

Jens B Nielsen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7159920/publications.pdf>

Version: 2024-02-01

895
papers

85,682
citations

511

128
h-index

932

240
g-index

1010
all docs

1010
docs citations

1010
times ranked

79571
citing authors

#	ARTICLE	IF	CITATIONS
1	Multiscale models quantifying yeast physiology: towards a whole-cell model. Trends in Biotechnology, 2022, 40, 291-305.	9.3	20
2	Microbial production of chemicals driven by CRISPR-Cas systems. Current Opinion in Biotechnology, 2022, 73, 34-42.	6.6	16
3	Professor John Villadsen, PhD, Dr. techn., Dr. h. c. mult (12.6.1936â€“22.7.2021). Biotechnology and Bioengineering, 2022, 119, 7-8.	3.3	0
4	Yeast synthetic biology advances biofuel production. Current Opinion in Microbiology, 2022, 65, 33-39.	5.1	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.	12.1	53
6	Genome-scale modeling of yeast metabolism: retrospectives and perspectives. FEMS Yeast Research, 2022, 22, .	2.3	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, .	7.1	11
8	Analysis of normal levels of free glycosaminoglycans in urine and plasma in adults. Journal of Biological Chemistry, 2022, 298, 101575.	3.4	13
9	Multimics Analysis Reveals the Impact of Microbiota on Host Metabolism in Hepatic Steatosis. Advanced Science, 2022, 9, e2104373.	11.2	23
10	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies. Nature Communications, 2022, 13, 801.	12.8	47
11	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	30.7	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, .	1.8	5
13	A Gene Co-Expression Network-Based Drug Repositioning Approach Identifies Candidates for Treatment of Hepatocellular Carcinoma. Cancers, 2022, 14, 1573.	3.7	8
14	Prediction of drug candidates for clear cell renal cell carcinoma using a systems biology-based drug repositioning approach. EBioMedicine, 2022, 78, 103963.	6.1	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.	3.8	14
16	Innovation trends in industrial biotechnology. Trends in Biotechnology, 2022, 40, 1160-1172.	9.3	30
17	The integration of bio-catalysis and electrocatalysis to produce fuels and chemicals from carbon dioxide. Chemical Society Reviews, 2022, 51, 4763-4785.	38.1	32
18	Improving recombinant protein production by yeast through genome-scale modeling using proteome constraints. Nature Communications, 2022, 13, .	12.8	18

#	ARTICLE	IF	CITATIONS
19	Proteome allocations change linearly with the specific growth rate of <i>Saccharomyces cerevisiae</i> under glucose limitation. <i>Nature Communications</i> , 2022, 13, .	12.8	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, .	2.3	2
21	Enhanced metabolism and negative regulation of ER stress support higher erythropoietin production in HEK293 cells. <i>Cell Reports</i> , 2022, 39, 110936.	6.4	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.	3.7	6
23	Reconstruction of a catalogue of genome-scale metabolic models with enzymatic constraints using GECKO 2.0. <i>Nature Communications</i> , 2022, 13, .	12.8	39
24	Deep learning-based kcat prediction enables improved enzyme-constrained model reconstruction. <i>Nature Catalysis</i> , 2022, 5, 662-672.	34.4	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, .	7.1	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.	0.4	5
27	The Translational Status of Cancer Liquid Biopsies. <i>Regenerative Engineering and Translational Medicine</i> , 2021, 7, 312-352.	2.9	39
28	Addressing the heterogeneity in liver diseases using biological networks. <i>Briefings in Bioinformatics</i> , 2021, 22, 1751-1766.	6.5	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.	6.0	28
30	Systems biology based drug repositioning for development of cancer therapy. <i>Seminars in Cancer Biology</i> , 2021, 68, 47-58.	9.6	54
31	Performance of Regression Models as a Function of Experiment Noise. <i>Bioinformatics and Biology Insights</i> , 2021, 15, 117793222110203.	2.0	9
32	Bayesian genome scale modelling identifies thermal determinants of yeast metabolism. <i>Nature Communications</i> , 2021, 12, 190.	12.8	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, .	2.3	4
35	Yeast based biorefineries for oleochemical production. <i>Current Opinion in Biotechnology</i> , 2021, 67, 26-34.	6.6	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.	2.2	13

#	ARTICLE	IF	CITATIONS
37	Mathematical modeling of proteome constraints within metabolism. <i>Current Opinion in Systems Biology</i> , 2021, 25, 50-56.	2.6	36
38	Production of Î²-carotene in <i>Saccharomyces cerevisiae</i> through altering yeast lipid metabolism. <i>Biotechnology and Bioengineering</i> , 2021, 118, 2043-2052.	3.3	30
39	Quantifying absolute gene expression profiles reveals distinct regulation of central carbon metabolism genes in yeast. <i>ELife</i> , 2021, 10, .	6.0	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.	3.7	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, .	7.1	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, .	7.1	22
43	Fatty acid synthesis is required for breast cancer brain metastasis. <i>Nature Cancer</i> , 2021, 2, 414-428.	13.2	147
44	Machine learning-based investigation of the cancer protein secretory pathway. <i>PLoS Computational Biology</i> , 2021, 17, e1008898.	3.2	7
45	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021, 49, W271-W276.	14.5	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.	3.2	16
47	Proteome constraints reveal targets for improving microbial fitness in nutrient-rich environments. <i>Molecular Systems Biology</i> , 2021, 17, e10093.	7.2	46
48	Informing Pharmacokinetic Models With Physiological Data: Oral Population Modeling of L-Serine in Humans. <i>Frontiers in Pharmacology</i> , 2021, 12, 643179.	3.5	3
49	Draft Genome Sequences of Five Fungal Strains Isolated from Kefir. <i>Microbiology Resource Announcements</i> , 2021, 10, e0019521.	0.6	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.	3.8	10
51	Strategies and challenges with the microbial conversion of methanol to high-value chemicals. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3655-3668.	3.3	12
52	Engineering yeast metabolism for the discovery and production of polyamines and polyamine analogues. <i>Nature Catalysis</i> , 2021, 4, 498-509.	34.4	26
53	BUTTERFLY: addressing the pooled amplification paradox with unique molecular identifiers in single-cell RNA-seq. <i>Genome Biology</i> , 2021, 22, 174.	8.8	5
54	Combined Metabolic Activators Accelerates Recovery in Mild-to-Moderate COVID-19. <i>Advanced Science</i> , 2021, 8, e2101222.	11.2	49

#	ARTICLE	IF	CITATIONS
55	Genome-scale insights into the metabolic versatility of <i>Limosilactobacillus reuteri</i> . <i>BMC Biotechnology</i> , 2021, 21, 46.	3.3	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, .	7.1	48
57	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	19.0	403
58	Rational gRNA design based on transcription factor binding data. <i>Synthetic Biology</i> , 2021, 6, ysab014.	2.2	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.	2.3	8
60	Stratification of patients with clear cell renal cell carcinoma to facilitate drug repositioning. <i>IScience</i> , 2021, 24, 102722.	4.1	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.	4.0	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, .	3.0	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, .	7.1	22
64	The yeastGemMap: A process diagram to assist yeast systems metabolic studies. <i>Biotechnology and Bioengineering</i> , 2021, 118, 4800-4814.	3.3	1
65	Metabolic network remodelling enhances yeast's fitness on xylose using aerobic glycolysis. <i>Nature Catalysis</i> , 2021, 4, 783-796.	34.4	23
66	A single chromosome strain of <i>S. cerevisiae</i> exhibits diminished ethanol metabolism and tolerance. <i>BMC Genomics</i> , 2021, 22, 688.	2.8	2
67	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	13.3	138
68	De novo biosynthesis of bioactive isoflavonoids by engineered yeast cell factories. <i>Nature Communications</i> , 2021, 12, 6085.	12.8	62
69	Combined metabolic activators therapy ameliorates liver fat in nonalcoholic fatty liver disease patients. <i>Molecular Systems Biology</i> , 2021, 17, e10459.	7.2	22
70	Yeast metabolic innovations emerged via expanded metabolic network and gene positive selection. <i>Molecular Systems Biology</i> , 2021, 17, e10427.	7.2	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.	4.1	7
72	Microbial community dynamics revisited. <i>Nature Computational Science</i> , 2021, 1, 640-641.	8.0	2

#	ARTICLE	IF	CITATIONS
73	A network-based approach reveals the dysregulated transcriptional regulation in non-alcoholic fatty liver disease. <i>IScience</i> , 2021, 24, 103222.	4.1	14
74	Synthetic Biology Advanced Natural Product Discovery. <i>Metabolites</i> , 2021, 11, 785.	2.9	8
75	Combinatorial, additive and dose-dependent drug-microbiome associations. <i>Nature</i> , 2021, 600, 500-505.	27.8	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, .	7.1	40
77	Pan-cancer analysis of the metabolic reaction network. <i>Metabolic Engineering</i> , 2020, 57, 51-62.	7.0	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.	3.7	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.	12.8	74
80	Engineering yeast phospholipid metabolism for de novo oleoylethanolamide production. <i>Nature Chemical Biology</i> , 2020, 16, 197-205.	8.0	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.	4.1	31
82	Yeast systems biology in understanding principles of physiology underlying complex human diseases. <i>Current Opinion in Biotechnology</i> , 2020, 63, 63-69.	6.6	7
83	Applications of Genome-Wide Screening and Systems Biology Approaches in Drug Repositioning. <i>Cancers</i> , 2020, 12, 2694.	3.7	14
84	Combining mechanistic and machine learning models for predictive engineering and optimization of tryptophan metabolism. <i>Nature Communications</i> , 2020, 11, 4880.	12.8	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.	4.1	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.	7.0	30
87	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. <i>Nature Communications</i> , 2020, 11, 5881.	12.8	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.	12.8	83
89	Pathway engineering in yeast for synthesizing the complex polyketide bikaverin. <i>Nature Communications</i> , 2020, 11, 6197.	12.8	29
90	Different Routes of Protein Folding Contribute to Improved Protein Production in <i>Saccharomyces cerevisiae</i> . <i>MBio</i> , 2020, 11, .	4.1	12

#	ARTICLE	IF	CITATIONS
91	Rewiring Central Carbon Metabolism Ensures Increased Provision of Acetyl-CoA and NADPH Required for 3-OH-Propionic Acid Production. ACS Synthetic Biology, 2020, 9, 3236-3244.	3.8	36
92	Proteome reallocation from amino acid biosynthesis to ribosomes enables yeast to grow faster in rich media. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 21804-21812.	7.1	44
93	Elucidating aromatic acid tolerance at low pH in <i>Saccharomyces cerevisiae</i> using adaptive laboratory evolution. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 27954-27961.	7.1	40
94	Engineering carboxylic acid reductase for selective synthesis of medium-chain fatty alcohols in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22974-22983.	7.1	27
95	Sources of variation in cell-type RNA-Seq profiles. PLoS ONE, 2020, 15, e0239495.	2.5	20
96	Editorial: yeast synthetic biology. FEMS Yeast Research, 2020, 20, .	2.3	0
97	Expressing a cytosolic pyruvate dehydrogenase complex to increase free fatty acid production in <i>Saccharomyces cerevisiae</i> . Microbial Cell Factories, 2020, 19, 226.	4.0	19
98	Evolution from adherent to suspension: systems biology of HEK293 cell line development. Scientific Reports, 2020, 10, 18996.	3.3	49
99	Stress-induced expression is enriched for evolutionarily young genes in diverse budding yeasts. Nature Communications, 2020, 11, 2144.	12.8	24
100	Quantitative analysis of amino acid metabolism in liver cancer links glutamate excretion to nucleotide synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10294-10304.	7.1	45
101	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	27.8	283
102	Absolute yeast mitochondrial proteome quantification reveals trade-off between biosynthesis and energy generation during diauxic shift. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7524-7535.	7.1	92
103	Rewiring carbon flux in <i>Escherichia coli</i> using a bifunctional molecular switch. Metabolic Engineering, 2020, 61, 47-57.	7.0	34
104	Current Status of COVID-19 Therapies and Drug Repositioning Applications. IScience, 2020, 23, 101303.	4.1	77
105	Bioprospecting Through Cloning of Whole Natural Product Biosynthetic Gene Clusters. Frontiers in Bioengineering and Biotechnology, 2020, 8, 526.	4.1	14
106	Third-generation biorefineries as the means to produce fuels and chemicals from CO ₂ . Nature Catalysis, 2020, 3, 274-288.	34.4	245
107	Exercise-Mediated Lowering of Glutamine Availability Suppresses Tumor Growth and Attenuates Muscle Wasting. IScience, 2020, 23, 100978.	4.1	10
108	Molecular natural history of breast cancer: Leveraging transcriptomics to predict breast cancer progression and aggressiveness. Cancer Medicine, 2020, 9, 3551-3562.	2.8	8

