

# Jack Jack T Pronk

## List of Publications by Year in descending order

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260  
papers

20,919  
citations

8749

75  
h-index

12585

132  
g-index

271  
all docs

271  
docs citations

271  
times ranked

13343  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Ehrlich Pathway for Fusel Alcohol Production: a Century of Research on <i>Saccharomyces cerevisiae</i> Metabolism. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2259-2266.	1.4	1,125
2	Pyruvate Metabolism in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1996, 12, 1607-1633.	0.8	650
3	Genome sequencing and analysis of the filamentous fungus <i>Penicillium chrysogenum</i> . <i>Nature Biotechnology</i> , 2008, 26, 1161-1168.	9.4	427
4	Alcoholic fermentation of carbon sources in biomass hydrolysates by <i>Saccharomyces cerevisiae</i> : current status. <i>Antonie Van Leeuwenhoek</i> , 2006, 90, 391-418.	0.7	411
5	Stoichiometry and compartmentation of NADH metabolism in <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Reviews</i> , 2001, 25, 15-37.	3.9	410
6	Microbial export of lactic and 3-hydroxypropanoic acid: implications for industrial fermentation processes. <i>Metabolic Engineering</i> , 2004, 6, 245-255.	3.6	409
7	Homofermentative Lactate Production Cannot Sustain Anaerobic Growth of Engineered <i>Saccharomyces cerevisiae</i> : Possible Consequence of Energy-Dependent Lactate Export. <i>Applied and Environmental Microbiology</i> , 2004, 70, 2898-2905.	1.4	365
8	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, .	1.1	360
9	Metabolic engineering of a xylose-isomerase-expressing strain for rapid anaerobic xylose fermentation. <i>FEMS Yeast Research</i> , 2005, 5, 399-409.	1.1	346
10	Malic Acid Production by <i>Saccharomyces cerevisiae</i> : Engineering of Pyruvate Carboxylation, Oxaloacetate Reduction, and Malate Export. <i>Applied and Environmental Microbiology</i> , 2008, 74, 2766-2777.	1.4	325
11	De novo production of the flavonoid naringenin in engineered <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 155.	1.9	302
12	High-level functional expression of a fungal xylose isomerase: the key to efficient ethanolic fermentation of xylose by ?. <i>FEMS Yeast Research</i> , 2003, 4, 69-78.	1.1	300
13	The Genome-wide Transcriptional Responses of <i>Saccharomyces cerevisiae</i> Grown on Glucose in Aerobic Chemostat Cultures Limited for Carbon, Nitrogen, Phosphorus, or Sulfur. <i>Journal of Biological Chemistry</i> , 2003, 278, 3265-3274.	1.6	292
14	Evolutionary engineering of mixed-sugar utilization by a xylose-fermenting strain. <i>FEMS Yeast Research</i> , 2005, 5, 925-934.	1.1	292
15	Role of Transcriptional Regulation in Controlling Fluxes in Central Carbon Metabolism of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 9125-9138.	1.6	264
16	Metabolic engineering of yeast for production of fuels and chemicals. <i>Current Opinion in Biotechnology</i> , 2013, 24, 398-404.	3.3	263
17	Effect of Specific Growth Rate on Fermentative Capacity of Baker's™ Yeast. <i>Applied and Environmental Microbiology</i> , 1998, 64, 4226-4233.	1.4	261
18	The <i>Saccharomyces cerevisiae</i> NDE1 and NDE2 Genes Encode Separate Mitochondrial NADH Dehydrogenases Catalyzing the Oxidation of Cytosolic NADH. <i>Journal of Biological Chemistry</i> , 1998, 273, 24529-24534.	1.6	247

