

Jens B Nielsen

List of Publications by Year in descending order

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Version: 2024-02-01

895
papers

85,682
citations

630

127
h-index

1082

240
g-index

1010
all docs

1010
docs citations

1010
times ranked

87273
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiscale models quantifying yeast physiology: towards a whole-cell model. Trends in Biotechnology, 2022, 40, 291-305.	4.9	20
2	Microbial production of chemicals driven by CRISPR-Cas systems. Current Opinion in Biotechnology, 2022, 73, 34-42.	3.3	16
3	Professor John Villadsen, PhD, Dr. techn., Dr. h. c. mult (12.6.1936–22.7.2021). Biotechnology and Bioengineering, 2022, 119, 7-8.	1.7	0
4	Yeast synthetic biology advances biofuel production. Current Opinion in Microbiology, 2022, 65, 33-39.	2.3	21
5	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. Gut, 2022, 71, 2463-2480.	6.1	53
6	Genome-scale modeling of yeast metabolism: retrospectives and perspectives. FEMS Yeast Research, 2022, 22, .	1.1	20
7	Yeast has evolved to minimize protein resource cost for synthesizing amino acids. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	11
8	Analysis of normal levels of free glycosaminoglycans in urine and plasma in adults. Journal of Biological Chemistry, 2022, 298, 101575.	1.6	13
9	Multimiomics Analysis Reveals the Impact of Microbiota on Host Metabolism in Hepatic Steatosis. Advanced Science, 2022, 9, e2104373.	5.6	23
10	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. Nature Communications, 2022, 13, 801.	5.8	47
11	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	15.2	102
12	Identification of a novel gene required for competitive growth at high temperature in the thermotolerant yeast Kluyveromyces marxianus. Microbiology (United Kingdom), 2022, 168, .	0.7	5
13	A Gene Co-Expression Network-Based Drug Repositioning Approach Identifies Candidates for Treatment of Hepatocellular Carcinoma. Cancers, 2022, 14, 1573.	1.7	8
14	Prediction of drug candidates for clear cell renal cell carcinoma using a systems biology-based drug repositioning approach. EBioMedicine, 2022, 78, 103963.	2.7	11
15	Mapping of Nonhomologous End Joining-Mediated Integration Facilitates Genome-Scale Trackable Mutagenesis in <i>Yarrowia lipolytica</i> . ACS Synthetic Biology, 2022, 11, 216-227.	1.9	14
16	Innovation trends in industrial biotechnology. Trends in Biotechnology, 2022, 40, 1160-1172.	4.9	30
17	The integration of bio-catalysis and electrocatalysis to produce fuels and chemicals from carbon dioxide. Chemical Society Reviews, 2022, 51, 4763-4785.	18.7	32
18	Improving recombinant protein production by yeast through genome-scale modeling using proteome constraints. Nature Communications, 2022, 13, .	5.8	18