#	ARTICLE	IF	CITATIONS
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.	7.1	32
110	An atlas of human metabolism. Science Signaling, 2020, 13, .	3.6	223
111	The transcription factor Leu3 shows differential binding behavior in response to changing leucine availability. FEMS Microbiology Letters, 2020, 367, .	1.8	1
112	Metabolic Engineering of <i>Saccharomyces cerevisiae</i> for Rosmarinic Acid Production. ACS Synthetic Biology, 2020, 9, 1978-1988.	3.8	25
113	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
114	Current state of aromatics production using yeast: achievements and challenges. Current Opinion in Biotechnology, 2020, 65, 65-74.	6.6	35
115	Multidimensional engineering of <i>Saccharomyces cerevisiae</i> for efficient synthesis of medium-chain fatty acids. Nature Catalysis, 2020, 3, 64-74.	34.4	80
116	Comprehensive understanding of <i>Saccharomyces cerevisiae</i> phenotypes with whole-cell model WM_S288C. Biotechnology and Bioengineering, 2020, 117, 1562-1574.	3.3	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.	7.2	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.	12.8	51
120	Meta-analysis of the gut microbiota in predicting response to cancer immunotherapy in metastatic melanoma. JCI Insight, 2020, 5, .	5.0	85
121	DSAVE: Detection of misclassified cells in single-cell RNA-Seq data. PLoS ONE, 2020, 15, e0243360.	2.5	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, .	3.8	8
123	A consensus <i>S. cerevisiae</i> metabolic model Yeast8 and its ecosystem for comprehensively probing cellular metabolism. Nature Communications, 2019, 10, 3586.	12.8	217
124	Expanding the Dynamic Range of a Transcription Factor-Based Biosensor in <i>Saccharomyces cerevisiae</i> . ACS Synthetic Biology, 2019, 8, 1968-1975.	3.8	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.	3.8	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.	14.5	11

#	ARTICLE	IF	CITATIONS
127	Modelling approaches for studying the microbiome. <i>Nature Microbiology</i> , 2019, 4, 1253-1267.	13.3	114
128	Metagenomic analysis of bile salt biotransformation in the human gut microbiome. <i>BMC Genomics</i> , 2019, 20, 517.	2.8	44
129	Systems biology perspective for studying the gut microbiota in human physiology and liver diseases. <i>EBioMedicine</i> , 2019, 49, 364-373.	6.1	25
130	Big data in yeast systems biology. <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	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, .	2.7	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, .	1.8	9
133	Complex I is bypassed during high intensity exercise. <i>Nature Communications</i> , 2019, 10, 5072.	12.8	32
134	Reconstruction and analysis of a <i>Kluyveromyces marxianus</i> genome-scale metabolic model. <i>BMC Bioinformatics</i> , 2019, 20, 551.	2.6	38
135	Rewiring carbon metabolism in yeast for high level production of aromatic chemicals. <i>Nature Communications</i> , 2019, 10, 4976.	12.8	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.	4.0	26
137	Genome-scale model of <i>Rhodotorula toruloides</i> metabolism. <i>Biotechnology and Bioengineering</i> , 2019, 116, 3396-3408.	3.3	55
138	Yeast cells handle stress by reprogramming their metabolism. <i>Nature</i> , 2019, 572, 184-185.	27.8	8
139	A bioinformatic pipeline to analyze ChIP-exo datasets. <i>Biology Methods and Protocols</i> , 2019, 4, bpz011.	2.2	3
140	Adaptive laboratory evolution of tolerance to dicarboxylic acids in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2019, 56, 130-141.	7.0	63
141	The pan-genome of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2019, 19, .	2.3	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.	3.8	39
143	Construction of mini-chemostats for high-throughput strain characterization. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1029-1038.	3.3	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

#	ARTICLE	IF	CITATIONS
145	Antibiotic Lethality Is Impacted by Nutrient Availabilities: New Insights from Machine Learning. <i>Cell</i> , 2019, 177, 1373-1374.	28.9	1
146	Engineering <i>Saccharomyces cerevisiae</i> cells for production of fatty acid-derived biofuels and chemicals. <i>Open Biology</i> , 2019, 9, 190049.	3.6	56
147	Dysregulated autophagy in muscle precursor cells from humans with type 2 diabetes. <i>Scientific Reports</i> , 2019, 9, 8169.	3.3	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.	6.6	88
150	Machine Learning Applied to Predicting Microorganism Growth Temperatures and Enzyme Catalytic Optima. <i>ACS Synthetic Biology</i> , 2019, 8, 1411-1420.	3.8	100
151	Comparative Transcriptome Analysis Shows Conserved Metabolic Regulation during Production of Secondary Metabolites in Filamentous Fungi. <i>MSystems</i> , 2019, 4, .	3.8	12
152	Cell factory engineering for improved production of natural products. <i>Natural Product Reports</i> , 2019, 36, 1233-1236.	10.3	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.	7.1	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.	12.8	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.	6.4	57
156	Simplified Intestinal Microbiota to Study Microbe-Diet-Host Interactions in a Mouse Model. <i>Cell Reports</i> , 2019, 26, 3772-3783.e6.	6.4	61
157	Strategies and challenges for metabolic rewiring. <i>Current Opinion in Systems Biology</i> , 2019, 15, 30-38.	2.6	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.	3.6	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.	4.0	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.	4.0	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.	14.5	20
162	Yeast Systems Biology: Model Organism and Cell Factory. <i>Biotechnology Journal</i> , 2019, 14, e1800421.	3.5	159

#	ARTICLE	IF	CITATIONS
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.	3.8	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, .	2.3	8
165	Harnessing xylose pathways for biofuels production. Current Opinion in Biotechnology, 2019, 57, 56-65.	6.6	71
166	Energy metabolism controls phenotypes by protein efficiency and allocation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 17592-17597.	7.1	96
167	The human secretome. Science Signaling, 2019, 12, .	3.6	259
168	Comparative genomics study reveals Red Sea Bacillus with characteristics associated with potential microbial cell factories (MCFs). Scientific Reports, 2019, 9, 19254.	3.3	6
169	Tackling Cancer with Yeast-Based Technologies. Trends in Biotechnology, 2019, 37, 592-603.	9.3	35
170	Lipid engineering combined with systematic metabolic engineering of <i>Saccharomyces cerevisiae</i> for high-yield production of lycopene. Metabolic Engineering, 2019, 52, 134-142.	7.0	251
171	Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. EBioMedicine, 2019, 40, 471-487.	6.1	38
172	Pyruvate kinase L/R is a regulator of lipid metabolism and mitochondrial function. Metabolic Engineering, 2019, 52, 263-272.	7.0	37
173	<i>Saccharomyces cerevisiae</i> displays a stable transcription start site landscape in multiple conditions. FEMS Yeast Research, 2019, 19, .	2.3	10
174	Synthetic Biology of Yeast. Biochemistry, 2019, 58, 1511-1520.	2.5	28
175	Genome-Scale Metabolic Modeling from Yeast to Human Cell Models of Complex Diseases: Latest Advances and Challenges. Methods in Molecular Biology, 2019, 2049, 329-345.	0.9	14
176	Recon3D enables a three-dimensional view of gene variation in human metabolism. Nature Biotechnology, 2018, 36, 272-281.	17.5	520
177	Targeting <i>CDK2</i> overcomes melanoma resistance against <i>BRAF</i> and Hsp90 inhibitors. Molecular Systems Biology, 2018, 14, e7858.	7.2	53
178	Metabolite secretion in microorganisms: the theory of metabolic overflow put to the test. Metabolomics, 2018, 14, 43.	3.0	66
179	Systems biology in hepatology: approaches and applications. Nature Reviews Gastroenterology and Hepatology, 2018, 15, 365-377.	17.8	117
180	Metabolite Depletion Affects Flux Profiling of Cell Lines. Trends in Biochemical Sciences, 2018, 43, 395-397.	7.5	8

#	ARTICLE	IF	CITATIONS
181	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for overproduction of triacylglycerols. <i>Metabolic Engineering Communications</i> , 2018, 6, 22-27.	3.6	63
182	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , 2018, 27, 559-571.e5.	16.2	321
183	Complete genomic and transcriptional landscape analysis using third-generation sequencing: a case study of <i>Saccharomyces cerevisiae</i> CEN.PK113-7D. <i>Nucleic Acids Research</i> , 2018, 46, e38-e38.	14.5	116
184	Redirection of lipid flux toward phospholipids in yeast increases fatty acid turnover and secretion. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 1262-1267.	7.1	51
185	Advancing biotechnology with CRISPR/Cas9: recent applications and patent landscape. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2018, 45, 467-480.	3.0	23
186	Engineering 1-Alkene Biosynthesis and Secretion by Dynamic Regulation in Yeast. <i>ACS Synthetic Biology</i> , 2018, 7, 584-590.	3.8	59
187	Modulation of saturation and chain length of fatty acids in <i>Saccharomyces cerevisiae</i> for production of cocoa butter-like lipids. <i>Biotechnology and Bioengineering</i> , 2018, 115, 932-942.	3.3	24
188	Screening of 2A peptides for polycistronic gene expression in yeast. <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	45
189	DCEO Biotechnology: Tools To Design, Construct, Evaluate, and Optimize the Metabolic Pathway for Biosynthesis of Chemicals. <i>Chemical Reviews</i> , 2018, 118, 4-72.	47.7	141
190	TCSBN: a database of tissue and cancer specific biological networks. <i>Nucleic Acids Research</i> , 2018, 46, D595-D600.	14.5	55
191	High-Throughput Microfluidics for the Screening of Yeast Libraries. <i>Methods in Molecular Biology</i> , 2018, 1671, 307-317.	0.9	8
192	Heterologous transporter expression for improved fatty alcohol secretion in yeast. <i>Metabolic Engineering</i> , 2018, 45, 51-58.	7.0	57
193	Multiplexed CRISPR/Cas9 Genome Editing and Gene Regulation Using Csy4 in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2018, 7, 10-15.	3.8	82
194	Metabolic network-based stratification of hepatocellular carcinoma reveals three distinct tumor subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11874-E11883.	7.1	149
195	Engineering the protein secretory pathway of <i>Saccharomyces cerevisiae</i> enables improved protein production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11025-E11032.	7.1	72
196	Identification of the decumbenone biosynthetic gene cluster in <i>Penicillium decumbens</i> and the importance for production of calbistrin. <i>Fungal Biology and Biotechnology</i> , 2018, 5, 18.	5.1	23
197	Regulation of Yeast-to-Hyphae Transition in <i>Yarrowia lipolytica</i> . <i>MSphere</i> , 2018, 3, .	2.9	35
198	Changes in lipid metabolism convey acid tolerance in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology for Biofuels</i> , 2018, 11, 297.	6.2	60

#	ARTICLE	IF	CITATIONS
199	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on <i>Streptomyces coelicolor</i> . PLoS Computational Biology, 2018, 14, e1006541.	3.2	228
200	Impact of forced fatty acid synthesis on metabolism and physiology of <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2018, 18, .	2.3	10
201	Yeast mitochondria: an overview of mitochondrial biology and the potential of mitochondrial systems biology. FEMS Yeast Research, 2018, 18, .	2.3	94
202	Plasma Glycosaminoglycans as Diagnostic and Prognostic Biomarkers in Surgically Treated Renal Cell Carcinoma. European Urology Oncology, 2018, 1, 364-377.	5.4	21
203	Barriers and opportunities in bio-based production of hydrocarbons. Nature Energy, 2018, 3, 925-935.	39.5	146
204	Gut microbiota dysbiosis is associated with malnutrition and reduced plasma amino acid levels: Lessons from genome-scale metabolic modeling. Metabolic Engineering, 2018, 49, 128-142.	7.0	65
205	Challenges in modeling the human gut microbiome. Nature Biotechnology, 2018, 36, 682-686.	17.5	25
206	Drug Repositioning for Effective Prostate Cancer Treatment. Frontiers in Physiology, 2018, 9, 500.	2.8	85
207	Metabolic Network-Based Identification and Prioritization of Anticancer Targets Based on Expression Data in Hepatocellular Carcinoma. Frontiers in Physiology, 2018, 9, 916.	2.8	38
208	Global rewiring of cellular metabolism renders <i>Saccharomyces cerevisiae</i> Crabtree negative. Nature Communications, 2018, 9, 3059.	12.8	79
209	Reconstruction of a Global Transcriptional Regulatory Network for Control of Lipid Metabolism in Yeast by Using Chromatin Immunoprecipitation with Lambda Exonuclease Digestion. MSystems, 2018, 3, .	3.8	32
210	Glucose-Dependent Promoters for Dynamic Regulation of Metabolic Pathways. Frontiers in Bioengineering and Biotechnology, 2018, 6, 63.	4.1	27
211	Expression of cocoa genes in <i>Saccharomyces cerevisiae</i> improves cocoa butter production. Microbial Cell Factories, 2018, 17, 11.	4.0	21
212	Balanced trafficking between the ER and the Golgi apparatus increases protein secretion in yeast. AMB Express, 2018, 8, 37.	3.0	21
213	Modular Pathway Rewiring of Yeast for Amino Acid Production. Methods in Enzymology, 2018, 608, 417-439.	1.0	12
214	Integrated analysis of the yeast NADPH-regulator Stb5 reveals distinct differences in NADPH requirements and regulation in different states of yeast metabolism. FEMS Yeast Research, 2018, 18, .	2.3	11
215	Reprogramming Yeast Metabolism from Alcoholic Fermentation to Lipogenesis. Cell, 2018, 174, 1549-1558.e14.	28.9	215
216	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of fatty acid-derived hydrocarbons. Biotechnology and Bioengineering, 2018, 115, 2139-2147.	3.3	25