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19	Auxotrophic Yeast Strains in Fundamental and Applied Research. Applied and Environmental Microbiology, 2002, 68, 2095-2100.	1.4	240
20	High-cell-density fed-batch cultivation of the docosahexaenoic acid producing marine alga <i>Cryptothecodinium cohnii</i> . Biotechnology and Bioengineering, 2003, 81, 666-672.	1.7	239
21	Novel Evolutionary Engineering Approach for Accelerated Utilization of Glucose, Xylose, and Arabinose Mixtures by Engineered <i>Saccharomyces cerevisiae</i> Strains. Applied and Environmental Microbiology, 2009, 75, 907-914.	1.4	238
22	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. Microbial Cell Factories, 2012, 11, 36.	1.9	238
23	The fluxes through glycolytic enzymes in <i>Saccharomyces cerevisiae</i> are predominantly regulated at posttranscriptional levels. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15753-15758.	3.3	223
24	Minimal metabolic engineering of for efficient anaerobic xylose fermentation: a proof of principle. FEMS Yeast Research, 2004, 4, 655-664.	1.1	220
25	Reproducibility of Oligonucleotide Microarray Transcriptome Analyses. Journal of Biological Chemistry, 2002, 277, 37001-37008.	1.6	208
26	The Two Acetyl-coenzyme A Synthetases of <i>Saccharomyces cerevisiae</i> Differ with Respect to Kinetic Properties and Transcriptional Regulation. Journal of Biological Chemistry, 1996, 271, 28953-28959.	1.6	204
27	Glucose Uptake Kinetics and Transcription of HXT Genes in Chemostat Cultures of <i>Saccharomyces cerevisiae</i> . Journal of Biological Chemistry, 1999, 274, 15350-15359.	1.6	197
28	Pyruvate decarboxylase: An indispensable enzyme for growth of <i>Saccharomyces cerevisiae</i> on glucose. Yeast, 1996, 12, 247-257.	0.8	196
29	Engineering of <i>Saccharomyces cerevisiae</i> for Efficient Anaerobic Alcoholic Fermentation of D-Arabinose. Applied and Environmental Microbiology, 2007, 73, 4881-4891.	1.4	192
30	Directed Evolution of Pyruvate Decarboxylase-Negative <i>Saccharomyces cerevisiae</i> , Yielding a C <sub>2</sub> -Independent, Glucose-Tolerant, and Pyruvate-Hyperproducing Yeast. Applied and Environmental Microbiology, 2004, 70, 159-166.	1.4	188
31	Kinetics of growth and sugar consumption in yeasts. Antonie Van Leeuwenhoek, 1993, 63, 343-352.	0.7	173
32	Identification and Characterization of Phenylpyruvate Decarboxylase Genes in <i>Saccharomyces cerevisiae</i> . Applied and Environmental Microbiology, 2003, 69, 4534-4541.	1.4	164
33	Identification and Characterization of <i>MAE1</i> , the <i>Saccharomyces cerevisiae</i> Structural Gene Encoding Mitochondrial Malic Enzyme. Journal of Bacteriology, 1998, 180, 2875-2882.	1.0	150
34	The Mitochondrial Alcohol Dehydrogenase Adh3p Is Involved in a Redox Shuttle in <i>Saccharomyces cerevisiae</i> . Journal of Bacteriology, 2000, 182, 4730-4737.	1.0	150
35	Pyruvate Decarboxylase: An Indispensable Enzyme for Growth of <i>Saccharomyces cerevisiae</i> on Glucose. Yeast, 1996, 12, 247-257.	0.8	149
36	Elimination of Glycerol Production in Anaerobic Cultures of a <i>Saccharomyces cerevisiae</i> Strain Engineered To Use Acetic Acid as an Electron Acceptor. Applied and Environmental Microbiology, 2010, 76, 190-195.	1.4	144

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37	Development of Efficient Xylose Fermentation in <i>Saccharomyces cerevisiae</i> : Xylose Isomerase as a Key Component. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2007, 108, 179-204.	0.6	143
38	<i>amdSYM</i> , a new dominant recyclable marker cassette for <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2013, 13, 126-139.	1.1	143
39	Regulation of carbon metabolism in chemostat cultures of <i>Saccharomyces cerevisiae</i> grown on mixtures of glucose and ethanol. <i>Yeast</i> , 1995, 11, 407-418.	0.8	141
40	<i>Saccharomyces cerevisiae</i> strains for second-generation ethanol production: from academic exploration to industrial implementation. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	140
41	Two-dimensional Transcriptome Analysis in Chemostat Cultures. <i>Journal of Biological Chemistry</i> , 2005, 280, 437-447.	1.6	137
42	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.	3.3	135
43	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of carboxylic acids: current status and challenges. <i>FEMS Yeast Research</i> , 2009, 9, 1123-1136.	1.1	134
44	In Vivo Analysis of the Mechanisms for Oxidation of Cytosolic NADH by <i>Saccharomyces cerevisiae</i> Mitochondria. <i>Journal of Bacteriology</i> , 2000, 182, 2823-2830.	1.0	127
45	Proteome analysis of yeast response to various nutrient limitations. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0026.	3.2	125
46	The <i>Saccharomyces cerevisiae</i> ICL2 Gene Encodes a Mitochondrial 2-Methylisocitrate Lyase Involved in Propionyl-Coenzyme A Metabolism. <i>Journal of Bacteriology</i> , 2000, 182, 7007-7013.	1.0	119
47	Xylose metabolism in the anaerobic fungus <i>Piromyces</i> sp. strain E2 follows the bacterial pathway. <i>Archives of Microbiology</i> , 2003, 180, 134-141.	1.0	117
48	Physiological Characterization of the ARO10-Dependent, Broad-Substrate-Specificity 2-Oxo Acid Decarboxylase Activity of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2005, 71, 3276-3284.	1.4	117
49	Carbon dioxide fixation by Calvin-Cycle enzymes improves ethanol yield in yeast. <i>Biotechnology for Biofuels</i> , 2013, 6, 125.	6.2	117
50	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.	3.6	117
51	Effects of acetic acid on the kinetics of xylose fermentation by an engineered, xylose-isomerase-based <i>Saccharomyces cerevisiae</i> strain. <i>FEMS Yeast Research</i> , 2009, 9, 358-364.	1.1	115
52	<i>S. cerevisiae</i> – <i>S. eubayanus</i> interspecific hybrid, the best of both worlds and beyond. <i>FEMS Yeast Research</i> , 2015, 15, .	1.1	112
53	Polycistronic expression of a $\beta$ -carotene biosynthetic pathway in <i>Saccharomyces cerevisiae</i> coupled to $\beta$ -ionone production. <i>Journal of Biotechnology</i> , 2014, 192, 383-392.	1.9	110
54	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

