

Jean-Marc Daran

List of Publications by Year in descending order

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135
papers

8,827
citations

41258

49
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87
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149
all docs

149
docs citations

149
times ranked

7624
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	Genome sequencing and analysis of the filamentous fungus <i>Penicillium chrysogenum</i> . <i>Nature Biotechnology</i> , 2008, 26, 1161-1168.	9.4	427
3	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
4	De novo production of the flavonoid naringenin in engineered <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 155.	1.9	302
5	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
6	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.	1.9	238
7	The fluxes through glycolytic enzymes in <i>Saccharomyces cerevisiae</i> are predominantly regulated at posttranscriptional levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15753-15758.	3.3	223
8	Alleviation of feedback inhibition in <i>Saccharomyces cerevisiae</i> aromatic amino acid biosynthesis: Quantification of metabolic impact. <i>Metabolic Engineering</i> , 2008, 10, 141-153.	3.6	174
9	<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
10	Two-dimensional Transcriptome Analysis in Chemostat Cultures. <i>Journal of Biological Chemistry</i> , 2005, 280, 437-447.	1.6	137
11	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
12	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
13	Carbon dioxide fixation by Calvin-Cycle enzymes improves ethanol yield in yeast. <i>Biotechnology for Biofuels</i> , 2013, 6, 125.	6.2	117
14	Fncpf1: a novel and efficient genome editing tool for <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2017, 45, 12585-12598.	6.5	116
15	Genetic and Biochemical Characterization of the UGP1 Gene Encoding the UDP-Glucose Pyrophosphorylase from <i>Saccharomyces cerevisiae</i> . <i>FEBS Journal</i> , 1995, 233, 520-530.	0.2	115
16	<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
17	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.	1.9	110
18	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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19	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
20	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
21	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
22	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
23	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
24	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
25	Nanopore sequencing enables near-complete de novo assembly of <i>Saccharomyces cerevisiae</i> reference strain CEN.PK113-7D. <i>FEMS Yeast Research</i> , 2017, 17, .	1.1	84
26	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
27	Multiplex genome editing of microorganisms using CRISPR-Cas. <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	80
28	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
29	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
30	Heterologous carotenoid production in <i>Saccharomyces cerevisiae</i> induces the pleiotropic drug resistance stress response. <i>Yeast</i> , 2010, 27, 983-998.	0.8	76
31	An internal deletion in <i>MTH1</i> 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
32	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
33	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
34	Vitamin requirements and biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2020, 37, 283-304.	0.8	74
35	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, 3920-3920.	1.4	71
36	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

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37	Construction of an <i>hdfA</i> <i>Penicillium chrysogenum</i> strain impaired in non-homologous end-joining and analysis of its potential for functional analysis studies. <i>Fungal Genetics and Biology</i> , 2009, 46, 418-426.	0.9	70
38	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
39	<i>De novo</i> detection of copy number variation by co-assembly. <i>Bioinformatics</i> , 2012, 28, 3195-3202.	1.8	69
40	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
41	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
42	Biological Parts for <i>Kluyveromyces marxianus</i> Synthetic Biology. <i>Frontiers in Bioengineering and Biotechnology</i> , 2019, 7, 97.	2.0	62
43	Industrial Relevance of Chromosomal Copy Number Variation in <i>Saccharomyces</i> Yeasts. <i>Applied and Environmental Microbiology</i> , 2017, 83, .	1.4	61
44	Mutations in <i>PMR1</i> 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
45	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
46	Engineering de novo anthocyanin production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2018, 17, 103.	1.9	58
47	Laboratory evolution of new lactate transporter genes in a <i>jen1^Δ</i> mutant of <i>Saccharomyces cerevisiae</i> and their identification as <i>ADY2</i> alleles by whole-genome resequencing and transcriptome analysis. <i>FEMS Yeast Research</i> , 2012, 12, 359-374.	1.1	56
48	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
49	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
50	CRISPR-Cas9 mediated gene deletions in lager yeast <i>Saccharomyces pastorianus</i> . <i>Microbial Cell Factories</i> , 2017, 16, 222.	1.9	53
51	Predicting Metabolic Fluxes Using Gene Expression Differences As Constraints. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 206-216.	1.9	52
52	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
53	Chemostat-Based Micro-Array Analysis in Baker's Yeast. <i>Advances in Microbial Physiology</i> , 2008, 54, 257-417.	1.0	50
54	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