#	ARTICLE	IF	CITATIONS
217	Reconstruction of 24 <i>Penicillium</i> genome-scale metabolic models shows diversity based on their secondary metabolism. <i>Biotechnology and Bioengineering</i> , 2018, 115, 2604-2612.	3.3	20
218	In vitro co-cultures of human gut bacterial species as predicted from co-occurrence network analysis. <i>PLoS ONE</i> , 2018, 13, e0195161.	2.5	41
219	Engineering lipid droplet assembly mechanisms for improved triacylglycerol accumulation in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2018, 18, .	2.3	16
220	A molecular genetic toolbox for <i>Yarrowia lipolytica</i> . <i>Biotechnology for Biofuels</i> , 2017, 10, 2.	6.2	62
221	Cocoa butter-like lipid production ability of non-oleaginous and oleaginous yeasts under nitrogen-limited culture conditions. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 3577-3585.	3.6	60
222	Expanding the product portfolio of fungal type I fatty acid synthases. <i>Nature Chemical Biology</i> , 2017, 13, 360-362.	8.0	97
223	Increasing cocoa butter-like lipid production of <i>Saccharomyces cerevisiae</i> by expression of selected cocoa genes. <i>AMB Express</i> , 2017, 7, 34.	3.0	24
224	Development of fungal cell factories for the production of secondary metabolites: Linking genomics and metabolism. <i>Synthetic and Systems Biotechnology</i> , 2017, 2, 5-12.	3.7	91
225	Systems Biology of Metabolism: A Driver for Developing Personalized and Precision Medicine. <i>Cell Metabolism</i> , 2017, 25, 572-579.	16.2	132
226	Personal model-assisted identification of NAD ⁺ and γ -glutathione metabolism as intervention target in NAFLD. <i>Molecular Systems Biology</i> , 2017, 13, 916.	7.2	147
227	Effects of acetoacetyl-CoA synthase expression on production of farnesene in <i>Saccharomyces cerevisiae</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 911-922.	3.0	30
228	Systematic inference of functional phosphorylation events in yeast metabolism. <i>Bioinformatics</i> , 2017, 33, 1995-2001.	4.1	9
229	Exploring the potential of <i>Saccharomyces cerevisiae</i> for biopharmaceutical protein production. <i>Current Opinion in Biotechnology</i> , 2017, 48, 77-84.	6.6	83
230	The yeast osmostress response is carbon source dependent. <i>Scientific Reports</i> , 2017, 7, 990.	3.3	55
231	Moderate Expression of <i>SEC16</i> Increases Protein Secretion by <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 2017, 83, .	3.1	43
232	Anticancer drug discovery through genome-scale metabolic modeling. <i>Current Opinion in Systems Biology</i> , 2017, 4, 1-8.	2.6	16
233	Metabolic engineering of yeast for fermentative production of flavonoids. <i>Bioresource Technology</i> , 2017, 245, 1645-1654.	9.6	129
234	Leucine Biosynthesis Is Involved in Regulating High Lipid Accumulation in <i>Yarrowia lipolytica</i> . <i>MBio</i> , 2017, 8, .	4.1	38

#	ARTICLE	IF	CITATIONS
235	Building a bio-based industry in the Middle East through harnessing the potential of the Red Sea biodiversity. <i>Applied Microbiology and Biotechnology</i> , 2017, 101, 4837-4851.	3.6	10
236	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of germacrene A, a precursor of beta-elemene. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2017, 44, 1065-1072.	3.0	43
237	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of very long chain fatty acid-derived chemicals. <i>Nature Communications</i> , 2017, 8, 15587.	12.8	82
238	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. <i>Nature Microbiology</i> , 2017, 2, 17044.	13.3	198
239	Absolute Quantification of Protein and mRNA Abundances Demonstrate Variability in Gene-Specific Translation Efficiency in Yeast. <i>Cell Systems</i> , 2017, 4, 495-504.e5.	6.2	178
240	In silico analysis of human metabolism: Reconstruction, contextualization and application of genome-scale models. <i>Current Opinion in Systems Biology</i> , 2017, 2, 29-38.	2.6	20
241	Systems Biology of Metabolism. <i>Annual Review of Biochemistry</i> , 2017, 86, 245-275.	11.1	173
242	Transcriptional reprogramming in yeast using dCas9 and combinatorial gRNA strategies. <i>Microbial Cell Factories</i> , 2017, 16, 46.	4.0	102
243	Dynamic regulation of fatty acid pools for improved production of fatty alcohols in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2017, 16, 45.	4.0	38
244	Engineering central metabolism – a grand challenge for plant biologists. <i>Plant Journal</i> , 2017, 90, 749-763.	5.7	78
245	Efficient protein production by yeast requires global tuning of metabolism. <i>Nature Communications</i> , 2017, 8, 1131.	12.8	80
246	Comparison of the metabolic response to over-production of p-coumaric acid in two yeast strains. <i>Metabolic Engineering</i> , 2017, 44, 265-272.	7.0	51
247	The Impact of Systems Biology on Bioprocessing. <i>Trends in Biotechnology</i> , 2017, 35, 1156-1168.	9.3	67
248	Network analyses identify liver-specific targets for treating liver diseases. <i>Molecular Systems Biology</i> , 2017, 13, 938.	7.2	112
249	Engineering Robustness of Microbial Cell Factories. <i>Biotechnology Journal</i> , 2017, 12, 1700014.	3.5	80
250	Enabling the synthesis of medium chain alkanes and 1-alkenes in yeast. <i>Metabolic Engineering</i> , 2017, 44, 81-88.	7.0	62
251	Exploiting off-targeting in guide RNA for CRISPR systems for simultaneous editing of multiple genes. <i>FEBS Letters</i> , 2017, 591, 3288-3295.	2.8	10
252	Human protein secretory pathway genes are expressed in a tissue-specific pattern to match processing demands of the secretome. <i>Npj Systems Biology and Applications</i> , 2017, 3, 22.	3.0	32

#	ARTICLE	IF	CITATIONS
253	Improving the economics of NASH/NAFLD treatment through the use of systems biology. Drug Discovery Today, 2017, 22, 1532-1538.	6.4	28
254	Selection of complementary foods based on optimal nutritional values. Scientific Reports, 2017, 7, 5413.	3.3	11
255	Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints. Molecular Systems Biology, 2017, 13, 935.	7.2	367
256	Elimination of the last reactions in ergosterol biosynthesis alters the resistance of <i>Saccharomyces cerevisiae</i> to multiple stresses. FEMS Yeast Research, 2017, 17, .	2.3	34
257	Genome-scale metabolic models applied to human health and disease. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2017, 9, e1393.	6.6	36
258	<i>In Vivo</i> Analysis of the Viable Microbiota and <i>Helicobacter pylori</i> Transcriptome in Gastric Infection and Early Stages of Carcinogenesis. Infection and Immunity, 2017, 85, .	2.2	55
259	Metabolism: Built on stable catalysts. Nature Microbiology, 2017, 2, 17085.	13.3	2
260	Functional screening of aldehyde decarbonylases for long-chain alkane production by <i>Saccharomyces cerevisiae</i> . Microbial Cell Factories, 2017, 16, 74.	4.0	32
261	Type 2 diabetes and obesity induce similar transcriptional reprogramming in human myocytes. Genome Medicine, 2017, 9, 47.	8.2	37
262	Predicting growth of the healthy infant using a genome scale metabolic model. Npj Systems Biology and Applications, 2017, 3, 3.	3.0	22
263	Evolutionary engineering reveals divergent paths when yeast is adapted to different acidic environments. Metabolic Engineering, 2017, 39, 19-28.	7.0	80
264	Establishing very long-chain fatty alcohol and wax ester biosynthesis in <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2017, 114, 1025-1035.	3.3	43
265	Genome scale metabolic modeling of cancer. Metabolic Engineering, 2017, 43, 103-112.	7.0	87
266	Affibody Scaffolds Improve Sesquiterpene Production in <i>Saccharomyces cerevisiae</i> . ACS Synthetic Biology, 2017, 6, 19-28.	3.8	66
267	Biobased production of alkanes and alkenes through metabolic engineering of microorganisms. Journal of Industrial Microbiology and Biotechnology, 2017, 44, 613-622.	3.0	77
268	Metabolic Models of Protein Allocation Call for the Kinetome. Cell Systems, 2017, 5, 538-541.	6.2	71
269	Engineering yeast metabolism for production of terpenoids for use as perfume ingredients, pharmaceuticals and biofuels. FEMS Yeast Research, 2017, 17, .	2.3	87
270	Physiological characterization of secondary metabolite producing <i>Penicillium</i> cell factories. Fungal Biology and Biotechnology, 2017, 4, 8.	5.1	26

#	ARTICLE	IF	CITATIONS
271	New Challenges to Study Heterogeneity in Cancer Redox Metabolism. <i>Frontiers in Cell and Developmental Biology</i> , 2017, 5, 65.	3.7	65
272	Bioproduction of Fuels: An Introduction. , 2017, , 3-25.		0
273	Prognostic Value of Plasma and Urine Glycosaminoglycan Scores in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2016, 6, 253.	2.8	22
274	EasyCloneMulti: A Set of Vectors for Simultaneous and Multiple Genomic Integrations in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2016, 11, e0150394.	2.5	49
275	Six Tissue Transcriptomics Reveals Specific Immune Suppression in Spleen by Dietary Polyunsaturated Fatty Acids. <i>PLoS ONE</i> , 2016, 11, e0155099.	2.5	13
276	Editorial: The Impact of Systems Medicine on Human Health and Disease. <i>Frontiers in Physiology</i> , 2016, 7, 552.	2.8	6
277	Genome-Wide Mapping of Binding Sites Reveals Multiple Biological Functions of the Transcription Factor Cst6p in <i>Saccharomyces cerevisiae</i> . <i>MBio</i> , 2016, 7, .	4.1	22
278	Transcriptomics resources of human tissues and Åorgans. <i>Molecular Systems Biology</i> , 2016, 12, 862.	7.2	130
279	Systems biology analysis of hepatitis C virus infection reveals the role of copy number increases in regions of chromosome 1q in hepatocellular carcinoma metabolism. <i>Molecular BioSystems</i> , 2016, 12, 1496-1506.	2.9	21
280	Dysregulated signaling hubs of liver lipid metabolism reveal hepatocellular carcinoma pathogenesis. <i>Nucleic Acids Research</i> , 2016, 44, 5529-5539.	14.5	35
281	Engineering and systems-level analysis of <i>Saccharomyces cerevisiae</i> for production of 3-hydroxypropionic acid via malonyl-CoA reductase-dependent pathway. <i>Microbial Cell Factories</i> , 2016, 15, 53.	4.0	98
282	The impact of respiration and oxidative stress response on recombinant Î±-amylase production by <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2016, 3, 205-210.	3.6	26
283	Systematic Analysis Reveals that Cancer Mutations Converge on Deregulated Metabolism of Arachidonate and Xenobiotics. <i>Cell Reports</i> , 2016, 16, 878-895.	6.4	21
284	Integrative analysis of human omics data using biomolecular networks. <i>Molecular BioSystems</i> , 2016, 12, 2953-2964.	2.9	33
285	In search for symmetries in the metabolism of cancer. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2016, 8, 23-35.	6.6	6
286	Adaptive Evolution of Phosphorus Metabolism in <i>Prochlorococcus</i> . <i>MSystems</i> , 2016, 1, .	3.8	19
287	Respiratory metabolism and calorie restriction relieve persistent endoplasmic reticulum stress induced by calcium shortage in yeast. <i>Scientific Reports</i> , 2016, 6, 27942.	3.3	11
288	Functional expression and evaluation of heterologous phosphoketolases in <i>Saccharomyces cerevisiae</i> . <i>AMB Express</i> , 2016, 6, 115.	3.0	39