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19	Proteome allocations change linearly with the specific growth rate of <i>Saccharomyces cerevisiae</i> under glucose limitation. <i>Nature Communications</i> , 2022, 13, .	5.8	28
20	Multi-omics analyses of the transition to the Crabtree effect in <i>S. cerevisiae</i> reveals a key role for the citric acid shuttle. <i>FEMS Yeast Research</i> , 2022, 22, .	1.1	2
21	Enhanced metabolism and negative regulation of ER stress support higher erythropoietin production in HEK293 cells. <i>Cell Reports</i> , 2022, 39, 110936.	2.9	4
22	Rewiring regulation on respiro-fermentative metabolism relieved Crabtree effects in <i>Saccharomyces cerevisiae</i> . <i>Synthetic and Systems Biotechnology</i> , 2022, 7, 1034-1043.	1.8	6
23	Reconstruction of a catalogue of genome-scale metabolic models with enzymatic constraints using GECKO 2.0. <i>Nature Communications</i> , 2022, 13, .	5.8	39
24	Deep learning-based kcat prediction enables improved enzyme-constrained model reconstruction. <i>Nature Catalysis</i> , 2022, 5, 662-672.	16.1	98
25	Genome-scale modeling drives 70-fold improvement of intracellular heme production in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	29
26	Plasma and Urine Free Glycosaminoglycans as Monitoring Biomarkers in Nonmetastatic Renal Cell Carcinoma—A Prospective Cohort Study. <i>European Urology Open Science</i> , 2022, 42, 30-39.	0.2	5
27	The Translational Status of Cancer Liquid Biopsies. <i>Regenerative Engineering and Translational Medicine</i> , 2021, 7, 312-352.	1.6	39
28	Addressing the heterogeneity in liver diseases using biological networks. <i>Briefings in Bioinformatics</i> , 2021, 22, 1751-1766.	3.2	9
29	A systems biology approach to understand gut microbiota and host metabolism in morbid obesity: design of the BARIA Longitudinal Cohort Study. <i>Journal of Internal Medicine</i> , 2021, 289, 340-354.	2.7	28
30	Systems biology based drug repositioning for development of cancer therapy. <i>Seminars in Cancer Biology</i> , 2021, 68, 47-58.	4.3	54
31	Performance of Regression Models as a Function of Experiment Noise. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110203.	1.0	9
32	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. <i>Nature Communications</i> , 2021, 12, 190.	5.8	25
33	Production of 10-methyl branched fatty acids in yeast. <i>Biotechnology for Biofuels</i> , 2021, 14, 12.	6.2	14
34	Transcriptomic response of <i>Saccharomyces cerevisiae</i> to octanoic acid production. <i>FEMS Yeast Research</i> , 2021, 21, .	1.1	4
35	Yeast based biorefineries for oleochemical production. <i>Current Opinion in Biotechnology</i> , 2021, 67, 26-34.	3.3	21
36	Benchmarking accuracy and precision of intensity-based absolute quantification of protein abundances in <i>Saccharomyces cerevisiae</i> . <i>Proteomics</i> , 2021, 21, e2000093.	1.3	13

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37	Mathematical modeling of proteome constraints within metabolism. <i>Current Opinion in Systems Biology</i> , 2021, 25, 50-56.	1.3	36
38	Production of β -carotene in <i>Saccharomyces cerevisiae</i> through altering yeast lipid metabolism. <i>Biotechnology and Bioengineering</i> , 2021, 118, 2043-2052.	1.7	30
39	Quantifying absolute gene expression profiles reveals distinct regulation of central carbon metabolism genes in yeast. <i>ELife</i> , 2021, 10, .	2.8	21
40	Expression of fungal biosynthetic gene clusters in <i>S. cerevisiae</i> for natural product discovery. <i>Synthetic and Systems Biotechnology</i> , 2021, 6, 20-22.	1.8	6
41	CODY enables quantitatively spatiotemporal predictions on in vivo gut microbial variability induced by diet intervention. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	17
42	Yeast optimizes metal utilization based on metabolic network and enzyme kinetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
43	Fatty acid synthesis is required for breast cancer brain metastasis. <i>Nature Cancer</i> , 2021, 2, 414-428.	5.7	147
44	Machine learning-based investigation of the cancer protein secretory pathway. <i>PLoS Computational Biology</i> , 2021, 17, e1008898.	1.5	7
45	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	6.5	25
46	A novel yeast hybrid modeling framework integrating Boolean and enzyme-constrained networks enables exploration of the interplay between signaling and metabolism. <i>PLoS Computational Biology</i> , 2021, 17, e1008891.	1.5	16
47	Proteome constraints reveal targets for improving microbial fitness in nutrient-rich environments. <i>Molecular Systems Biology</i> , 2021, 17, e10093.	3.2	46
48	Informing Pharmacokinetic Models With Physiological Data: Oral Population Modeling of L-Serine in Humans. <i>Frontiers in Pharmacology</i> , 2021, 12, 643179.	1.6	3
49	Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. <i>Microbiology Resource Announcements</i> , 2021, 10, e0019521.	0.3	1
50	GTR 2.0: gRNA-tRNA Array and Cas9-NG Based Genome Disruption and Single-Nucleotide Conversion in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2021, 10, 1328-1337.	1.9	10
51	Strategies and challenges with the microbial conversion of methanol to high-value chemicals. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3655-3668.	1.7	12
52	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	16.1	26
53	BUTTERFLY: addressing the pooled amplification paradox with unique molecular identifiers in single-cell RNA-seq. <i>Genome Biology</i> , 2021, 22, 174.	3.8	5
54	Combined Metabolic Activators Accelerates Recovery in Mild to Moderate COVID-19. <i>Advanced Science</i> , 2021, 8, e2101222.	5.6	49

