombination sequences. <i>Microbial Cell Factories</i> , 2013 , 12, 47	6.4	74

174	Long-term adaptation of <i>Saccharomyces cerevisiae</i> to the burden of recombinant insulin production. <i>Biotechnology and Bioengineering</i> , 2013 , 110, 2749-63	4.9	23
173	Functional analysis and transcriptional regulation of two orthologs of ARO10, encoding broad-substrate-specificity 2-oxo-acid decarboxylases, in the brewing yeast <i>Saccharomyces pastorianus</i> CBS1483. <i>FEMS Yeast Research</i> , 2013 , 13, 505-17	3.1	30
172	Carbon dioxide fixation by Calvin-Cycle enzymes improves ethanol yield in yeast. <i>Biotechnology for Biofuels</i> , 2013 , 6, 125	7.8	93
171	Genome duplication and mutations in ACE2 cause multicellular, fast-sedimenting phenotypes in evolved <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, E4223-31	11.5	71
170	amdSYM, a new dominant recyclable marker cassette for <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2013 , 13, 126-39	3.1	106
169	Crystal ball 2013. <i>Microbial Biotechnology</i> , 2013 , 6, 3-16	6.3	6
168	Metabolic engineering of yeast for production of fuels and chemicals. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 398-404	11.4	231
167	Fsy1, the sole hexose-proton transporter characterized in <i>Saccharomyces</i> yeasts, exhibits a variable fructose:H(+) stoichiometry. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 201-7	3.8	22
166	Resolving Phenylalanine Metabolism Sheds Light on Natural Synthesis of Penicillin G in <i>Penicillium chrysogenum</i> . <i>Eukaryotic Cell</i> , 2013 , 12, 151-151		78
165	One-step assembly and targeted integration of multigene constructs assisted by the I-SceI meganuclease in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2013 , 13, 769-81	3.1	42
164	Transcriptome-based characterization of interactions between <i>Saccharomyces cerevisiae</i> and <i>Lactobacillus delbrueckii</i> subsp. <i>bulgaricus</i> in lactose-grown chemostat cocultures. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 5949-61	4.8	36
163	Laboratory evolution of new lactate transporter genes in a <i>jen1</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012 , 12, 359-374	3.1	44
162	Energy coupling in <i>Saccharomyces cerevisiae</i> : selected opportunities for metabolic engineering. <i>FEMS Yeast Research</i> , 2012 , 12, 387-97	3.1	54
161	Metabolic engineering of β -oxidation in <i>Penicillium chrysogenum</i> for improved semi-synthetic cephalosporin biosynthesis. <i>Metabolic Engineering</i> , 2012 , 14, 437-48	9.7	22
160	Galacturonic acid inhibits the growth of <i>Saccharomyces cerevisiae</i> on galactose, xylose, and arabinose. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5052-9	4.8	23
159	Toward pectin fermentation by <i>Saccharomyces cerevisiae</i> : expression of the first two steps of a bacterial pathway for D-galacturonate metabolism. <i>Journal of Biotechnology</i> , 2012 , 162, 303-10	3.7	23
158	An internal deletion in MTH1 enables growth on glucose of pyruvate-decarboxylase negative, non-fermentative <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012 , 11, 131	6.4	65
157	De novo production of the flavonoid naringenin in engineered <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012 , 11, 155	6.4	235