#	ARTICLE	IF	CITATIONS
289	Engineering yeast for high-level production of stilbenoid antioxidants. <i>Scientific Reports</i> , 2016, 6, 36827.	3.3	122
290	<i>Penicillium arizonense</i> , a new, genome sequenced fungal species, reveals a high chemical diversity in secreted metabolites. <i>Scientific Reports</i> , 2016, 6, 35112.	3.3	33
291	Regulation of amino-acid metabolism controls flux to lipid accumulation in <i>Yarrowia lipolytica</i> . <i>Npj Systems Biology and Applications</i> , 2016, 2, 16005.	3.0	141
292	Harnessing Yeast Peroxisomes for Biosynthesis of Fatty-Acid-Derived Biofuels and Chemicals with Relieved Side-Pathway Competition. <i>Journal of the American Chemical Society</i> , 2016, 138, 15368-15377.	13.7	157
293	Flux control through protein phosphorylation in yeast. <i>FEMS Yeast Research</i> , 2016, 16, fow096.	2.3	29
294	Production of fatty acid-derived oleochemicals and biofuels by synthetic yeast cell factories. <i>Nature Communications</i> , 2016, 7, 11709.	12.8	306
295	Human gut microbiota and healthy aging: Recent developments and future prospective. <i>Nutrition and Healthy Aging</i> , 2016, 4, 3-16.	1.1	150
296	Thermotolerant yeasts selected by adaptive evolution express heat stress response at 30°C. <i>Scientific Reports</i> , 2016, 6, 27003.	3.3	62
297	Metabolic Trade-offs in Yeast are Caused by F1FO-ATP synthase. <i>Scientific Reports</i> , 2016, 6, 22264.	3.3	121
298	Genome-scale metabolic model of <i>Pichia pastoris</i> with native and humanized glycosylation of recombinant proteins. <i>Biotechnology and Bioengineering</i> , 2016, 113, 961-969.	3.3	43
299	Adaptation to different types of stress converge on mitochondrial metabolism. <i>Molecular Biology of the Cell</i> , 2016, 27, 2505-2514.	2.1	59
300	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016, 24, 172-184.	16.2	133
301	Engineering of synthetic, stress-responsive yeast promoters. <i>Nucleic Acids Research</i> , 2016, 44, e136-e136.	14.5	99
302	Glycosaminoglycan Profiling in Patients' Plasma and Urine Predicts the Occurrence of Metastatic Clear Cell Renal Cell Carcinoma. <i>Cell Reports</i> , 2016, 15, 1822-1836.	6.4	55
303	Improving the flux distributions simulated with genome-scale metabolic models of <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2016, 3, 153-163.	3.6	51
304	Industrial systems biology and its impact on synthetic biology of yeast cell factories. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1164-1170.	3.3	40
305	Flux Control at the Malonyl-CoA Node through Hierarchical Dynamic Pathway Regulation in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2016, 5, 224-233.	3.8	131
306	Improved production of fatty acids by <i>Saccharomyces cerevisiae</i> through screening a cDNA library from the oleaginous yeast <i>Yarrowia lipolytica</i> . <i>FEMS Yeast Research</i> , 2016, 16, fow108.	2.3	21

#	ARTICLE	IF	CITATIONS
307	Physiological and transcriptional characterization of <i>Saccharomyces cerevisiae</i> engineered for production of fatty acid ethyl esters. FEMS Yeast Research, 2016, 16, fov105.	2.3	10
308	Production of farnesene and santalene by <i>Saccharomyces cerevisiae</i> using fed-batch cultivations with RQ-controlled feed. Biotechnology and Bioengineering, 2016, 113, 72-81.	3.3	102
309	Voluntary Running Suppresses Tumor Growth through Epinephrine- and IL-6-Dependent NK Cell Mobilization and Redistribution. Cell Metabolism, 2016, 23, 554-562.	16.2	572
310	Engineering Cellular Metabolism. Cell, 2016, 164, 1185-1197.	28.9	953
311	Biobased organic acids production by metabolically engineered microorganisms. Current Opinion in Biotechnology, 2016, 37, 165-172.	6.6	130
312	Heme metabolism in stress regulation and protein production: From Cinderella to a key player. Bioengineered, 2016, 7, 112-115.	3.2	10
313	Improved quantification of farnesene during microbial production from <i>Saccharomyces cerevisiae</i> in two-liquid-phase fermentations. Talanta, 2016, 146, 100-106.	5.5	24
314	Bioproduction of Fuels: An Introduction. , 2016, , 1-23.		0
315	Extensive weight loss reveals distinct gene expression changes in human subcutaneous and visceral adipose tissue. Scientific Reports, 2015, 5, 14841.	3.3	62
316	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
317	The gut microbiota modulates host amino acid and glutathione metabolism in mice. Molecular Systems Biology, 2015, 11, 834.	7.2	291
318	Human metabolic atlas: an online resource for human metabolism. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav068.	3.0	76
319	Engineering the oxygen sensing regulation results in an enhanced recombinant human hemoglobin production by <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2015, 112, 181-188.	3.3	24
320	Long-chain alkane production by the yeast <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2015, 112, 1275-1279.	3.3	101
321	Modifying Yeast Tolerance to Inhibitory Conditions of Ethanol Production Processes. Frontiers in Bioengineering and Biotechnology, 2015, 3, 184.	4.1	93
322	From next-generation sequencing to systematic modeling of the gut microbiome. Frontiers in Genetics, 2015, 6, 219.	2.3	99
323	Adaptive mutations in sugar metabolism restore growth on glucose in a pyruvate decarboxylase negative yeast strain. Microbial Cell Factories, 2015, 14, 116.	4.0	19
324	Cancer Metabolism: A Modeling Perspective. Frontiers in Physiology, 2015, 6, 382.	2.8	58

#	ARTICLE	IF	CITATIONS
325	Functional pyruvate formate lyase pathway expressed with two different electron donors in <i>Saccharomyces cerevisiae</i> at aerobic growth. <i>FEMS Yeast Research</i> , 2015, 15, fov024.	2.3	17
326	Flux balance analysis predicts essential genes in clear cell renal cell carcinoma metabolism. <i>Scientific Reports</i> , 2015, 5, 10738.	3.3	95
327	Genome scale models of yeast: towards standardized evaluation and consistent omic integration. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 846-858.	1.3	66
328	Stratification of Hepatocellular Carcinoma Patients Based on Acetate Utilization. <i>Cell Reports</i> , 2015, 13, 2014-2026.	6.4	113
329	Metabolic pathway engineering for fatty acid ethyl ester production in <i>Saccharomyces cerevisiae</i> using stable chromosomal integration. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 477-486.	3.0	37
330	Production of natural products through metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Biotechnology</i> , 2015, 35, 7-15.	6.6	170
331	Metabolic engineering strategies for microbial synthesis of oleochemicals. <i>Metabolic Engineering</i> , 2015, 29, 1-11.	7.0	152
332	Identifying anti-growth factors for human cancer cell lines through genome-scale metabolic modeling. <i>Scientific Reports</i> , 2015, 5, 8183.	3.3	60
333	New paradigms for metabolic modeling of human cells. <i>Current Opinion in Biotechnology</i> , 2015, 34, 91-97.	6.6	86
334	Tissue-based map of the human proteome. <i>Science</i> , 2015, 347, 1260419.	12.6	10,802
335	Impact of synthetic biology and metabolic engineering on industrial production of fine chemicals. <i>Biotechnology Advances</i> , 2015, 33, 1395-1402.	11.7	195
336	Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome. <i>Cell Metabolism</i> , 2015, 22, 320-331.	16.2	345
337	Roux-en-Y Gastric Bypass and Vertical Banded Gastroplasty Induce Long-Term Changes on the Human Gut Microbiome Contributing to Fat Mass Regulation. <i>Cell Metabolism</i> , 2015, 22, 228-238.	16.2	638
338	Editorial. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 315-316.	3.0	1
339	Metabolic Needs and Capabilities of <i>Toxoplasma gondii</i> through Combined Computational and Experimental Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004261.	3.2	92
340	Logical transformation of genome-scale metabolic models for gene level applications and analysis. <i>Bioinformatics</i> , 2015, 31, 2324-2331.	4.1	43
341	Molecular Mechanism of Flocculation Self-Recognition in Yeast and Its Role in Mating and Survival. <i>MBio</i> , 2015, 6, .	4.1	62
342	Proteome- and Transcriptome-Driven Reconstruction of the Human Myocyte Metabolic Network and Its Use for Identification of Markers for Diabetes. <i>Cell Reports</i> , 2015, 11, 921-933.	6.4	112

#	ARTICLE	IF	CITATIONS
343	Ach1 is involved in shuttling mitochondrial acetyl units for cytosolic C2 provision in <i>Saccharomyces cerevisiae</i> lacking pyruvate decarboxylase. <i>FEMS Yeast Research</i> , 2015, 15, .	2.3	28
344	Controllability analysis of transcriptional regulatory networks reveals circular control patterns among transcription factors. <i>Integrative Biology (United Kingdom)</i> , 2015, 7, 560-568.	1.3	18
345	Enhanced amino acid utilization sustains growth of cells lacking Snf1/AMPK. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2015, 1853, 1615-1625.	4.1	29
346	Glucose repression in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov068.	2.3	220
347	Production of 3-hydroxypropionic acid from glucose and xylose by metabolically engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering Communications</i> , 2015, 2, 132-136.	3.6	59
348	Finding directionality and gene-disease predictions in disease associations. <i>BMC Systems Biology</i> , 2015, 9, 35.	3.0	10
349	Microfluidic screening and whole-genome sequencing identifies mutations associated with improved protein secretion by yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4689-96.	7.1	138
350	The human cardiac and skeletal muscle proteomes defined by transcriptomics and antibody-based profiling. <i>BMC Genomics</i> , 2015, 16, 475.	2.8	58
351	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015, 11, 625-631.	8.0	715
352	Thermotolerant Yeast Strains Adapted by Laboratory Evolution Show Trade-Off at Ancestral Temperatures and Preadaptation to Other Stresses. <i>MBio</i> , 2015, 6, e00431.	4.1	108
353	De novo production of resveratrol from glucose or ethanol by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015, 32, 1-11.	7.0	242
354	Modular pathway rewiring of <i>Saccharomyces cerevisiae</i> enables high-level production of L-ornithine. <i>Nature Communications</i> , 2015, 6, 8224.	12.8	97
355	Improving heterologous protein secretion at aerobic conditions by activating hypoxia-induced genes in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov070.	2.3	13
356	Yeast cell factories on the horizon. <i>Science</i> , 2015, 349, 1050-1051.	12.6	62
357	Advancing metabolic engineering through systems biology of industrial microorganisms. <i>Current Opinion in Biotechnology</i> , 2015, 36, 8-15.	6.6	92
358	Establishment of a yeast platform strain for production of p-coumaric acid through metabolic engineering of aromatic amino acid biosynthesis. <i>Metabolic Engineering</i> , 2015, 31, 181-188.	7.0	213
359	Expanded metabolite coverage of <i>Saccharomyces cerevisiae</i> extract through improved chloroform/methanol extraction and tert-butyl dimethylsilyl derivatization. <i>Analytical Chemistry Research</i> , 2015, 6, 9-16.	2.0	14
360	Genetic and nutrient modulation of acetyl-CoA levels in <i>Synechocystis</i> for n-butanol production. <i>Microbial Cell Factories</i> , 2015, 14, 167.	4.0	92

