

Jack Jack T Pronk

List of Publications by Year in descending order

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Version: 2024-02-01

260
papers

20,919
citations

8755

75
h-index

12597

132
g-index

271
all docs

271
docs citations

271
times ranked

13343
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathway engineering strategies for improved product yield in yeast-based industrial ethanol production. <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 554-566.	3.7	21
2	Respiratory reoxidation of NADH is a key contributor to high oxygen requirements of oxygen-limited cultures of <i>Ogataea parapolymorpha</i> . <i>FEMS Yeast Research</i> , 2022, 22, .	2.3	2
3	Uncoupling growth and succinic acid production in an industrial <i>Saccharomyces cerevisiae</i> strain. <i>Biotechnology and Bioengineering</i> , 2021, 118, 1557-1567.	3.3	12
4	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.	7.0	10
5	Critical parameters and procedures for anaerobic cultivation of yeasts in bioreactors and anaerobic chambers. <i>FEMS Yeast Research</i> , 2021, 21, .	2.3	12
6	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.	4.1	11
7	A squalene-hopene cyclase in <i>Schizosaccharomyces japonicus</i> 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, .	7.1	9
8	Engineering the thermotolerant industrial yeast <i>Kluyveromyces marxianus</i> for anaerobic growth. <i>Metabolic Engineering</i> , 2021, 67, 347-364.	7.0	14
9	Engineering oxygen-independent biotin biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021, 67, 88-103.	7.0	5
10	Elimination of aromatic fusel alcohols as by-products of <i>Saccharomyces cerevisiae</i> strains engineered for phenylpropanoid production by 2-oxo-acid decarboxylase replacement. <i>Metabolic Engineering Communications</i> , 2021, 13, e00183.	3.6	1
11	Class-II dihydroorotate dehydrogenases from three phylogenetically distant fungi support anaerobic pyrimidine biosynthesis. <i>Fungal Biology and Biotechnology</i> , 2021, 8, 10.	5.1	9
12	Physiological responses of <i>Saccharomyces cerevisiae</i> to industrially relevant conditions: Slow growth, low pH, and high CO ₂ levels. <i>Biotechnology and Bioengineering</i> , 2020, 117, 721-735.	3.3	15
13	Squalene-Tetrahymanol Cyclase Expression Enables Sterol-Independent Growth of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	12
14	Contribution of Complex I NADH Dehydrogenase to Respiratory Energy Coupling in Glucose-Grown Cultures of <i>Ogataea parapolymorpha</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	7
15	Improving Industrially Relevant Phenotypic Traits by Engineering Chromosome Copy Number in <i>Saccharomyces pastorianus</i> . <i>Frontiers in Genetics</i> , 2020, 11, 518.	2.3	12
16	<i>Candidatus Galacturonibacter soehngeni</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.	3.5	6
17	Vitamin requirements and biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020, 37, 283-304.	1.7	74
18	Exploiting the Diversity of Saccharomycotina Yeasts To Engineer Biotin-Independent Growth of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	9

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19	Adaptive Laboratory Evolution and Reverse Engineering of Single-Vitamin Prototrophies in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	18
20	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, .	2.3	21
21	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, .	3.1	12
22	Himalayan <i>Saccharomyces eubayanus</i> Genome Sequences Reveal Genetic Markers Explaining Heterotrophic Maltotriose Consumption by <i>Saccharomyces pastorianus</i> Hybrids. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	21
23	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.	7.0	70
24	Lager-brewing yeasts in the era of modern genetics. <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	23
25	Functional expression of a bacterial α -ketoglutarate dehydrogenase in the cytosol of <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019, 56, 190-197.	7.0	6
26	Phenotype-Independent Isolation of Interspecies <i>Saccharomyces</i> Hybrids by Dual-Dye Fluorescent Staining and Fluorescence-Activated Cell Sorting. <i>Frontiers in Microbiology</i> , 2019, 10, 871.	3.5	8
27	Laboratory Evolution of a <i>Saccharomyces cerevisiae</i> \times <i>S. eubayanus</i> Hybrid Under Simulated Lager-Brewing Conditions. <i>Frontiers in Genetics</i> , 2019, 10, 242.	2.3	35
28	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.	3.5	29
29	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.	14.5	32
30	A toolkit for rapid CRISPR-Cas9 assisted construction of hexose-transport-deficient <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	25
31	A Novel D-Galacturonate Fermentation Pathway in <i>Lactobacillus suebicus</i> Links Initial Reactions of the Galacturonate-Isomerase Route With the Phosphoketolase Pathway. <i>Frontiers in Microbiology</i> , 2019, 10, 3027.	3.5	14
32	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, .	2.3	75
33	The <i>Penicillium chrysogenum</i> transporter PcAraT enables high-affinity, glucose-insensitive L-arabinose transport in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 63.	6.2	29
34	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.	6.6	135
35	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.	7.0	24
36	Evaluation of a novel cloud-based software platform for structured experiment design and linked data analytics. <i>Scientific Data</i> , 2018, 5, 180195.	5.3	10