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55	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
56	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
57	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
58	Physiological and morphological effects of genetic alterations leading to a reduced synthesis of UDP-glucose in <i>Saccharomyces cerevisiae</i> . <i>FEMS Microbiology Letters</i> , 2006, 153, 89-96.	0.7	46
59	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
60	Integrating genome assemblies with MAIA. <i>Bioinformatics</i> , 2010, 26, i433-i439.	1.8	45
61	Toward Developing a Yeast Cell Factory for the Production of Prenylated Flavonoids. <i>Journal of Agricultural and Food Chemistry</i> , 2019, 67, 13478-13486.	2.4	45
62	Chromosome level assembly and comparative genome analysis confirm lager-brewing yeasts originated from a single hybridization. <i>BMC Genomics</i> , 2019, 20, 916.	1.2	43
63	Exploiting combinatorial cultivation conditions to infer transcriptional regulation. <i>BMC Genomics</i> , 2007, 8, 25.	1.2	42
64	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
65	Determination of the Cytosolic NADPH/NADP Ratio in <i>Saccharomyces cerevisiae</i> using Shikimate Dehydrogenase as Sensor Reaction. <i>Scientific Reports</i> , 2015, 5, 12846.	1.6	41
66	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.	1.4	40
67	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.	1.1	39
68	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.	0.9	36
69	Alternative reactions at the interface of glycolysis and citric acid cycle in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2016, 16, fow017.	1.1	36
70	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.	1.5	36
71	An atypical <i>PMR2</i> locus is responsible for hypersensitivity to sodium and lithium cations in the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>FEMS Yeast Research</i> , 2009, 9, 789-792.	1.1	35
72	Deletion of the <i>Saccharomyces cerevisiae</i> <i>ARO8</i> gene, encoding an aromatic amino acid transaminase, enhances phenylethanol production from glucose. <i>Yeast</i> , 2014, 32, n/a-n/a.	0.8	35