#	ARTICLE	IF	CITATIONS
361	Establishing a synthetic pathway for high-level production of 3-hydroxypropionic acid in <i>Saccharomyces cerevisiae</i> via β^2 -alanine. <i>Metabolic Engineering</i> , 2015, 27, 57-64.	7.0	185
362	Microbial acetyl-CoA metabolism and metabolic engineering. <i>Metabolic Engineering</i> , 2015, 28, 28-42.	7.0	237
363	Networking in metabolism and human disease. <i>Oncotarget</i> , 2015, 6, 15708-15709.	1.8	3
364	Defining the human gallbladder proteome by transcriptomics and affinity proteomics. <i>Proteomics</i> , 2014, 14, 2498-2507.	2.2	19
365	Chromosome 3p loss of heterozygosity is associated with a unique metabolic network in clear cell renal carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E866-75.	7.1	128
366	Enabling Technologies to Advance Microbial Isoprenoid Production. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2014, 148, 143-160.	1.1	10
367	Metagenomic Data Utilization and Analysis (MEDUSA) and Construction of a Global Gut Microbial Gene Catalogue. <i>PLoS Computational Biology</i> , 2014, 10, e1003706.	3.2	55
368	Genome-Scale Metabolic Models: A Link between Bioinformatics and Systems Biology. , 2014, , 165-173.		0
369	Synthetic Biology for Engineering Acetyl Coenzyme A Metabolism in Yeast. <i>MBio</i> , 2014, 5, e02153.	4.1	88
370	Evolution reveals a glutathione-dependent mechanism of 3-hydroxypropionic acid tolerance. <i>Metabolic Engineering</i> , 2014, 26, 57-66.	7.0	74
371	Genome-scale analysis of the high-efficient protein secretion system of <i>Aspergillus oryzae</i> . <i>BMC Systems Biology</i> , 2014, 8, 73.	3.0	30
372	Kiwi: a tool for integration and visualization of network topology and gene-set analysis. <i>BMC Bioinformatics</i> , 2014, 15, 408.	2.6	12
373	BioMet Toolbox 2.0: genome-wide analysis of metabolism and omics data. <i>Nucleic Acids Research</i> , 2014, 42, W175-W181.	14.5	40
374	Dynamic Metabolic Footprinting Reveals the Key Components of Metabolic Network in Yeast <i>Saccharomyces cerevisiae</i> . <i>International Journal of Genomics</i> , 2014, 2014, 1-14.	1.6	16
375	Improved production of fatty acid ethyl esters in <i>Saccharomyces cerevisiae</i> through up-regulation of the ethanol degradation pathway and expression of the heterologous phosphoketolase pathway. <i>Microbial Cell Factories</i> , 2014, 13, 39.	4.0	115
376	Enhanced ethanol production and reduced glycerol formation in <i>fps1Δ</i> mutants of <i>Saccharomyces cerevisiae</i> engineered for improved redox balancing. <i>AMB Express</i> , 2014, 4, 86.	3.0	23
377	Coupled incremental precursor and co-factor supply improves 3-hydroxypropionic acid production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2014, 22, 104-109.	7.0	123
378	Physiological characterization of the high malic acid-producing <i>Aspergillus oryzae</i> strain 2103a-68. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 3517-3527.	3.6	53

#	ARTICLE	IF	CITATIONS
379	Genome scale metabolic modeling of the riboflavin overproducer <i>Ashbya gossypii</i> . Biotechnology and Bioengineering, 2014, 111, 1191-1199.	3.3	35
380	Advances in metabolic engineering of yeast <i>Saccharomyces cerevisiae</i> for production of chemicals. Biotechnology Journal, 2014, 9, 609-620.	3.5	221
381	EasyClone: method for iterative chromosomal integration of multiple genes <i>Saccharomyces cerevisiae</i> . FEMS Yeast Research, 2014, 14, 238-248.	2.3	236
382	Gcn4p and the Crabtree effect of yeast: drawing the causal model of the Crabtree effect in <i>Saccharomyces cerevisiae</i> and explaining evolutionary trade-offs of adaptation to galactose through systems biology. FEMS Yeast Research, 2014, 14, 654-662.	2.3	14
383	Engineering synergy in biotechnology. Nature Chemical Biology, 2014, 10, 319-322.	8.0	147
384	Engineering of chromosomal wax ester synthase integrated <i>Saccharomyces cerevisiae</i> mutants for improved biosynthesis of fatty acid ethyl esters. Biotechnology and Bioengineering, 2014, 111, 1740-1747.	3.3	72
385	Kinetic models in industrial biotechnology – Improving cell factory performance. Metabolic Engineering, 2014, 24, 38-60.	7.0	238
386	Management of the endoplasmic reticulum stress by activation of the heat shock response in yeast. FEMS Yeast Research, 2014, 14, 481-494.	2.3	38
387	Genome-scale metabolic modelling of hepatocytes reveals serine deficiency in patients with non-alcoholic fatty liver disease. Nature Communications, 2014, 5, 3083.	12.8	461
388	High-throughput screening for industrial enzyme production hosts by droplet microfluidics. Lab on A Chip, 2014, 14, 806-813.	6.0	195
389	Balanced globin protein expression and heme biosynthesis improve production of human hemoglobin in <i>Saccharomyces cerevisiae</i> . Metabolic Engineering, 2014, 21, 9-16.	7.0	64
390	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. Molecular and Cellular Proteomics, 2014, 13, 397-406.	3.8	2,819
391	The human liver-specific proteome defined by transcriptomics and antibody-based profiling. FASEB Journal, 2014, 28, 2901-2914.	0.5	73
392	Biopharmaceutical protein production by <i>Saccharomyces cerevisiae</i> : current state and future prospects. Pharmaceutical Bioprocessing, 2014, 2, 167-182.	0.8	40
393	Identification of anticancer drugs for hepatocellular carcinoma through personalized genome-scale metabolic modeling. Molecular Systems Biology, 2014, 10, 721.	7.2	331
394	Applications of computational modeling in metabolic engineering of yeast. FEMS Yeast Research, 2014, 15, n/a-n/a.	2.3	28
395	A dedicated database system for handling multi-level data in systems biology. Source Code for Biology and Medicine, 2014, 9, 17.	1.7	2
396	Altered sterol composition renders yeast thermotolerant. Science, 2014, 346, 75-78.	12.6	368

#	ARTICLE	IF	CITATIONS
397	Impact of protein uptake and degradation on recombinant protein secretion in yeast. Applied Microbiology and Biotechnology, 2014, 98, 7149-7159.	3.6	23
398	Bridging the gaps in systems biology. Molecular Genetics and Genomics, 2014, 289, 727-734.	2.1	38
399	Improved Production of a Heterologous Amylase in <i>Saccharomyces cerevisiae</i> by Inverse Metabolic Engineering. Applied and Environmental Microbiology, 2014, 80, 5542-5550.	3.1	29
400	The future of genome-scale modeling of yeast through integration of a transcriptional regulatory network. Quantitative Biology, 2014, 2, 30-46.	0.5	8
401	Genome-scale metabolic reconstructions of <i>Bifidobacterium adolescentis</i> L2-32 and <i>Faecalibacterium prausnitzii</i> A2-165 and their interaction. BMC Systems Biology, 2014, 8, 41.	3.0	88
402	Defining the Human Adipose Tissue Proteome To Reveal Metabolic Alterations in Obesity. Journal of Proteome Research, 2014, 13, 5106-5119.	3.7	55
403	Improving Production of Malonyl Coenzyme A-Derived Metabolites by Abolishing Snf1-Dependent Regulation of Acc1. MBio, 2014, 5, e01130-14.	4.1	194
404	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of fatty acid ethyl esters, an advanced biofuel, by eliminating non-essential fatty acid utilization pathways. Applied Energy, 2014, 115, 226-232.	10.1	99
405	Maintaining a strong yeast research community. FEMS Yeast Research, 2014, 14, 527-528.	2.3	2
406	Elucidating the interactions between the human gut microbiota and its host through metabolic modeling. Frontiers in Genetics, 2014, 5, 86.	2.3	72
407	Fatty Acid-Derived Biofuels and Chemicals Production in <i>Saccharomyces cerevisiae</i> . Frontiers in Bioengineering and Biotechnology, 2014, 2, 32.	4.1	65
408	Genetic Engineering Tools for <i>Saccharomyces cerevisiae</i> . , 2014, , 287-301.		2
409	Succinate dehydrogenase inhibition leads to epithelial-mesenchymal transition and reprogrammed carbon metabolism. Cancer & Metabolism, 2014, 2, 21.	5.0	137
410	Systems Biology: Developments and Applications. , 2014, , 83-96.		3
411	Specific growth rate and substrate dependent polyhydroxybutyrate production in <i>Saccharomyces cerevisiae</i> . AMB Express, 2013, 3, 18.	3.0	17
412	Improved polyhydroxybutyrate production by <i>Saccharomyces cerevisiae</i> through the use of the phosphoketolase pathway. Biotechnology and Bioengineering, 2013, 110, 2216-2224.	3.3	86
413	Improving biobutanol production in engineered <i>Saccharomyces cerevisiae</i> by manipulation of acetyl-CoA metabolism. Journal of Industrial Microbiology and Biotechnology, 2013, 40, 1051-1056.	3.0	96
414	FANTOM: Functional and taxonomic analysis of metagenomes. BMC Bioinformatics, 2013, 14, 38.	2.6	35

#	ARTICLE	IF	CITATIONS
415	Mapping condition-dependent regulation of metabolism in yeast through genome-scale modeling. BMC Systems Biology, 2013, 7, 36.	3.0	101
416	Mapping global effects of the anti-sigma factor MucA in <i>Pseudomonas fluorescens</i> SBW25 through genome-scale metabolic modeling. BMC Systems Biology, 2013, 7, 19.	3.0	32
417	Application of Genome-Scale Metabolic Models in Metabolic Engineering. Industrial Biotechnology, 2013, 9, 203-214.	0.8	26
418	From flavors and pharmaceuticals to advanced biofuels: Production of isoprenoids in <i>Saccharomyces cerevisiae</i> . Biotechnology Journal, 2013, 8, 1435-1444.	3.5	91
419	Advances in metabolic pathway and strain engineering paving the way for sustainable production of chemical building blocks. Current Opinion in Biotechnology, 2013, 24, 965-972.	6.6	111
420	Understanding the interactions between bacteria in the human gut through metabolic modeling. Scientific Reports, 2013, 3, 2532.	3.3	224
421	Transcriptome signatures in <i>Helicobacter pylori</i> -infected mucosa identifies acidic mammalian chitinase loss as a corpus atrophy marker. BMC Medical Genomics, 2013, 6, 41.	1.5	52
422	Integrated analysis, transcriptome-lipidome, reveals the effects of INO- level (INO2 and INO4) on lipid metabolism in yeast. BMC Systems Biology, 2013, 7, S7.	3.0	22
423	A universal fixation method based on quaternary ammonium salts (RNAlater) for omics-technologies: <i>Saccharomyces cerevisiae</i> as a case study. Biotechnology Letters, 2013, 35, 891-900.	2.2	19
424	Economic and environmental impacts of microbial biodiesel. Nature Biotechnology, 2013, 31, 789-793.	17.5	77
425	Assessing the Human Gut Microbiota in Metabolic Diseases. Diabetes, 2013, 62, 3341-3349.	0.6	384
426	Anaerobic α -Amylase Production and Secretion with Fumarate as the Final Electron Acceptor in <i>Saccharomyces cerevisiae</i> . Applied and Environmental Microbiology, 2013, 79, 2962-2967.	3.1	23
427	Using Transcriptomics To Improve Butanol Tolerance of <i>Synechocystis</i> sp. Strain PCC 6803. Applied and Environmental Microbiology, 2013, 79, 7419-7427.	3.1	85
428	Adaptively evolved yeast mutants on galactose show trade-offs in carbon utilization on glucose. Metabolic Engineering, 2013, 16, 78-86.	7.0	29
429	Correlation of cell growth and heterologous protein production by <i>Saccharomyces cerevisiae</i> . Applied Microbiology and Biotechnology, 2013, 97, 8955-8962.	3.6	41
430	A community-driven global reconstruction of human metabolism. Nature Biotechnology, 2013, 31, 419-425.	17.5	920
431	Toward systems metabolic engineering of <i>Aspergillus</i> and <i>Pichia</i> species for the production of chemicals and biofuels. Biotechnology Journal, 2013, 8, 534-544.	3.5	18
432	Establishing a platform cell factory through engineering of yeast acetyl-CoA metabolism. Metabolic Engineering, 2013, 15, 48-54.	7.0	268

#	ARTICLE	IF	CITATIONS
433	Metabolic engineering of yeast for production of fuels and chemicals. Current Opinion in Biotechnology, 2013, 24, 398-404.	6.6	263
434	Advanced biofuel production by the yeast <i>Saccharomyces cerevisiae</i> . Current Opinion in Chemical Biology, 2013, 17, 480-488.	6.1	173
435	Genome-scale modeling of human metabolism – a systems biology approach. Biotechnology Journal, 2013, 8, 985-996.	3.5	101
436	Quantitative Analysis of Glycerol Accumulation, Glycolysis and Growth under Hyper Osmotic Stress. PLoS Computational Biology, 2013, 9, e1003084.	3.2	95
437	Genome-scale modeling enables metabolic engineering of <i>Saccharomyces cerevisiae</i> for succinic acid production. Journal of Industrial Microbiology and Biotechnology, 2013, 40, 735-747.	3.0	64
438	The role of biofuels in the future energy supply. Energy and Environmental Science, 2013, 6, 1077.	30.8	145
439	Gut metagenome in European women with normal, impaired and diabetic glucose control. Nature, 2013, 498, 99-103.	27.8	2,401
440	Heat shock response improves heterologous protein secretion in <i>Saccharomyces cerevisiae</i> . Applied Microbiology and Biotechnology, 2013, 97, 3559-3568.	3.6	45
441	Rapid Quantification of Yeast Lipid using Microwave-Assisted Total Lipid Extraction and HPLC-CAD. Analytical Chemistry, 2013, 85, 4912-4919.	6.5	110
442	A maternal diet of fatty fish reduces body fat of offspring compared with a maternal diet of beef and a post-weaning diet of fish improves insulin sensitivity and lipid profile in adult C57BL/6 male mice. Acta Physiologica, 2013, 209, 220-234.	3.8	25
443	The RAVEN Toolbox and Its Use for Generating a Genome-scale Metabolic Model for <i>Penicillium chrysogenum</i> . PLoS Computational Biology, 2013, 9, e1002980.	3.2	364
444	Novel insights into obesity and diabetes through genome-scale metabolic modeling. Frontiers in Physiology, 2013, 4, 92.	2.8	38
445	Mapping Condition-Dependent Regulation of Lipid Metabolism in <i>Saccharomyces cerevisiae</i> . G3: Genes, Genomes, Genetics, 2013, 3, 1979-1995.	1.8	18
446	Adipose Tissue Resting Energy Expenditure and Expression of Genes Involved in Mitochondrial Function Are Higher in Women than in Men. Journal of Clinical Endocrinology and Metabolism, 2013, 98, E370-E378.	3.6	89
447	Systems biology methods and developments of filamentous fungi in relation to the production of food ingredients. , 2013, , 19-41.		0
448	Industrial Systems Biology of <i>Saccharomyces cerevisiae</i> Enables Novel Succinic Acid Cell Factory. PLoS ONE, 2013, 8, e54144.	2.5	142
449	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. Nucleic Acids Research, 2013, 41, 4378-4391.	14.5	684
450	Integration of clinical data with a genome-scale metabolic model of the human adipocyte. Molecular Systems Biology, 2013, 9, 649.	7.2	217