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37	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. FEMS Yeast Research, 2018, 18, .	2.3	16
38	Selection of Pof-Saccharomyces eubayanus Variants for the Construction of <i>S. cerevisiae</i> Å— <i>S. eubayanus</i> Hybrids With Reduced 4-Vinyl Guaiacol Formation. Frontiers in Microbiology, 2018, 9, 1640.	3.5	25
39	Reassessment of requirements for anaerobic xylose fermentation by engineered, non-evolved <i>Saccharomyces cerevisiae</i> strains. FEMS Yeast Research, 2018, 19, .	2.3	6
40	Laboratory evolution and physiological analysis of <i>Saccharomyces cerevisiae</i> strains dependent on sucrose uptake via the <i>Phaseolus vulgaris</i> <i>Suf1</i> transporter. Yeast, 2018, 35, 639-652.	1.7	6
41	Laboratory evolution for forced glucose-xylose co-consumption enables identification of mutations that improve mixed-sugar fermentation by xylose-fermenting <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2018, 18, .	2.3	42
42	Galacturonate Metabolism in Anaerobic Chemostat Enrichment Cultures: Combined Fermentation and Acetogenesis by the Dominant sp. nov. <i>Candidatus Galacturonibacter soehngenii</i> . Applied and Environmental Microbiology, 2018, 84, .	3.1	16
43	Structural, Physiological and Regulatory Analysis of Maltose Transporter Genes in <i>Saccharomyces eubayanus</i> CBS 12357T. Frontiers in Microbiology, 2018, 9, 1786.	3.5	47
44	Fermentation of glucose-xylose-arabinose mixtures by a synthetic consortium of single-sugar-fermenting <i>Saccharomyces cerevisiae</i> strains. FEMS Yeast Research, 2018, 18, .	2.3	33
45	Optimizing anaerobic growth rate and fermentation kinetics in <i>Saccharomyces cerevisiae</i> strains expressing Calvin-cycle enzymes for improved ethanol yield. Biotechnology for Biofuels, 2018, 11, 17.	6.2	57
46	Metabolic engineering strategies for optimizing acetate reduction, ethanol yield and osmotolerance in <i>Saccharomyces cerevisiae</i> . Biotechnology for Biofuels, 2017, 10, 107.	6.2	33
47	<i>Saccharomyces cerevisiae</i> strains for second-generation ethanol production: from academic exploration to industrial implementation. FEMS Yeast Research, 2017, 17, .	2.3	140
48	Laboratory Evolution of a Biotin-Requiring <i>Saccharomyces cerevisiae</i> Strain for Full Biotin Prototrophy and Identification of Causal Mutations. Applied and Environmental Microbiology, 2017, 83, .	3.1	30
49	Industrial Relevance of Chromosomal Copy Number Variation in <i>Saccharomyces</i> Yeasts. Applied and Environmental Microbiology, 2017, 83, .	3.1	61
50	Mutations in PMR1 stimulate xylose isomerase activity and anaerobic growth on xylose of engineered <i>Saccharomyces cerevisiae</i> by influencing manganese homeostasis. Scientific Reports, 2017, 7, 46155.	3.3	61
51	A Simulator-Assisted Workshop for Teaching Chemostat Cultivation in Academic Classes on Microbial Physiology. Journal of Microbiology and Biology Education, 2017, 18, .	1.0	3
52	Extreme calorie restriction in yeast retentostats induces uniform non-quiescent growth arrest. Biochimica Et Biophysica Acta - Molecular Cell Research, 2017, 1864, 231-242.	4.1	10
53	Elimination of sucrose transport and hydrolysis in <i>Saccharomyces cerevisiae</i> : a platform strain for engineering sucrose metabolism. FEMS Yeast Research, 2017, 17, .	2.3	34
54	A CRISPR/Cas9-based exploration into the elusive mechanism for lactate export in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2017, 17, .	2.3	35