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73	Pathway swapping: Toward modular engineering of essential cellular processes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 15060-15065.	3.3	35
74	A CRISPR/Cas9-based exploration into the elusive mechanism for lactate export in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2017, 17, .	1.1	35
75	Laboratory Evolution of a <i>Saccharomyces cerevisiae</i> × <i>S. eubayanus</i> Hybrid Under Simulated Lager-Brewing Conditions. Frontiers in Genetics, 2019, 10, 242.	1.1	35
76	Elimination of sucrose transport and hydrolysis in <i>Saccharomyces cerevisiae</i> : a platform strain for engineering sucrose metabolism. FEMS Yeast Research, 2017, 17, .	1.1	34
77	Identity of the Growth-Limiting Nutrient Strongly Affects Storage Carbohydrate Accumulation in Anaerobic Chemostat Cultures of <i>Saccharomyces cerevisiae</i> . Applied and Environmental Microbiology, 2009, 75, 6876-6885.	1.4	33
78	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. FEMS Yeast Research, 2012, 12, n/a-n/a.	1.1	33
79	Fermentation of glucose-xylose-arabinose mixtures by a synthetic consortium of single-sugar-fermenting <i>Saccharomyces cerevisiae</i> strains. FEMS Yeast Research, 2018, 18, .	1.1	33
80	Allele-specific genome editing using CRISPR-Cas9 is associated with loss of heterozygosity in diploid yeast. Nucleic Acids Research, 2019, 47, 1362-1372.	6.5	32
81	Excessive by-product formation: A key contributor to low isobutanol yields of engineered <i>Saccharomyces cerevisiae</i> strains. Metabolic Engineering Communications, 2016, 3, 39-51.	1.9	30
82	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, .	1.4	30
83	Long-term adaptation of <i>Saccharomyces cerevisiae</i> to the burden of recombinant insulin production. Biotechnology and Bioengineering, 2013, 110, 2749-2763.	1.7	29
84	The <i>Penicillium chrysogenum</i> transporter PcAraT enables high-affinity, glucose-insensitive L-arabinose transport in <i>Saccharomyces cerevisiae</i> . Biotechnology for Biofuels, 2018, 11, 63.	6.2	29
85	In vivo recombination of <i>Saccharomyces eubayanus</i> maltose-transporter genes yields a chimeric transporter that enables maltotriose fermentation. PLoS Genetics, 2019, 15, e1007853.	1.5	29
86	The genome sequence of the popular hexose-transport-deficient <i>Saccharomyces cerevisiae</i> strain EB.YW4000 reveals LoxP/Cre-induced translocations and gene loss. FEMS Yeast Research, 2015, 15, .	1.1	28
87	Degeneration of penicillin production in ethanol-limited chemostat cultivations of <i>Penicillium chrysogenum</i> : A systems biology approach. BMC Systems Biology, 2011, 5, 132.	3.0	27
88	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. OMICS A Journal of Integrative Biology, 2012, 16, 320-333.	1.0	27
89	Efficient simultaneous excision of multiple selectable marker cassettes using I-SceI-induced double-strand DNA breaks in <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2014, 14, 741-754.	1.1	27
90	A protocol for introduction of multiple genetic modifications in <i>Saccharomyces cerevisiae</i> using CRISPR/Cas9. FEMS Yeast Research, 2018, 18, .	1.1	27

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91	Metabolic engineering of β^2 -oxidation in <i>Penicillium chrysogenum</i> for improved semi-synthetic cephalosporin biosynthesis. <i>Metabolic Engineering</i> , 2012, 14, 437-448.	3.6	26
92	Correlation between transcript profiles and fitness of deletion mutants in anaerobic chemostat cultures of <i>Saccharomyces cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 2007, 153, 877-886.	0.7	25
93	Selection of Pof- <i>Saccharomyces eubayanus</i> Variants for the Construction of <i>S. cerevisiae</i> Δ - <i>S. eubayanus</i> Hybrids With Reduced 4-Vinyl Guaiacol Formation. <i>Frontiers in Microbiology</i> , 2018, 9, 1640.	1.5	25
94	A toolkit for rapid CRISPR-Cas9 assisted construction of hexose-transport-deficient <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	25
95	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
96	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.	3.6	24
97	Stress-induced expression is enriched for evolutionarily young genes in diverse budding yeasts. <i>Nature Communications</i> , 2020, 11, 2144.	5.8	24
98	Functional characterization of the oxaloacetase encoding gene and elimination of oxalate formation in the β^2 -lactam producer <i>Penicillium chrysogenum</i> . <i>Fungal Genetics and Biology</i> , 2011, 48, 831-839.	0.9	23
99	Transcriptional responses to glucose in <i>Saccharomyces cerevisiae</i> strains lacking a functional protein kinase A. <i>BMC Genomics</i> , 2011, 12, 405.	1.2	23
100	Lager-brewing yeasts in the era of modern genetics. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	23
101	Characterisation of the broad substrate specificity 2-keto acid decarboxylase Aro10p of <i>Saccharomyces kudriavzevii</i> and its implication in aroma development. <i>Microbial Cell Factories</i> , 2016, 15, 51.	1.9	21
102	Himalayan <i>Saccharomyces eubayanus</i> Genome Sequences Reveal Genetic Markers Explaining Heterotic Maltotriose Consumption by <i>Saccharomyces pastorianus</i> Hybrids. <i>Applied and Environmental Microbiology</i> , 2019, 85, .	1.4	21
103	A supernumerary designer chromosome for modular <i>in vivo</i> pathway assembly in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2021, 49, 1769-1783.	6.5	20
104	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.	1.2	19
105	Functional expression of a heterologous nickel-dependent, ATP-independent urease in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 30, 130-140.	3.6	19
106	Requirements for Carnitine Shuttle-Mediated Translocation of Mitochondrial Acetyl Moieties to the Yeast Cytosol. <i>MBio</i> , 2016, 7, .	1.8	19
107	Adaptive Laboratory Evolution and Reverse Engineering of Single-Vitamin Prototrophies in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	18
108	Membrane potential independent transport of NH ₃ in the absence of ammonium permeases in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2017, 11, 49.	3.0	17