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55	Genome-scale insights into the metabolic versatility of <i>Limosilactobacillus reuteri</i> . <i>BMC Biotechnology</i> , 2021, 21, 46.	1.7	8
56	Genome-scale metabolic network reconstruction of model animals as a platform for translational research. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
57	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	9.0	403
58	Rational gRNA design based on transcription factor binding data. <i>Synthetic Biology</i> , 2021, 6, ysab014.	1.2	0
59	Analytical performance of a standardized kit for mass spectrometry-based measurements of human glycosaminoglycans. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2021, 1177, 122761.	1.2	8
60	Stratification of patients with clear cell renal cell carcinoma to facilitate drug repositioning. <i>IScience</i> , 2021, 24, 102722.	1.9	8
61	Expression of antibody fragments in <i>Saccharomyces cerevisiae</i> strains evolved for enhanced protein secretion. <i>Microbial Cell Factories</i> , 2021, 20, 134.	1.9	21
62	Characterization of cross-species transcription and splicing from <i>Penicillium</i> to <i>Saccharomyces cerevisiae</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2021, 48, .	1.4	0
63	In vitro turnover numbers do not reflect in vivo activities of yeast enzymes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	22
64	The yeastGemMap: A process diagram to assist yeast systemsâ€™ metabolic studies. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4800-4814.	1.7	1
65	Metabolic network remodelling enhances yeastâ€™s fitness on xylose using aerobic glycolysis. <i>Nature Catalysis</i> , 2021, 4, 783-796.	16.1	23
66	A single chromosome strain of <i>S. cerevisiae</i> exhibits diminished ethanol metabolism and tolerance. <i>BMC Genomics</i> , 2021, 22, 688.	1.2	2
67	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	5.9	138
68	De novo biosynthesis of bioactive isoflavonoids by engineered yeast cell factories. <i>Nature Communications</i> , 2021, 12, 6085.	5.8	62
69	Combined metabolic activators therapy ameliorates liver fat in nonalcoholic fatty liver disease patients. <i>Molecular Systems Biology</i> , 2021, 17, e10459.	3.2	22
70	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. <i>Molecular Systems Biology</i> , 2021, 17, e10427.	3.2	17
71	Constraint-based modeling of yeast mitochondria reveals the dynamics of protein import and iron-sulfur cluster biogenesis. <i>IScience</i> , 2021, 24, 103294.	1.9	7
72	Microbial community dynamics revisited. <i>Nature Computational Science</i> , 2021, 1, 640-641.	3.8	2

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73	A network-based approach reveals the dysregulated transcriptional regulation in non-alcoholic fatty liver disease. <i>IScience</i> , 2021, 24, 103222.	1.9	14
74	Synthetic Biology Advanced Natural Product Discovery. <i>Metabolites</i> , 2021, 11, 785.	1.3	8
75	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	13.7	102
76	Adaptations in metabolism and protein translation give rise to the Crabtree effect in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	40
77	Pan-cancer analysis of the metabolic reaction network. <i>Metabolic Engineering</i> , 2020, 57, 51-62.	3.6	29
78	Metabolic Profiling and Compound-Class Identification Reveal Alterations in Serum Triglyceride Levels in Mice Immunized with Human Vaccine Adjuvant Alum. <i>Journal of Proteome Research</i> , 2020, 19, 269-278.	1.8	5
79	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. <i>Nature Communications</i> , 2020, 11, 68.	5.8	74
80	Engineering yeast phospholipid metabolism for de novo oleoylethanolamide production. <i>Nature Chemical Biology</i> , 2020, 16, 197-205.	3.9	16
81	Optimizing cultivation of <i>Cordyceps militaris</i> for fast growth and cordycepin overproduction using rational design of synthetic media. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1-8.	1.9	31
82	Yeast systems biology in understanding principles of physiology underlying complex human diseases. <i>Current Opinion in Biotechnology</i> , 2020, 63, 63-69.	3.3	7
83	Applications of Genome-Wide Screening and Systems Biology Approaches in Drug Repositioning. <i>Cancers</i> , 2020, 12, 2694.	1.7	14
84	Combining mechanistic and machine learning models for predictive engineering and optimization of tryptophan metabolism. <i>Nature Communications</i> , 2020, 11, 4880.	5.8	137
85	Advances in Metabolic Engineering of <i>Saccharomyces cerevisiae</i> for Cocoa Butter Equivalent Production. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 594081.	2.0	23
86	Promiscuous phosphoketolase and metabolic rewiring enables novel non-oxidative glycolysis in yeast for high-yield production of acetyl-CoA derived products. <i>Metabolic Engineering</i> , 2020, 62, 150-160.	3.6	30
87	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	5.8	122
88	Deep learning suggests that gene expression is encoded in all parts of a co-evolving interacting gene regulatory structure. <i>Nature Communications</i> , 2020, 11, 6141.	5.8	83
89	Pathway engineering in yeast for synthesizing the complex polyketide bikaverin. <i>Nature Communications</i> , 2020, 11, 6197.	5.8	29
90	Different Routes of Protein Folding Contribute to Improved Protein Production in <i>Saccharomyces cerevisiae</i> . <i>MBio</i> , 2020, 11, .	1.8	12