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55	Metabolic Engineering of Glycerol Production in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2002, 68, 2814-2821.	1.4	108
56	Quantitative proteomics and transcriptomics of anaerobic and aerobic yeast cultures reveals post-transcriptional regulation of key cellular processes. <i>Microbiology (United Kingdom)</i> , 2007, 153, 3864-3878.	0.7	108
57	Regulation of fermentative capacity and levels of glycolytic enzymes in chemostat cultures of <i>Saccharomyces cerevisiae</i> . <i>Enzyme and Microbial Technology</i> , 2000, 26, 724-736.	1.6	107
58	Acclimation of <i>Saccharomyces cerevisiae</i> to Low Temperature: A Chemostat-based Transcriptome Analysis. <i>Molecular Biology of the Cell</i> , 2007, 18, 5100-5112.	0.9	106
59	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.	1.9	102
60	Prolonged selection in aerobic, glucose-limited chemostat cultures of <i>Saccharomyces cerevisiae</i> causes a partial loss of glycolytic capacity. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1657-1669.	0.7	101
61	Regulation of alcoholic fermentation in batch and chemostat cultures of <i>Kluyveromyces lactis</i> CBS 2359. , 1998, 14, 459-469.		100
62	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	5.8	100
63	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.	3.3	100
64	Oxidation and Reduction of Iron by Acidophilic Bacteria. <i>Geomicrobiology Journal</i> , 1992, 10, 153-171.	1.0	99
65	Fermentative capacity in high-cell-density fed-batch cultures of baker's yeast. <i>Biotechnology and Bioengineering</i> , 2000, 68, 517-523.	1.7	99
66	Growth requirements of pyruvate-decarboxylase-negative <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Letters</i> , 1999, 174, 73-79.	0.7	98
67	Engineering topology and kinetics of sucrose metabolism in <i>Saccharomyces cerevisiae</i> for improved ethanol yield. <i>Metabolic Engineering</i> , 2011, 13, 694-703.	3.6	98
68	Effects of growth conditions on mitochondrial morphology in <i>Saccharomyces cerevisiae</i> . <i>Antonie Van Leeuwenhoek</i> , 1995, 67, 243-253.	0.7	97
69	Quantitative Physiology of <i>Saccharomyces cerevisiae</i> at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5607-5614.	1.4	95
70	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.	3.6	93
71	Carbonic anhydrase (Nce103p): an essential biosynthetic enzyme for growth of <i>Saccharomyces cerevisiae</i> at atmospheric carbon dioxide pressure. <i>Biochemical Journal</i> , 2005, 391, 311-316.	1.7	88
72	Generic and specific transcriptional responses to different weak organic acids in anaerobic chemostat cultures of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2007, 7, 819-833.	1.1	85