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55	Evolutionary Engineering in Chemostat Cultures for Improved Maltotriose Fermentation Kinetics in <i>Saccharomyces pastorianus</i> Lager Brewing Yeast. <i>Frontiers in Microbiology</i> , 2017, 8, 1690.	3.5	36
56	Requirements for Carnitine Shuttle-Mediated Translocation of Mitochondrial Acetyl Moieties to the Yeast Cytosol. <i>MBio</i> , 2016, 7, .	4.1	19
57	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.	7.1	35
58	Alternative reactions at the interface of glycolysis and citric acid cycle in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2016, 16, fow017.	2.3	36
59	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.	6.2	109
60	<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.	3.1	52
61	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.	2.3	13
62	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.	4.0	45
63	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.	4.0	49
64	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.	7.0	117
65	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.	4.0	26
66	How to set up collaborations between academia and industrial biotech companies. <i>Nature Biotechnology</i> , 2015, 33, 237-240.	17.5	23
67	<i>S. cerevisiae</i> Å— <i>S. eubayanus</i> interspecific hybrid, the best of both worlds and beyond. <i>FEMS Yeast Research</i> , 2015, 15, .	2.3	112
68	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5662-5670.	3.1	42
69	A Minimal Set of Glycolytic Genes Reveals Strong Redundancies in <i>Saccharomyces cerevisiae</i> Central Metabolism. <i>Eukaryotic Cell</i> , 2015, 14, 804-816.	3.4	42
70	Editorial overview: Energy biotechnology. <i>Current Opinion in Biotechnology</i> , 2015, 33, viii-xi.	6.6	2
71	Functional expression of a heterologous nickel-dependent, ATP-independent urease in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 30, 130-140.	7.0	19
72	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, .	2.3	28

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73	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, .	2.3	360
74	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, 6253-6267.	3.1	79
75	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015, 32, 1-7.	6.6	74
76	Oxygen availability strongly affects chronological lifespan and thermotolerance in batch cultures of <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell</i> , 2015, 2, 429-444.	3.2	25
77	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.	1.6	0
78	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, 369-389.	2.5	19
79	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.	3.3	12
80	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, 383-392.	3.8	110
81	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.	7.0	93
82	Deletion of the <i>Saccharomyces cerevisiae</i> ARO8 gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2014, 32, n/a-n/a.	1.7	35
83	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, 1020-1030.	4.1	24
84	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, 741-754.	2.3	27
85	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.	4.1	84
86	Proteome Adaptation of <i>Saccharomyces cerevisiae</i> to Severe Calorie Restriction in Retentostat Cultures. <i>Journal of Proteome Research</i> , 2014, 13, 3542-3553.	3.7	17
87	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, 1196-1205.	2.3	44
88	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, 4433-4449.	3.1	6
89	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.	4.2	36
90	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.	6.2	68