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91	Rewiring Central Carbon Metabolism Ensures Increased Provision of Acetyl-CoA and NADPH Required for 3-OH-Propionic Acid Production. <i>ACS Synthetic Biology</i> , 2020, 9, 3236-3244.	1.9	36
92	Proteome reallocation from amino acid biosynthesis to ribosomes enables yeast to grow faster in rich media. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 21804-21812.	3.3	44
93	Elucidating aromatic acid tolerance at low pH in <i>Saccharomyces cerevisiae</i> using adaptive laboratory evolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 27954-27961.	3.3	40
94	Engineering carboxylic acid reductase for selective synthesis of medium-chain fatty alcohols in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 22974-22983.	3.3	27
95	Sources of variation in cell-type RNA-Seq profiles. <i>PLoS ONE</i> , 2020, 15, e0239495.	1.1	20
96	Editorial: yeast synthetic biology. <i>FEMS Yeast Research</i> , 2020, 20, .	1.1	0
97	Expressing a cytosolic pyruvate dehydrogenase complex to increase free fatty acid production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2020, 19, 226.	1.9	19
98	Evolution from adherent to suspension: systems biology of HEK293 cell line development. <i>Scientific Reports</i> , 2020, 10, 18996.	1.6	49
99	Stress-induced expression is enriched for evolutionarily young genes in diverse budding yeasts. <i>Nature Communications</i> , 2020, 11, 2144.	5.8	24
100	Quantitative analysis of amino acid metabolism in liver cancer links glutamate excretion to nucleotide synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 10294-10304.	3.3	45
101	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020, 581, 310-315.	13.7	283
102	Absolute yeast mitochondrial proteome quantification reveals trade-off between biosynthesis and energy generation during diauxic shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 7524-7535.	3.3	92
103	Rewiring carbon flux in <i>Escherichia coli</i> using a bifunctional molecular switch. <i>Metabolic Engineering</i> , 2020, 61, 47-57.	3.6	34
104	Current Status of COVID-19 Therapies and Drug Repositioning Applications. <i>IScience</i> , 2020, 23, 101303.	1.9	77
105	Bioprospecting Through Cloning of Whole Natural Product Biosynthetic Gene Clusters. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 526.	2.0	14
106	Third-generation biorefineries as the means to produce fuels and chemicals from CO ₂ . <i>Nature Catalysis</i> , 2020, 3, 274-288.	16.1	245
107	Exercise-Mediated Lowering of Glutamine Availability Suppresses Tumor Growth and Attenuates Muscle Wasting. <i>IScience</i> , 2020, 23, 100978.	1.9	10
108	Molecular natural history of breast cancer: Leveraging transcriptomics to predict breast cancer progression and aggressiveness. <i>Cancer Medicine</i> , 2020, 9, 3551-3562.	1.3	8