#	ARTICLE	IF	CITATIONS
451	Investigation of Malic Acid Production in <i>Aspergillus oryzae</i> under Nitrogen Starvation Conditions. <i>Applied and Environmental Microbiology</i> , 2013, 79, 6050-6058.	3.1	69
452	Production of biopharmaceutical proteins by yeast. <i>Bioengineered</i> , 2013, 4, 207-211.	3.2	199
453	Genome-Scale Modeling of the Protein Secretory Machinery in Yeast. <i>PLoS ONE</i> , 2013, 8, e63284.	2.5	71
454	Reconstruction of Genome-Scale Active Metabolic Networks for 69 Human Cell Types and 16 Cancer Types Using INIT. <i>PLoS Computational Biology</i> , 2012, 8, e1002518.	3.2	381
455	Profiling of Cytosolic and Peroxisomal Acetyl-CoA Metabolism in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e42475.	2.5	100
456	Recovery of Phenotypes Obtained by Adaptive Evolution through Inverse Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2012, 78, 7579-7586.	3.1	18
457	Identification and treatment of heme depletion attributed to overexpression of a lineage of evolved P450 monooxygenases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 19504-19509.	7.1	72
458	Pharmaceutical protein production by yeast: towards production of human blood proteins by microbial fermentation. <i>Current Opinion in Biotechnology</i> , 2012, 23, 965-971.	6.6	82
459	Bridging Omics Technologies with Synthetic Biology in Yeast Industrial Biotechnology. , 2012, , 271-327.		2
460	Symptomatic atherosclerosis is associated with an altered gut metagenome. <i>Nature Communications</i> , 2012, 3, 1245.	12.8	970
461	<i>Aspergilli</i> : Systems biology and industrial applications. <i>Biotechnology Journal</i> , 2012, 7, 1147-1155.	3.5	32
462	Mapping the polysaccharide degradation potential of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2012, 13, 313.	2.8	35
463	Combined metabolic engineering of precursor and co-factor supply to increase Î±-santalene production by <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 117.	4.0	130
464	<i>Scheffersomyces stipitis</i> : a comparative systems biology study with the Crabtree positive yeast <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012, 11, 136.	4.0	57
465	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
466	Genome-scale metabolic reconstructions of <i>Pichia stipitis</i> and <i>Pichia pastoris</i> and in silico evaluation of their potentials. <i>BMC Systems Biology</i> , 2012, 6, 24.	3.0	101
467	Engineering of acetyl-CoA metabolism for the improved production of polyhydroxybutyrate in <i>Saccharomyces cerevisiae</i> . <i>AMB Express</i> , 2012, 2, 52.	3.0	83
468	Metabolic Engineering of Isoprenoid Production: Reconstruction of Multistep Heterologous Pathways in Tractable Hosts. , 2012, , 73-89.		1

#	ARTICLE	IF	CITATIONS
469	Fifteen years of large scale metabolic modeling of yeast: Developments and impacts. <i>Biotechnology Advances</i> , 2012, 30, 979-988.	11.7	106
470	Systems biology of yeast: enabling technology for development of cell factories for production of advanced biofuels. <i>Current Opinion in Biotechnology</i> , 2012, 23, 624-630.	6.6	83
471	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <i>Gut</i> , 2012, 61, 1124-1131.	12.1	321
472	Physiological characterization of recombinant <i>Saccharomyces cerevisiae</i> expressing the <i>Aspergillus nidulans</i> phosphoketolase pathway: validation of activity through ¹³ C-based metabolic flux analysis. <i>Applied Microbiology and Biotechnology</i> , 2012, 95, 1001-1010.	3.6	32
473	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012, 40, 10084-10097.	14.5	285
474	Lipid biosynthesis monitored at the single-cell level in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology Journal</i> , 2012, 7, 594-601.	3.5	11
475	Different expression systems for production of recombinant proteins in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1259-1268.	3.3	128
476	Genome-scale metabolic representation of <i>Amycolatopsis balhimycina</i> . <i>Biotechnology and Bioengineering</i> , 2012, 109, 1798-1807.	3.3	19
477	Metabolic engineering of <i>Saccharomyces cerevisiae</i> : a key cell factory platform for future biorefineries. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 2671-2690.	5.4	367
478	Fast and accurate preparation fatty acid methyl esters by microwave-assisted derivatization in the yeast <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2012, 94, 1637-1646.	3.6	66
479	Integrated analysis of transcriptome and lipid profiling reveals the co-influences of inositol and Snf1 in controlling lipid biosynthesis in yeast. <i>Molecular Genetics and Genomics</i> , 2012, 287, 541-554.	2.1	16
480	Translational and systems medicine. <i>Journal of Internal Medicine</i> , 2012, 271, 108-110.	6.0	14
481	Systems medicine and metabolic modelling. <i>Journal of Internal Medicine</i> , 2012, 271, 142-154.	6.0	133
482	A systems-level approach for metabolic engineering of yeast cell factories. <i>FEMS Yeast Research</i> , 2012, 12, 228-248.	2.3	90
483	Evolutionary engineering of <i>Saccharomyces cerevisiae</i> for efficient aerobic xylose consumption. <i>FEMS Yeast Research</i> , 2012, 12, 582-597.	2.3	81
484	Enhancing the copy number of episomal plasmids in <i>Saccharomyces cerevisiae</i> for improved protein production. <i>FEMS Yeast Research</i> , 2012, 12, 598-607.	2.3	66
485	Metabolic engineering of recombinant protein secretion by <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2012, 12, 491-510.	2.3	157
486	Dynamic ¹³ C-labeling experiments prove important differences in protein turnover rate between two <i>Saccharomyces cerevisiae</i> strains. <i>FEMS Yeast Research</i> , 2012, 12, 741-747.	2.3	19

#	ARTICLE	IF	CITATIONS
487	Engineering of vesicle trafficking improves heterologous protein secretion in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2012, 14, 120-127.	7.0	97
488	Dynamic control of gene expression in <i>Saccharomyces cerevisiae</i> engineered for the production of plant sesquiterpene β -santalene in a fed-batch mode. <i>Metabolic Engineering</i> , 2012, 14, 91-103.	7.0	215
489	Imbalance of heterologous protein folding and disulfide bond formation rates yields runaway oxidative stress. <i>BMC Biology</i> , 2012, 10, 16.	3.8	72
490	Functional expression and characterization of five wax ester synthases in <i>Saccharomyces cerevisiae</i> and their utility for biodiesel production. <i>Biotechnology for Biofuels</i> , 2012, 5, 7.	6.2	71
491	Industrial glucoamylase fed-batch benefits from oxygen limitation and high osmolarity. <i>Biotechnology and Bioengineering</i> , 2012, 109, 116-124.	3.3	19
492	Functional expression and characterization of five wax ester synthases in <i>Saccharomyces cerevisiae</i> and their utility for biodiesel production. <i>Biotechnology for Biofuels</i> , 2012, 5, 7.	6.2	93
493	Reconstruction and Evaluation of the Synthetic Bacterial MEP Pathway in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2012, 7, e52498.	2.5	54
494	Linking Genotype and Phenotype of <i>Saccharomyces cerevisiae</i> Strains Reveals Metabolic Engineering Targets and Leads to Triterpene Hyper-Producers. <i>PLoS ONE</i> , 2011, 6, e14763.	2.5	42
495	Bioreaction Engineering Principles. , 2011, , .		168
496	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	5.5	329
497	Genome-Scale Metabolic Models of <i>Saccharomyces cerevisiae</i> . <i>Methods in Molecular Biology</i> , 2011, 759, 445-463.	0.9	18
498	Growth Kinetics of Cell Cultures. , 2011, , 271-357.		2
499	Synergies between synthetic biology and metabolic engineering. <i>Nature Biotechnology</i> , 2011, 29, 693-695.	17.5	128
500	Mapping the interaction of Snf1 with TORC1 in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2011, 7, 545.	7.2	163
501	Unraveling Molecular Signatures of Immunostimulatory Adjuvants in the Female Genital Tract through Systems Biology. <i>PLoS ONE</i> , 2011, 6, e20448.	2.5	17
502	Transcriptional control of metabolic fluxes. <i>Molecular Systems Biology</i> , 2011, 7, 478.	7.2	10
503	Chimeric synthetic pathways. <i>Nature Chemical Biology</i> , 2011, 7, 195-196.	8.0	9
504	Mathematical models of cell factories: moving towards the core of industrial biotechnology. <i>Microbial Biotechnology</i> , 2011, 4, 572-584.	4.2	24

#	ARTICLE	IF	CITATIONS
505	Molecular Basis for Mycophenolic Acid Biosynthesis in <i>Penicillium brevicompactum</i> . <i>Applied and Environmental Microbiology</i> , 2011, 77, 3035-3043.	3.1	130
506	Prospects for microbial biodiesel production. <i>Biotechnology Journal</i> , 2011, 6, 277-285.	3.5	70
507	Opportunities for yeast metabolic engineering: Lessons from synthetic biology. <i>Biotechnology Journal</i> , 2011, 6, 262-276.	3.5	101
508	Heterologous production of polyunsaturated fatty acids in <i>Saccharomyces cerevisiae</i> causes a global transcriptional response resulting in reduced proteasomal activity and increased oxidative stress. <i>Biotechnology Journal</i> , 2011, 6, 343-356.	3.5	51
509	Elemental and Redox Balances. , 2011, , 63-118.		1
510	Biochemical Reaction Networks. , 2011, , 151-214.		1
511	Enzyme Kinetics and Metabolic Control Analysis. , 2011, , 215-269.		0
512	Population Balance Equations. , 2011, , 359-381.		0
513	Scale-Up of Bioprocesses. , 2011, , 497-546.		4
514	A Closer Look at Bacteroides: Phylogenetic Relationship and Genomic Implications of a Life in the Human Gut. <i>Microbial Ecology</i> , 2011, 61, 473-485.	2.8	135
515	Revealing the beneficial effect of protease supplementation to high gravity beer fermentations using "omics" techniques. <i>Microbial Cell Factories</i> , 2011, 10, 27.	4.0	27
516	Molecular and process design for rotavirus-like particle production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2011, 10, 33.	4.0	47
517	MEMOSys: Bioinformatics platform for genome-scale metabolic models. <i>BMC Systems Biology</i> , 2011, 5, 20.	3.0	29
518	Codon usage variability determines the correlation between proteome and transcriptome fold changes. <i>BMC Systems Biology</i> , 2011, 5, 33.	3.0	33
519	Integrated analysis of the global transcriptional response to α -amylase overproduction by <i>Aspergillus oryzae</i> . <i>Biotechnology and Bioengineering</i> , 2011, 108, 1130-1139.	3.3	12
520	Comparative metabolic capabilities for <i>Micrococcus luteus</i> NCTC 2665, the "Fleming" strain, and actinobacteria. <i>Biotechnology and Bioengineering</i> , 2011, 108, 2770-2775.	3.3	6
521	Prospects for systems biology and modeling of the gut microbiome. <i>Trends in Biotechnology</i> , 2011, 29, 251-258.	9.3	74
522	Versatile Enzyme Expression and Characterization System for <i>Aspergillus nidulans</i> , with the <i>Penicillium brevicompactum</i> Polyketide Synthase Gene from the Mycophenolic Acid Gene Cluster as a Test Case. <i>Applied and Environmental Microbiology</i> , 2011, 77, 3044-3051.	3.1	86