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91	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.	4.0	102
92	Long-term adaptation of <i>Saccharomyces cerevisiae</i> to the burden of recombinant insulin production. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2749-2763.	3.3	29
93	Functional analysis and transcriptional regulation of two orthologs of <i>ARO10</i> , encoding broad-substrate-specificity 2-oxo-acid decarboxylases, in the brewing yeast <i>Saccharomyces pastorianus</i> CBS1483. <i>FEMS Yeast Research</i> , 2013, 13, 505-517.	2.3	39
94	Carbon dioxide fixation by Calvin-Cycle enzymes improves ethanol yield in yeast. <i>Biotechnology for Biofuels</i> , 2013, 6, 125.	6.2	117
95	Genome duplication and mutations in <i>ACE2</i> 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.	7.1	100
96	<i>amdSYM</i> , a new dominant recyclable marker cassette for <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2013, 13, 126-139.	2.3	143
97	Crystal ball “ 2013. <i>Microbial Biotechnology</i> , 2013, 6, 3-16.	4.2	6
98	Metabolic engineering of yeast for production of fuels and chemicals. <i>Current Opinion in Biotechnology</i> , 2013, 24, 398-404.	6.6	263
99	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, 201-207.	2.6	26
100	Resolving Phenylalanine Metabolism Sheds Light on Natural Synthesis of Penicillin G in <i>Penicillium chrysogenum</i> . <i>Eukaryotic Cell</i> , 2013, 12, 151-151.	3.4	0
101	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, 769-781.	2.3	49
102	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, 5949-5961.	3.1	50
103	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, 320-333.	2.0	27
104	Substrate Specificity of Thiamine Pyrophosphate-Dependent 2-Oxo-Acid Decarboxylases in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2012, 78, 7538-7548.	3.1	81
105	Resolving Phenylalanine Metabolism Sheds Light on Natural Synthesis of Penicillin G in <i>Penicillium chrysogenum</i> . <i>Eukaryotic Cell</i> , 2012, 11, 238-249.	3.4	24
106	Laboratory evolution of new lactate transporter genes in a <i>jen1Δ</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, n/a-n/a.	2.3	33
107	Metabolic engineering of β -oxidation in <i>Penicillium chrysogenum</i> for improved semi-synthetic cephalosporin biosynthesis. <i>Metabolic Engineering</i> , 2012, 14, 437-448.	7.0	26
108	Galacturonic Acid Inhibits the Growth of <i>Saccharomyces cerevisiae</i> on Galactose, Xylose, and Arabinose. <i>Applied and Environmental Microbiology</i> , 2012, 78, 5052-5059.	3.1	33

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109	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, 303-310.	3.8	26
110	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.	4.0	76
111	De novo production of the flavonoid naringenin in engineered <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 155.	4.0	302
112	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.	4.0	238
113	Similar temperature dependencies of glycolytic enzymes: an evolutionary adaptation to temperature dynamics?. <i>BMC Systems Biology</i> , 2012, 6, 151.	3.0	29
114	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, 401-406.	1.7	9
115	Genome-wide analytical approaches for reverse metabolic engineering of industrially relevant phenotypes in yeast. <i>FEMS Yeast Research</i> , 2012, 12, 183-196.	2.3	75
116	Metabolic engineering, synthetic biology and systems biology. <i>FEMS Yeast Research</i> , 2012, 12, 103-103.	2.3	12
117	Laboratory evolution of new lactate transporter genes in a <i>jen1^Δ</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.	2.3	56
118	Energy coupling in <i>Saccharomyces cerevisiae</i> : selected opportunities for metabolic engineering. <i>FEMS Yeast Research</i> , 2012, 12, 387-397.	2.3	75
119	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.	2.9	29
120	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.	2.3	79
121	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, 603-620.	2.3	43
122	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, 518-526.	7.0	49
123	Engineering topology and kinetics of sucrose metabolism in <i>Saccharomyces cerevisiae</i> for improved ethanol yield. <i>Metabolic Engineering</i> , 2011, 13, 694-703.	7.0	98
124	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, 2133-2144.	4.1	29
125	Anaplerotic Role for Cytosolic Malic Enzyme in Engineered <i>Saccharomyces cerevisiae</i> Strains. <i>Applied and Environmental Microbiology</i> , 2011, 77, 732-738.	3.1	47
126	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	12.8	100

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127	Metabolome, transcriptome and metabolic flux analysis of arabinose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2010, 12, 537-551.	7.0	75
128	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, 367-384.	2.3	4
129	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, 318-328.	3.1	40
130	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, 744-750.	3.1	64
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