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109	Building blocks are synthesized on demand during the yeast cell cycle. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7575-7583.	3.3	32
110	An atlas of human metabolism. Science Signaling, 2020, 13, .	1.6	223
111	The transcription factor Leu3 shows differential binding behavior in response to changing leucine availability. FEMS Microbiology Letters, 2020, 367, .	0.7	1
112	Metabolic Engineering of <i>Saccharomyces cerevisiae</i> for Rosmarinic Acid Production. ACS Synthetic Biology, 2020, 9, 1978-1988.	1.9	25
113	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
114	Current state of aromatics production using yeast: achievements and challenges. Current Opinion in Biotechnology, 2020, 65, 65-74.	3.3	35
115	Multidimensional engineering of <i>Saccharomyces cerevisiae</i> for efficient synthesis of medium-chain fatty acids. Nature Catalysis, 2020, 3, 64-74.	16.1	80
116	Comprehensive understanding of <i>Saccharomyces cerevisiae</i> phenotypes with whole-cell model WM_S288C. Biotechnology and Bioengineering, 2020, 117, 1562-1574.	1.7	23
117	The acute effect of metabolic cofactor supplementation: a potential therapeutic strategy against non-alcoholic fatty liver disease. Molecular Systems Biology, 2020, 16, e9495.	3.2	39
118	Improvement in the Current Therapies for Hepatocellular Carcinoma Using a Systems Medicine Approach. Advanced Biology, 2020, 4, e2000030.	3.0	7
119	Nitrogen limitation reveals large reserves in metabolic and translational capacities of yeast. Nature Communications, 2020, 11, 1881.	5.8	51
120	Meta-analysis of the gut microbiota in predicting response to cancer immunotherapy in metastatic melanoma. JCI Insight, 2020, 5, .	2.3	85
121	DSAVE: Detection of misclassified cells in single-cell RNA-Seq data. PLoS ONE, 2020, 15, e0243360.	1.1	2
122	Integrated Metabolic Modeling, Culturing, and Transcriptomics Explain Enhanced Virulence of <i>Vibrio cholerae</i> during Coinfection with Enterotoxigenic <i>Escherichia coli</i> . MSystems, 2020, 5, .	1.7	8
123	A consensus <i>S. cerevisiae</i> metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. Nature Communications, 2019, 10, 3586.	5.8	217
124	Expanding the Dynamic Range of a Transcription Factor-Based Biosensor in <i>Saccharomyces cerevisiae</i> . ACS Synthetic Biology, 2019, 8, 1968-1975.	1.9	44
125	FadR-Based Biosensor-Assisted Screening for Genes Enhancing Fatty Acyl-CoA Pools in <i>Saccharomyces cerevisiae</i> . ACS Synthetic Biology, 2019, 8, 1788-1800.	1.9	44
126	ChIP-exo analysis highlights Fkh1 and Fkh2 transcription factors as hubs that integrate multi-scale networks in budding yeast. Nucleic Acids Research, 2019, 47, 7825-7841.	6.5	11

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127	Modelling approaches for studying the microbiome. <i>Nature Microbiology</i> , 2019, 4, 1253-1267.	5.9	114
128	Metagenomic analysis of bile salt biotransformation in the human gut microbiome. <i>BMC Genomics</i> , 2019, 20, 517.	1.2	44
129	Systems biology perspective for studying the gut microbiota in human physiology and liver diseases. <i>EBioMedicine</i> , 2019, 49, 364-373.	2.7	25
130	Big data in yeast systems biology. <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	15
131	Carbohydrate active enzymes are affected by diet transition from milk to solid food in infant gut microbiota. <i>FEMS Microbiology Ecology</i> , 2019, 95, .	1.3	10
132	Identification and characterisation of two high-affinity glucose transporters from the spoilage yeast <i>Brettanomyces bruxellensis</i> . <i>FEMS Microbiology Letters</i> , 2019, 366, .	0.7	9
133	Complex I is bypassed during high intensity exercise. <i>Nature Communications</i> , 2019, 10, 5072.	5.8	32
134	Reconstruction and analysis of a <i>Kluyveromyces marxianus</i> genome-scale metabolic model. <i>BMC Bioinformatics</i> , 2019, 20, 551.	1.2	38
135	Rewiring carbon metabolism in yeast for high level production of aromatic chemicals. <i>Nature Communications</i> , 2019, 10, 4976.	5.8	177
136	Metabolic engineering and transcriptomic analysis of <i>Saccharomyces cerevisiae</i> producing p-coumaric acid from xylose. <i>Microbial Cell Factories</i> , 2019, 18, 191.	1.9	26
137	Genome-scale model of <i>Rhodotorula toruloides</i> metabolism. <i>Biotechnology and Bioengineering</i> , 2019, 116, 3396-3408.	1.7	55
138	Yeast cells handle stress by reprogramming their metabolism. <i>Nature</i> , 2019, 572, 184-185.	13.7	8
139	A bioinformatic pipeline to analyze ChIP-exo datasets. <i>Biology Methods and Protocols</i> , 2019, 4, bpz011.	1.0	3
140	Adaptive laboratory evolution of tolerance to dicarboxylic acids in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019, 56, 130-141.	3.6	63
141	The pan-genome of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	1.1	12
142	Model-Assisted Fine-Tuning of Central Carbon Metabolism in Yeast through dCas9-Based Regulation. <i>ACS Synthetic Biology</i> , 2019, 8, 2457-2463.	1.9	39
143	Construction of mini-chemostats for high-throughput strain characterization. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1029-1038.	1.7	16
144	SLIMER: probing flexibility of lipid metabolism in yeast with an improved constraint-based modeling framework. <i>BMC Systems Biology</i> , 2019, 13, 4.	3.0	43