#	ARTICLE	IF	CITATIONS
523	Unravelling evolutionary strategies of yeast for improving galactose utilization through integrated systems level analysis. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 12179-12184.	7.1	137
524	Diversion of Flux toward Sesquiterpene Production in <i>Saccharomyces cerevisiae</i> by Fusion of Host and Heterologous Enzymes. Applied and Environmental Microbiology, 2011, 77, 1033-1040.	3.1	194
525	Chemicals from Metabolic Pathways. , 2011, , 7-62.		5
526	Phosphoglycerate mutase knock-out mutant <i>Saccharomyces cerevisiae</i> : Physiological investigation and transcriptome analysis. Biotechnology Journal, 2010, 5, 1016-1027.	3.5	11
527	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. Nature Communications, 2010, 1, 145.	12.8	100
528	Whole genome sequencing of <i>Saccharomyces cerevisiae</i> : from genotype to phenotype for improved metabolic engineering applications. BMC Genomics, 2010, 11, 723.	2.8	64
529	OptFlux: an open-source software platform for in silico metabolic engineering. BMC Systems Biology, 2010, 4, 45.	3.0	321
530	Use of genome-scale metabolic models for understanding microbial physiology. FEBS Letters, 2010, 584, 2556-2564.	2.8	81
531	Industrial systems biology. Biotechnology and Bioengineering, 2010, 105, 439-460.	3.3	130
532	Enhancement of farnesyl diphosphate pool as direct precursor of sesquiterpenes through metabolic engineering of the mevalonate pathway in <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2010, 106, 86-96.	3.3	127
533	Implementation of communication-mediated domains for non-ribosomal peptide production in <i>Saccharomyces cerevisiae</i> . Biotechnology and Bioengineering, 2010, 106, 841-844.	3.3	17
534	Integrative analysis using proteome and transcriptome data from yeast to unravel regulatory patterns at post-transcriptional level. Biotechnology and Bioengineering, 2010, 107, 865-875.	3.3	16
535	Pathway kinetics and metabolic control analysis of a high-yielding strain of <i>Penicillium chrysogenum</i> during fed batch cultivations. Biotechnology and Bioengineering, 2010, 52, 631-631.	3.3	0
536	Identification of flux control in metabolic networks using non-equilibrium thermodynamics. Metabolic Engineering, 2010, 12, 369-377.	7.0	24
537	Increased glycopeptide production after overexpression of shikimate pathway genes being part of the balhimycin biosynthetic gene cluster. Metabolic Engineering, 2010, 12, 455-461.	7.0	49
538	Reconstruction of the yeast protein-protein interaction network involved in nutrient sensing and global metabolic regulation. BMC Systems Biology, 2010, 4, 68.	3.0	9
539	Characterization of different promoters for designing a new expression vector in <i>Saccharomyces cerevisiae</i> . Yeast, 2010, 27, 955-964.	1.7	281
540	Prospects of yeast systems biology for human health: integrating lipid, protein and energy metabolism. FEMS Yeast Research, 2010, 10, 1046-1059.	2.3	59

#	ARTICLE	IF	CITATIONS
541	Measuring enzyme activities under standardized <i>in vivo</i> -like conditions for systems biology. FEBS Journal, 2010, 277, 749-760.	4.7	147
542	The β -subunits of the Snf1 kinase in <i>Saccharomyces cerevisiae</i> , Gal83 and Sip2, but not Sip1, are redundant in glucose derepression and regulation of sterol biosynthesis. Molecular Microbiology, 2010, 77, 371-383.	2.5	23
543	Identifying Molecular Effects of Diet through Systems Biology: Influence of Herring Diet on Sterol Metabolism and Protein Turnover in Mice. PLoS ONE, 2010, 5, e12361.	2.5	17
544	Analysis of Genome-Wide Coexpression and Coevolution of <i>Aspergillus oryzae</i> and <i>Aspergillus niger</i> . OMICS A Journal of Integrative Biology, 2010, 14, 165-175.	2.0	5
545	Sampling the Solution Space in Genome-Scale Metabolic Networks Reveals Transcriptional Regulation in Key Enzymes. PLoS Computational Biology, 2010, 6, e1000859.	3.2	164
546	BioMet Toolbox: genome-wide analysis of metabolism. Nucleic Acids Research, 2010, 38, W144-W149.	14.5	91
547	Systems Biology of Industrial Microorganisms. , 2010, 120, 51-99.		14
548	Toward design-based engineering of industrial microbes. Current Opinion in Microbiology, 2010, 13, 255-262.	5.1	82
549	Systems biology of energy homeostasis in yeast. Current Opinion in Microbiology, 2010, 13, 382-388.	5.1	30
550	Yeast Biological Networks Unfold the Interplay of Antioxidants, Genome and Phenotype, and Reveal a Novel Regulator of the Oxidative Stress Response. PLoS ONE, 2010, 5, e13606.	2.5	14
551	Comparative Transcriptomic Approach To Investigate Differences in Wine Yeast Physiology and Metabolism during Fermentation. Applied and Environmental Microbiology, 2009, 75, 6600-6612.	3.1	34
552	Reconstruction of the yeast Snf1 kinase regulatory network reveals its role as a global energy regulator. Molecular Systems Biology, 2009, 5, 319.	7.2	97
553	Genome-wide analysis of maltose utilization and regulation in aspergilli. Microbiology (United Kingdom) 153, 185-194. doi:10.1099/mic/0/000000.0	1.85	34
554	Studies of the Production of Fungal Polyketides in <i>Aspergillus nidulans</i> by Using Systems Biology Tools. Applied and Environmental Microbiology, 2009, 75, 2212-2220.	3.1	31
555	Global transcriptional response of <i>Saccharomyces cerevisiae</i> to the deletion of SDH3. BMC Systems Biology, 2009, 3, 17.	3.0	23
556	Reconstruction and logical modeling of glucose repression signaling pathways in <i>Saccharomyces cerevisiae</i> . BMC Systems Biology, 2009, 3, 7.	3.0	50
557	Systems biology of lipid metabolism: From yeast to human. FEBS Letters, 2009, 583, 3905-3913.	2.8	97
558	In silico genome-scale reconstruction and validation of the <i>Corynebacterium glutamicum</i> metabolic network. Biotechnology and Bioengineering, 2009, 102, 583-597.	3.3	162

#	ARTICLE	IF	CITATIONS
559	Physiology of <i>Aspergillus niger</i> in oxygen-limited continuous cultures: Influence of aeration, carbon source concentration and dilution rate. <i>Biotechnology and Bioengineering</i> , 2009, 103, 956-965.	3.3	33
560	Uncovering transcriptional regulation of glycerol metabolism in <i>Aspergilli</i> through genome-wide gene expression data analysis. <i>Molecular Genetics and Genomics</i> , 2009, 282, 571-86.	2.1	56
561	Physiological characterisation of <i>acuB</i> deletion in <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2009, 84, 157-167.	3.6	12
562	Characterization of chromosomal integration sites for heterologous gene expression in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009, 26, 545-551.	1.7	233
563	Recombinant bacterial hemoglobin alters metabolism of <i>Aspergillus niger</i> . <i>Metabolic Engineering</i> , 2009, 11, 8-12.	7.0	17
564	Overexpression of isocitrate lyase-glyoxylate bypass influence on metabolism in <i>Aspergillus niger</i> . <i>Metabolic Engineering</i> , 2009, 11, 107-116.	7.0	37
565	Enhancing sesquiterpene production in <i>Saccharomyces cerevisiae</i> through in silico driven metabolic engineering. <i>Metabolic Engineering</i> , 2009, 11, 328-334.	7.0	199
566	Heterologous production of non-ribosomal peptide LLD-ACV in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2009, 11, 391-397.	7.0	38
567	Disruption of the NADPH-dependent glutamate dehydrogenase affects the morphology of two industrial strains of <i>Penicillium chrysogenum</i> . <i>Journal of Biotechnology</i> , 2009, 139, 280-282.	3.8	10
568	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6477-6482.	7.1	154
569	Current status of systems biology in <i>Aspergilli</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S180-S190.	2.1	43
570	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	2.1	133
571	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	2.1	99
572	Nutritional Systems Biology: Definitions and Approaches. <i>Annual Review of Nutrition</i> , 2009, 29, 329-339.	10.1	75
573	Systemic analysis of the response of <i>Aspergillus niger</i> to ambient pH. <i>Genome Biology</i> , 2009, 10, R47.	9.6	99
574	Gene deletion of cytosolic ATP: citrate lyase leads to altered organic acid production in <i>Aspergillus niger</i> . <i>Journal of Industrial Microbiology and Biotechnology</i> , 2009, 36, 1275-1280.	3.0	28
575	Structure and Flux Analysis of Metabolic Networks. , 2009, , .		0
576	The yeast metabolome addressed by electrospray ionization mass spectrometry: Initiation of a mass spectral library and its applications for metabolic footprinting by direct infusion mass spectrometry. <i>Metabolomics</i> , 2008, 4, 393-405.	3.0	27

#	ARTICLE	IF	CITATIONS
577	Production of plant sesquiterpenes in <i>Saccharomyces cerevisiae</i> : Effect of <i>ERG9</i> repression on sesquiterpene biosynthesis. <i>Biotechnology and Bioengineering</i> , 2008, 99, 666-677.	3.3	216
578	The roles of galactitol, galactose-1-phosphate, and phosphoglucomutase in galactose-induced toxicity in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2008, 101, 317-326.	3.3	58
579	Enhanced citrate production through gene insertion in <i>Aspergillus niger</i> . <i>Metabolic Engineering</i> , 2008, 10, 87-96.	7.0	67
580	Production of the polyketide 6-MSA in yeast engineered for increased malonyl-CoA supply. <i>Metabolic Engineering</i> , 2008, 10, 246-254.	7.0	98
581	Impact of systems biology on metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2008, 8, 122-131.	2.3	131
582	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008, 26, 1155-1160.	17.5	530
583	Metabolic Control Analysis of Xylose Catabolism in <i>Aspergillus</i> . <i>Biotechnology Progress</i> , 2008, 19, 1136-1141.	2.6	23
584	Natural computation meta-heuristics for the in silico optimization of microbial strains. <i>BMC Bioinformatics</i> , 2008, 9, 499.	2.6	90
585	Analysis of <i>Aspergillus nidulans</i> metabolism at the genome-scale. <i>BMC Genomics</i> , 2008, 9, 163.	2.8	77
586	Improved annotation through genome-scale metabolic modeling of <i>Aspergillus oryzae</i> . <i>BMC Genomics</i> , 2008, 9, 245.	2.8	88
587	Transcription factor control of growth rate dependent genes in <i>Saccharomyces cerevisiae</i> : A three factor design. <i>BMC Genomics</i> , 2008, 9, 341.	2.8	50
588	Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. <i>BMC Systems Biology</i> , 2008, 2, 17.	3.0	121
589	The genome-scale metabolic model iIN800 of <i>Saccharomyces cerevisiae</i> and its validation: a scaffold to query lipid metabolism. <i>BMC Systems Biology</i> , 2008, 2, 71.	3.0	141
590	Reconstruction of a bacterial isoprenoid biosynthetic pathway in <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 2008, 582, 4032-4038.	2.8	36
591	Metabolic footprinting in microbiology: methods and applications in functional genomics and biotechnology. <i>Trends in Biotechnology</i> , 2008, 26, 490-497.	9.3	122
592	Can yeast systems biology contribute to the understanding of human disease?. <i>Trends in Biotechnology</i> , 2008, 26, 584-590.	9.3	87
593	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i> . <i>Molecular Systems Biology</i> , 2008, 4, 178.	7.2	190
594	Physiological characterization of glucose repression in the strains with SNF1 and SNF4 genes deleted. <i>Journal of Biotechnology</i> , 2008, 133, 73-81.	3.8	11