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73	Physiological and Transcriptional Responses to High Concentrations of Lactic Acid in Anaerobic Chemostat Cultures of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2008, 74, 5759-5768.	1.4	85
74	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.	1.8	84
75	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.	1.4	81
76	High-Level Expression of <i>Plasmodium vivax</i> Apical Membrane Antigen 1 (AMA-1) in <i>Pichia pastoris</i> : Strong Immunogenicity in <i>Macaca mulatta</i> Immunized with <i>P. vivax</i> AMA-1 and Adjuvant SBAS2. <i>Infection and Immunity</i> , 1999, 67, 43-49.	1.0	81
77	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.	1.1	79
78	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.	1.4	79
79	Transcriptional responses of <i>Saccharomyces cerevisiae</i> to preferred and nonpreferred nitrogen sources in glucose-limited chemostat cultures. <i>FEMS Yeast Research</i> , 2007, 7, 604-620.	1.1	78
80	Pyruvate decarboxylase: an indispensable enzyme for growth of <i>Saccharomyces cerevisiae</i> on glucose. <i>Yeast</i> , 1996, 12, 247-57.	0.8	78
81	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.	1.9	76
82	Catalase Overexpression Reduces Lactic Acid-Induced Oxidative Stress in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2009, 75, 2320-2325.	1.4	75
83	Metabolome, transcriptome and metabolic flux analysis of arabinose fermentation by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2010, 12, 537-551.	3.6	75
84	Genome-wide analytical approaches for reverse metabolic engineering of industrially relevant phenotypes in yeast. <i>FEMS Yeast Research</i> , 2012, 12, 183-196.	1.1	75
85	Energy coupling in <i>Saccharomyces cerevisiae</i> : selected opportunities for metabolic engineering. <i>FEMS Yeast Research</i> , 2012, 12, 387-397.	1.1	75
86	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, .	1.1	75
87	Dynamics of Glycolytic Regulation during Adaptation of <i>Saccharomyces cerevisiae</i> to Fermentative Metabolism. <i>Applied and Environmental Microbiology</i> , 2008, 74, 5710-5723.	1.4	74
88	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015, 32, 1-7.	3.3	74
89	Vitamin requirements and biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020, 37, 283-304.	0.8	74
90	Glucose metabolism and gluconic acid production by <i>Acetobacter diazotrophicus</i> . <i>Journal of Bioscience and Bioengineering</i> , 1991, 72, 101-105.	0.9	72

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91	Exploring and dissecting genome-wide gene expression responses of <i>Penicillium chrysogenum</i> to phenylacetic acid consumption and penicillinG production. <i>BMC Genomics</i> , 2009, 10, 75.	1.2	70
92	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.	3.6	70
93	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
94	Effects of Pyruvate Decarboxylase Overproduction on Flux Distribution at the Pyruvate Branch Point in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 1998, 64, 2133-2140.	1.4	66
95	A new physiological role for Pdr12p in <i>Saccharomyces cerevisiae</i> : export of aromatic and branched-chain organic acids produced in amino acid catabolism. <i>FEMS Yeast Research</i> , 2006, 6, 937-945.	1.1	64
96	Key Process Conditions for Production of C <sub>4</sub> Dicarboxylic Acids in Bioreactor Batch Cultures of an Engineered <i>Saccharomyces cerevisiae</i> Strain. <i>Applied and Environmental Microbiology</i> , 2010, 76, 744-750.	1.4	64
97	Validation of a Metabolic Network for <i>Saccharomyces cerevisiae</i> Using Mixed Substrate Studies. <i>Biotechnology Progress</i> , 1996, 12, 434-448.	1.3	63
98	Pyruvate Decarboxylase Catalyzes Decarboxylation of Branched-Chain 2-Oxo Acids but Is Not Essential for Fusel Alcohol Production by <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 1998, 64, 1303-1307.	1.4	62
99	Industrial Relevance of Chromosomal Copy Number Variation in <i>Saccharomyces</i> Yeasts. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	61
100	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.	1.6	61
101	Functional analysis of structural genes for NAD <sup>+</sup> -dependent formate dehydrogenase in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2002, 19, 509-520.	0.8	60
102	Metabolic flux analysis of a glycerol-overproducing <i>Saccharomyces cerevisiae</i> strain based on GC-MS, LC-MS and NMR-derived <sup>13</sup> C-labelling data. <i>FEMS Yeast Research</i> , 2007, 7, 216-231.	1.1	60
103	Control of the Glycolytic Flux in <i>Saccharomyces cerevisiae</i> Grown at Low Temperature. <i>Journal of Biological Chemistry</i> , 2007, 282, 10243-10251.	1.6	59
104	Optimizing anaerobic growth rate and fermentation kinetics in <i>Saccharomyces cerevisiae</i> strains expressing Calvin-cycle enzymes for improved ethanol yield. <i>Biotechnology for Biofuels</i> , 2018, 11, 17.	6.2	57
105	Prolonged Maltose-Limited Cultivation of <i>Saccharomyces cerevisiae</i> Selects for Cells with Improved Maltose Affinity and Hypersensitivity. <i>Applied and Environmental Microbiology</i> , 2004, 70, 1956-1963.	1.4	56
106	Laboratory evolution of new lactate transporter genes in a <i>jen1<sup>Δ</sup></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.	1.1	56
107	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.	1.2	55
108	Oxidation of reduced sulphur compounds by intact cells of <i>Thiobacillus acidophilus</i> . <i>Archives of Microbiology</i> , 1992, 157, 161-168.	1.0	54