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145	Antibiotic Lethality Is Impacted by Nutrient Availabilities: New Insights from Machine Learning. <i>Cell</i> , 2019, 177, 1373-1374.	13.5	1
146	Engineering <i>Saccharomyces cerevisiae</i> cells for production of fatty acid-derived biofuels and chemicals. <i>Open Biology</i> , 2019, 9, 190049.	1.5	56
147	Dysregulated autophagy in muscle precursor cells from humans with type 2 diabetes. <i>Scientific Reports</i> , 2019, 9, 8169.	1.6	16
148	Proteome analysis of xylose metabolism in <i>Rhodotorula toruloides</i> during lipid production. <i>Biotechnology for Biofuels</i> , 2019, 12, 137.	6.2	61
149	Recent trends in metabolic engineering of microbial chemical factories. <i>Current Opinion in Biotechnology</i> , 2019, 60, 188-197.	3.3	88
150	Machine Learning Applied to Predicting Microorganism Growth Temperatures and Enzyme Catalytic Optima. <i>ACS Synthetic Biology</i> , 2019, 8, 1411-1420.	1.9	100
151	Comparative Transcriptome Analysis Shows Conserved Metabolic Regulation during Production of Secondary Metabolites in Filamentous Fungi. <i>MSystems</i> , 2019, 4, .	1.7	12
152	Cell factory engineering for improved production of natural products. <i>Natural Product Reports</i> , 2019, 36, 1233-1236.	5.2	37
153	RNAi expression tuning, microfluidic screening, and genome recombineering for improved protein production in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 9324-9332.	3.3	54
154	A gRNA-tRNA array for CRISPR-Cas9 based rapid multiplexed genome editing in <i>Saccharomyces cerevisiae</i> . <i>Nature Communications</i> , 2019, 10, 1053.	5.8	164
155	A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome. <i>Cell Reports</i> , 2019, 26, 2622-2635.e5.	2.9	57
156	Simplified Intestinal Microbiota to Study Microbe-Diet-Host Interactions in a Mouse Model. <i>Cell Reports</i> , 2019, 26, 3772-3783.e6.	2.9	61
157	Strategies and challenges for metabolic rewiring. <i>Current Opinion in Systems Biology</i> , 2019, 15, 30-38.	1.3	27
158	Identification of genes involved in shea butter biosynthesis from <i>Vitellaria paradoxa</i> fruits through transcriptomics and functional heterologous expression. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 3727-3736.	1.7	19
159	Heterologous phosphoketolase expression redirects flux towards acetate, perturbs sugar phosphate pools and increases respiratory demand in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2019, 18, 25.	1.9	27
160	Increasing jojoba-like wax ester production in <i>Saccharomyces cerevisiae</i> by enhancing very long-chain, monounsaturated fatty acid synthesis. <i>Microbial Cell Factories</i> , 2019, 18, 49.	1.9	20
161	Predictive models of eukaryotic transcriptional regulation reveals changes in transcription factor roles and promoter usage between metabolic conditions. <i>Nucleic Acids Research</i> , 2019, 47, 4986-5000.	6.5	20
162	Yeast Systems Biology: Model Organism and Cell Factory. <i>Biotechnology Journal</i> , 2019, 14, e1800421.	1.8	159

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163	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. ACS Synthetic Biology, 2019, 8, 976-988.	1.9	1
164	Effects of overexpression of <i>STB5</i> in <i>Saccharomyces cerevisiae</i> on fatty acid biosynthesis, physiology and transcriptome. FEMS Yeast Research, 2019, 19, .	1.1	8
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