156	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. <i>Microbial Cell Factories</i> , 2012 , 11, 36	6.4	183
155	Similar temperature dependencies of glycolytic enzymes: an evolutionary adaptation to temperature dynamics?. <i>BMC Systems Biology</i> , 2012 , 6, 151	3.5	21
154	In vivo analysis of <i>Saccharomyces cerevisiae</i> plasma membrane ATPase Pma1p isoforms with increased in vitro H ⁺ /ATP stoichiometry. <i>Antonie Van Leeuwenhoek</i> , 2012 , 102, 401-6	2.1	9
153	Genome-wide analytical approaches for reverse metabolic engineering of industrially relevant phenotypes in yeast. <i>FEMS Yeast Research</i> , 2012 , 12, 183-96	3.1	64
152	Impact of velvet complex on transcriptome and penicillin G production in glucose-limited chemostat cultures of a β -lactam high-producing <i>Penicillium chrysogenum</i> strain. <i>OMICS A Journal of Integrative Biology</i> , 2012 , 16, 320-33	3.8	23
151	Substrate specificity of thiamine pyrophosphate-dependent 2-oxo-acid decarboxylases in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2012 , 78, 7538-48	4.8	68
150	Resolving phenylalanine metabolism sheds light on natural synthesis of penicillin G in <i>Penicillium chrysogenum</i> . <i>Eukaryotic Cell</i> , 2012 , 11, 238-49		20
149	Laboratory evolution of new lactate transporter genes in a <i>jen1</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as ADY2 alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012 , 12, 359-374	3.1	33
148	The diversity of protein turnover and abundance under nitrogen-limited steady-state conditions in <i>Saccharomyces cerevisiae</i> . <i>Molecular BioSystems</i> , 2011 , 7, 3316-26		24
147	Batch and continuous culture-based selection strategies for acetic acid tolerance in xylose-fermenting <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2011 , 11, 299-306	3.1	71
146	Cellular responses of <i>Saccharomyces cerevisiae</i> at near-zero growth rates: transcriptome analysis of anaerobic retentostat cultures. <i>FEMS Yeast Research</i> , 2011 , 11, 603-20	3.1	36
145	Increasing free-energy (ATP) conservation in maltose-grown <i>Saccharomyces cerevisiae</i> by expression of a heterologous maltose phosphorylase. <i>Metabolic Engineering</i> , 2011 , 13, 518-26	9.7	48
144	Engineering topology and kinetics of sucrose metabolism in <i>Saccharomyces cerevisiae</i> for improved ethanol yield. <i>Metabolic Engineering</i> , 2011 , 13, 694-703	9.7	74
143	Extreme calorie restriction and energy source starvation in <i>Saccharomyces cerevisiae</i> represent distinct physiological states. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2011 , 1813, 2133-44	9.9	24
142	Anaplerotic role for cytosolic malic enzyme in engineered <i>Saccharomyces cerevisiae</i> strains. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 732-8	4.8	37
141	Involvement of Snf7p and Rim101p in the transcriptional regulation of TIR1 and other anaerobically upregulated genes in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2010 , 10, 367-84	3.1	2
140	Involvement of vacuolar sequestration and active transport in tolerance of <i>Saccharomyces cerevisiae</i> to hop iso- α -acids. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 318-28	4.8	34
139	Key process conditions for production of C(4) dicarboxylic acids in bioreactor batch cultures of an engineered <i>Saccharomyces cerevisiae</i> strain. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 744-50	4.8	57

138	Phosphoenolpyruvate carboxykinase as the sole anaplerotic enzyme in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2010 , 76, 5383-9	4.8	36
137	Elimination of glycerol production in anaerobic cultures of a <i>Saccharomyces cerevisiae</i> strain engineered to use acetic acid as an electron acceptor. <i>Applied and Environmental Microbiology</i> , 2010 , 76, 190-5	4.8	121
136	The <i>Penicillium chrysogenum</i> <i>aclA</i> gene encodes a broad-substrate-specificity acyl-coenzyme A ligase involved in activation of adipic acid, a side-chain precursor for cephem antibiotics. <i>Fungal Genetics and Biology</i> , 2010 , 47, 33-42	3.9	32
135	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010 , 1, 145	17.4	78
134	Metabolome, transcriptome and metabolic flux analysis of arabinose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2010 , 12, 537-51	9.7	66
133	Catalase overexpression reduces lactic acid-induced oxidative stress in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2009 , 75, 2320-5	4.8	62
132	Quantitative physiology of <i>Saccharomyces cerevisiae</i> at near-zero specific growth rates. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 5607-14	4.8	78
131	Identity of the growth-limiting nutrient strongly affects storage carbohydrate accumulation in anaerobic chemostat cultures of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2009 , 75, 6876-85	4.8	28
130	Novel evolutionary engineering approach for accelerated utilization of glucose, xylose, and arabinose mixtures by engineered <i>Saccharomyces cerevisiae</i> strains. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 907-14	4.8	215
129	Combinatorial effects of environmental parameters on transcriptional regulation in <i>Saccharomyces cerevisiae</i> : a quantitative analysis of a compendium of chemostat-based transcriptome data. <i>BMC Genomics</i> , 2009 , 10, 53	4.5	46
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10	Allele-specific genome editing using CRISPR-Cas9 causes off-target mutations in diploid yeast	1
9	Maltotriose consumption by hybrid <i>Saccharomyces pastorianus</i> is heterotic and results from regulatory cross-talk between parental sub-genomes	3
8	Stoichiometry and compartmentation of NADH metabolism in <i>Saccharomyces cerevisiae</i>	12
7	Growth requirements of pyruvate-decarboxylase-negative <i>Saccharomyces cerevisiae</i>	1
6	Adaptive laboratory evolution and reverse engineering of single-vitamin prototrophies in <i>Saccharomyces cerevisiae</i>	1
5	In vivo recombination of <i>Saccharomyces eubayanus</i> maltose-transporter genes yields a chimeric transporter that enables maltotriose fermentation	4
4	Laboratory evolution of a <i>Saccharomyces cerevisiae</i> x <i>S. eubayanus</i> hybrid under simulated lager-brewing conditions: genetic diversity and phenotypic convergence	3
3	Re-oxidation of cytosolic NADH is a major contributor to the high oxygen requirements of the thermotolerant yeast <i>Ogataea parapolymorpha</i> in oxygen-limited cultures	1
2	Engineering the thermotolerant industrial yeast <i>Kluyveromyces marxianus</i> for anaerobic growth	1
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