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109	Physiological and Transcriptional Responses of <i>Saccharomyces cerevisiae</i> to Zinc Limitation in Chemostat Cultures. <i>Applied and Environmental Microbiology</i> , 2007, 73, 7680-7692.	1.4	53
110	<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.	1.4	52
111	Comparative genotyping of the laboratory strains S288C and CEN.PK113-7D using oligonucleotide microarrays. <i>FEMS Yeast Research</i> , 2003, 4, 259-269.	1.1	50
112	Transcription factor control of growth rate dependent genes in <i>Saccharomyces cerevisiae</i> : A three factor design. <i>BMC Genomics</i> , 2008, 9, 341.	1.2	50
113	Chemostat-Based Micro-Array Analysis in Baker's Yeast. <i>Advances in Microbial Physiology</i> , 2008, 54, 257-417.	1.0	50
114	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.	1.4	50
115	Physiological and genome-wide transcriptional responses of to high carbon dioxide concentrations. <i>FEMS Yeast Research</i> , 2005, 5, 579-593.	1.1	49
116	Engineering of <i>Penicillium chrysogenum</i> for fermentative production of a novel carbamoylated cephem antibiotic precursor. <i>Metabolic Engineering</i> , 2009, 11, 125-137.	3.6	49
117	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.	3.6	49
118	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.	1.1	49
119	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.	1.9	49
120	Physiological and genetic engineering of cytosolic redox metabolism in <i>Saccharomyces cerevisiae</i> for improved glycerol production. <i>Metabolic Engineering</i> , 2006, 8, 532-542.	3.6	48
121	Anaplerotic Role for Cytosolic Malic Enzyme in Engineered <i>Saccharomyces cerevisiae</i> Strains. <i>Applied and Environmental Microbiology</i> , 2011, 77, 732-738.	1.4	47
122	Structural, Physiological and Regulatory Analysis of Maltose Transporter Genes in <i>Saccharomyces eubayanus</i> CBS 12357T. <i>Frontiers in Microbiology</i> , 2018, 9, 1786.	1.5	47
123	Contribution of the transcriptional regulator Leu3p to physiology and gene expression in nitrogen- and carbon-limited chemostat cultures. <i>FEMS Yeast Research</i> , 2005, 5, 885-897.	1.1	45
124	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.	1.9	45
125	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.	1.1	44
126	Hydrolytic activity in baker's yeast limits the yield of asymmetric 3-oxo ester reduction. <i>Biotechnology and Bioengineering</i> , 2000, 69, 370-376.	1.7	43



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127	Oxygen Requirements of the Food Spoilage Yeast <i>Zygosaccharomyces bailii</i> in Synthetic and Complex Media. <i>Applied and Environmental Microbiology</i> , 2001, 67, 2123-2128.	1.4	43
128	Two mechanisms for oxidation of cytosolic NADPH by <i>Kluyveromyces lactis</i> mitochondria. <i>Yeast</i> , 2002, 19, 813-824.	0.8	43
129	Overproduction of Threonine Aldolase Circumvents the Biosynthetic Role of Pyruvate Decarboxylase in Glucose-Limited Chemostat Cultures of <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2003, 69, 2094-2099.	1.4	43
130	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.	1.1	43
131	Enzymic analysis of NADPH metabolism in $\beta$ -lactam-producing <i>Penicillium chrysogenum</i> : Presence of a mitochondrial NADPH dehydrogenase. <i>Metabolic Engineering</i> , 2006, 8, 91-101.	3.6	42
132	Exploiting combinatorial cultivation conditions to infer transcriptional regulation. <i>BMC Genomics</i> , 2007, 8, 25.	1.2	42
133	Physiological and Transcriptional Responses of Different Industrial Microbes at Near-Zero Specific Growth Rates. <i>Applied and Environmental Microbiology</i> , 2015, 81, 5662-5670.	1.4	42
134	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
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