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109	Comparative assessment of native and heterologous 2-oxo acid decarboxylases for application in isobutanol production by <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 204.	6.2	16
110	Laboratory evolution of a glucose-phosphorylation-deficient, arabinose-fermenting <i>S. cerevisiae</i> strain reveals mutations in <i>GAL2</i> that enable glucose-insensitive l-arabinose uptake. <i>FEMS Yeast Research</i> , 2018, 18, .	1.1	16
111	The Genetic Makeup and Expression of the Glycolytic and Fermentative Pathways Are Highly Conserved Within the <i>Saccharomyces</i> Genus. <i>Frontiers in Genetics</i> , 2018, 9, 504.	1.1	15
112	Engineering and Analysis of a <i>Saccharomyces cerevisiae</i> Strain That Uses Formaldehyde as an Auxiliary Substrate. <i>Applied and Environmental Microbiology</i> , 2008, 74, 3182-3188.	1.4	14
113	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.	1.1	13
114	Full humanization of the glycolytic pathway in <i>Saccharomyces cerevisiae</i> . <i>Cell Reports</i> , 2022, 39, 111010.	2.9	13
115	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.	1.3	12
116	Improving Industrially Relevant Phenotypic Traits by Engineering Chromosome Copy Number in <i>Saccharomyces pastorianus</i> . <i>Frontiers in Genetics</i> , 2020, 11, 518.	1.1	12
117	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.	1.8	11
118	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.	3.6	10
119	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.	0.7	9
120	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, .	1.4	9
121	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.	1.5	8
122	Design and Experimental Evaluation of a Minimal, Innocuous Watermarking Strategy to Distinguish Near-Identical DNA and RNA Sequences. <i>ACS Synthetic Biology</i> , 2020, 9, 1361-1375.	1.9	8
123	Exploring the abundance of oleate hydratases in the genus <i>Rhodococcus</i> —discovery of novel enzymes with complementary substrate scope. <i>Applied Microbiology and Biotechnology</i> , 2020, 104, 5801-5812.	1.7	8
124	The complete genome sequence of the nitrile biocatalyst <i>Rhodococcus rhodochrous</i> ATCC BAA-870. <i>BMC Genomics</i> , 2020, 21, 3.	1.2	7
125	Crystal ball “ 2013. <i>Microbial Biotechnology</i> , 2013, 6, 3-16.	2.0	6
126	Modular, synthetic chromosomes as new tools for large scale engineering of metabolism. <i>Metabolic Engineering</i> , 2022, 72, 1-13.	3.6	6

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127	Engineering oxygen-independent biotin biosynthesis in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2021, 67, 88-103.	3.6	5
128	Genetic bases for the metabolism of the DMS precursor S-methylmethionine by <i>Saccharomyces cerevisiae</i> . <i>Food Microbiology</i> , 2022, 106, 104041.	2.1	5
129	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.	1.1	4
130	gEL DNA: A Cloning- and Polymerase Chain Reaction-Free Method for CRISPR-Based Multiplexed Genome Editing. <i>CRISPR Journal</i> , 2021, , .	1.4	4
131	Engineering of molybdenum-cofactor-dependent nitrate assimilation in <i>Yarrowia lipolytica</i> . <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	4
132	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.	1.9	1
133	Entering GATTACA: yeast genomes: analysis, insights and applications. <i>FEMS Yeast Research</i> , 2021, 20, .	1.1	1
134	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
135	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.	1.8	0