#	ARTICLE	IF	CITATIONS
595	Characterization of Global Yeast Quantitative Proteome Data Generated from the Wild-Type and Glucose Repression <i>Saccharomyces cerevisiae</i> Strains: The Comparison of Two Quantitative Methods. Journal of Proteome Research, 2008, 7, 266-275.	3.7	101
596	Antibiotic Overproduction in Streptomyces coelicolor A3(2) Mediated by Phosphofructokinase Deletion*. Journal of Biological Chemistry, 2008, 283, 25186-25199.	3.4	131
597	A trispecies<i>Aspergillus</i>microarray: Comparative transcriptomics of three<i>Aspergillus</i>species. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4387-4392.	7.1	152
598	Design and Application of Genome-Scale Reconstructed Metabolic Models. Methods in Molecular Biology, 2008, 416, 409-431.	0.9	47
599	Growth Temperature Exerts Differential Physiological and Transcriptional Responses in Laboratory and Wine Strains of <i>Saccharomyces cerevisiae</i>. Applied and Environmental Microbiology, 2008, 74, 6358-6368.	3.1	91
600	NADPH-dependent glutamate dehydrogenase in Penicillium chrysogenum is involved in regulation of β -lactam production. Microbiology (United Kingdom), 2008, 154, 1242-1250.	1.8	11
601	Systems Analysis Unfolds the Relationship between the Phosphoketolase Pathway and Growth in Aspergillus nidulans. PLoS ONE, 2008, 3, e3847.	2.5	40
602	Increasing NADH oxidation reduces overflow metabolism in Saccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2402-2407.	7.1	302
603	Transient Marker System for Iterative Gene Targeting of a Prototrophic Fungus. Applied and Environmental Microbiology, 2007, 73, 7240-7245.	3.1	12
604	Principles of optimal metabolic network operation. Molecular Systems Biology, 2007, 3, 126.	7.2	28
605	The Metabolic Response of Heterotrophic Arabidopsis Cells to Oxidative Stress. Plant Physiology, 2007, 143, 312-325.	4.8	234
606	The role of metabolomics in systems biology. Topics in Current Genetics, 2007, , 1-10.	0.7	26
607	Data acquisition, analysis, and mining: Integrative tools for discerning metabolic function in Saccharomyces cerevisiae. Topics in Current Genetics, 2007, , 159-187.	0.7	0
608	From Gene Expression to Metabolic Fluxes. , 2007, , 37-66.		2
609	A systems biology approach to study glucose repression in the yeast Saccharomyces cerevisiae. Biotechnology and Bioengineering, 2007, 96, 134-145.	3.3	71
610	A comparison of direct infusion MS and GC-MS for metabolic footprinting of yeast mutants. Biotechnology and Bioengineering, 2007, 96, 1014-1022.	3.3	45
611	Optimization of heterologous production of the polyketide 6-MSA in Saccharomyces cerevisiae. Biotechnology and Bioengineering, 2007, 97, 893-900.	3.3	47
612	Understanding signaling in yeast: Insights from network analysis. Biotechnology and Bioengineering, 2007, 97, 1246-1258.	3.3	28

#	ARTICLE	IF	CITATIONS
613	Identification of flux regulation coefficients from elementary flux modes: A systems biology tool for analysis of metabolic networks. <i>Biotechnology and Bioengineering</i> , 2007, 97, 1535-1549.	3.3	33
614	Physiological characterization of xylose metabolism in <i>Aspergillus niger</i> under oxygen-limited conditions. <i>Biotechnology and Bioengineering</i> , 2007, 98, 462-475.	3.3	30
615	Evidence, through C13-labelling analysis, of phosphoketolase activity in fungi. <i>Process Biochemistry</i> , 2007, 42, 1050-1055.	3.7	13
616	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	17.5	1,047
617	Effect of carbon source perturbations on transcriptional regulation of metabolic fluxes in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2007, 1, 18.	3.0	38
618	Systems biology of antibiotic production by microorganisms. <i>Natural Product Reports</i> , 2007, 24, 1262.	10.3	151
619	Standard reporting requirements for biological samples in metabolomics experiments: microbial and in vitro biology experiments. <i>Metabolomics</i> , 2007, 3, 189-194.	3.0	50
620	Elucidating the mode-of-action of compounds from metabolite profiling studies. , 2007, 64, 103-129.		2
621	Metabolic network driven analysis of genome-wide transcription data from <i>Aspergillus nidulans</i> . <i>Genome Biology</i> , 2006, 7, R108.	9.6	52
622	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006, 7, R107.	9.6	205
623	Integration of metabolome data with metabolic networks reveals reporter reactions. <i>Molecular Systems Biology</i> , 2006, 2, 50.	7.2	131
624	Transcription analysis using high-density micro-arrays of <i>Aspergillus nidulans</i> wild-type and <i>creA</i> mutant during growth on glucose or ethanol. <i>Fungal Genetics and Biology</i> , 2006, 43, 593-603.	2.1	59
625	Yeast systems biology to unravel the network of life. <i>Yeast</i> , 2006, 23, 227-238.	1.7	66
626	In silico aided metabolic engineering of <i>Saccharomyces cerevisiae</i> for improved bioethanol production. <i>Metabolic Engineering</i> , 2006, 8, 102-111.	7.0	311
627	Fungal metabolite analysis in genomics and phenomics. <i>Current Opinion in Biotechnology</i> , 2006, 17, 191-197.	6.6	89
628	Polyol synthesis in <i>Aspergillus niger</i> : Influence of oxygen availability, carbon and nitrogen sources on the metabolism. <i>Biotechnology and Bioengineering</i> , 2006, 94, 899-908.	3.3	54
629	Global Transcriptional and Physiological Responses of <i>Saccharomyces cerevisiae</i> to Ammonium, l-Alanine, or l-Glutamine Limitation. <i>Applied and Environmental Microbiology</i> , 2006, 72, 6194-6203.	3.1	52
630	Robust multi-scale clustering of large DNA microarray datasets with the consensus algorithm. <i>Bioinformatics</i> , 2006, 22, 58-67.	4.1	72

#	ARTICLE	IF	CITATIONS
631	Deletion of RTS1 , Encoding a Regulatory Subunit of Protein Phosphatase 2A, Results in Constitutive Amino Acid Signaling via Increased Stp1p Processing. <i>Eukaryotic Cell</i> , 2006, 5, 174-179.	3.4	22
632	Hap4 Is Not Essential for Activation of Respiration at Low Specific Growth Rates in <i>Saccharomyces cerevisiae</i> *. <i>Journal of Biological Chemistry</i> , 2006, 281, 12308-12314.	3.4	31
633	From Glucose to Antibiotics: What Controls the Fluxes?., 2005, , 195-214.		0
634	High-throughput metabolic state analysis: the missing link in integrated functional genomics of yeasts. <i>Biochemical Journal</i> , 2005, 388, 669-677.	3.7	147
635	Biosynthesis of glyoxylate from glycine in. <i>FEMS Yeast Research</i> , 2005, 5, 703-709.	2.3	31
636	Comparative metabolic network analysis of two xylose fermenting recombinant <i>Saccharomyces cerevisiae</i> strains. <i>Metabolic Engineering</i> , 2005, 7, 437-444.	7.0	65
637	From genomes to in silico cells via metabolic networks. <i>Current Opinion in Biotechnology</i> , 2005, 16, 350-355.	6.6	78
638	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005, 6, 308.	2.6	374
639	The next wave in metabolome analysis. <i>Trends in Biotechnology</i> , 2005, 23, 544-546.	9.3	204
640	Modeling <i>Lactococcus lactis</i> using a genome-scale flux model. <i>BMC Microbiology</i> , 2005, 5, 39.	3.3	231
641	Teaching microbial physiology using glucose repression phenomenon in baker's yeast as an example. <i>Biochemistry and Molecular Biology Education</i> , 2005, 33, 404-410.	1.2	4
642	Mass spectrometry in metabolome analysis. <i>Mass Spectrometry Reviews</i> , 2005, 24, 613-646.	5.4	513
643	Analysis of acyl CoA ester intermediates of the mevalonate pathway in <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2005, 67, 119-124.	3.6	23
644	Grr1p is required for transcriptional induction of amino acid permease genes and proper transcriptional regulation of genes in carbon metabolism of <i>Saccharomyces cerevisiae</i> . <i>Current Genetics</i> , 2005, 47, 139-149.	1.7	15
645	The role of high-throughput transcriptome analysis in metabolic engineering. <i>Biotechnology and Bioprocess Engineering</i> , 2005, 10, 385-399.	2.6	14
646	Global metabolite analysis of yeast: evaluation of sample preparation methods. <i>Yeast</i> , 2005, 22, 1155-1169.	1.7	365
647	CreA influences the metabolic fluxes of <i>Aspergillus nidulans</i> during growth on glucose and xylose. <i>Microbiology (United Kingdom)</i> , 2005, 151, 2209-2221.	1.8	40
648	Metabolite profiling of fungi and yeast: from phenotype to metabolome by MS and informatics. <i>Journal of Experimental Botany</i> , 2005, 56, 273-286.	4.8	172

#	ARTICLE	IF	CITATIONS
649	Improvement of Galactose Uptake in <i>Saccharomyces cerevisiae</i> through Overexpression of Phosphoglucumutase: Example of Transcript Analysis as a Tool in Inverse Metabolic Engineering. <i>Applied and Environmental Microbiology</i> , 2005, 71, 6465-6472.	3.1	116
650	Genome-scale analysis of <i>Streptomyces coelicolor</i> A3(2) metabolism. <i>Genome Research</i> , 2005, 15, 820-829.	5.5	215
651	Intracellular metabolite profiling of <i>Fusarium oxysporum</i> converting glucose to ethanol. <i>Journal of Biotechnology</i> , 2005, 115, 425-434.	3.8	78
652	Uncovering transcriptional regulation of metabolism by using metabolic network topology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2685-2689.	7.1	553
653	Microbial Isoprenoid Production: An Example of Green Chemistry through Metabolic Engineering. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2005, 100, 19-51.	1.1	70
654	Metabolic Network Analysis of <i>Streptomyces tenebrarius</i> , a <i>Streptomyces</i> Species with an Active Entner-Doudoroff Pathway. <i>Applied and Environmental Microbiology</i> , 2005, 71, 2294-2302.	3.1	54
655	Modelling of Fungal Metabolism. , 2005, , 195-214.		0
656	Control of Fluxes Towards Antibiotics and the Role of Primary Metabolism in Production of Antibiotics. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2004, 88, 137-178.	1.1	22
657	Protein kinase A is involved in the control of morphology and branching during aerobic growth of <i>Mucor circinelloides</i> . <i>Microbiology (United Kingdom)</i> , 2004, 150, 143-150.	1.8	17
658	Identification of the Entner-Doudoroff pathway in an antibiotic-producing actinomycete species. <i>Molecular Microbiology</i> , 2004, 52, 895-902.	2.5	39
659	Pyruvate decarboxylases from the petite-negative yeast <i>Saccharomyces kluyveri</i> . <i>Molecular Genetics and Genomics</i> , 2004, 270, 558-568.	2.1	16
660	Elucidation of the role of Grr1p in glucose sensing by through genome-wide transcription analysis. <i>FEMS Yeast Research</i> , 2004, 5, 193-204.	2.3	14
661	Characterisation of the <i>Mucor circinelloides</i> regulated promoter <i>gpd1P</i> . <i>Current Genetics</i> , 2004, 45, 225-234.	1.7	15
662	Aerobic and anaerobic ethanol production by <i>Mucor circinelloides</i> during submerged growth. <i>Applied Microbiology and Biotechnology</i> , 2004, 63, 543-548.	3.6	39
663	The effect of CreA in glucose and xylose catabolism in <i>Aspergillus nidulans</i> . <i>Applied Microbiology and Biotechnology</i> , 2004, 63, 748-753.	3.6	32
664	Lipase production by recombinant strains of <i>Aspergillus niger</i> expressing a lipase-encoding gene from <i>Thermomyces lanuginosus</i> . <i>Applied Microbiology and Biotechnology</i> , 2004, 65, 714-719.	3.6	30
665	Transcriptional profiling of extracellular amino acid sensing in <i>Saccharomyces cerevisiae</i> and the role of Stp1p and Stp2p. <i>Yeast</i> , 2004, 21, 635-648.	1.7	29
666	Phenotypic characterization of glucose repression mutants of <i>Saccharomyces cerevisiae</i> using experiments with ¹³ C-labelled glucose. <i>Yeast</i> , 2004, 21, 769-779.	1.7	50

#	ARTICLE	IF	CITATIONS
667	Genome-wide transcriptional response of a <i>Saccharomyces cerevisiae</i> strain with an altered redox metabolism. <i>Biotechnology and Bioengineering</i> , 2004, 85, 269-276.	3.3	32
668	Impact of transamination reactions and protein turnover on labeling dynamics in ^{13}C -labeling experiments. <i>Biotechnology and Bioengineering</i> , 2004, 86, 209-216.	3.3	35
669	Glucose metabolism in the antibiotic producing actinomycete <i>Nonomuraea</i> sp. ATCC 39727. <i>Biotechnology and Bioengineering</i> , 2004, 88, 652-663.	3.3	18
670	The First International Workshop on Systems Biology of Yeast, St. Louis, USA, 9 November, 2003. <i>FEMS Yeast Research</i> , 2004, 4, 757-758.	2.3	1
671	Impact of ^{13}C -analyses on inverse metabolic engineering. <i>Metabolic Engineering</i> , 2004, 6, 204-211.	7.0	96
672	Integration of gene expression data into genome-scale metabolic models. <i>Metabolic Engineering</i> , 2004, 6, 285-293.	7.0	198
673	Metabolic network analysis on <i>Phaffia rhodozyma</i> yeast using ^{13}C -labeled glucose and gas chromatography-mass spectrometry. <i>Metabolic Engineering</i> , 2004, 6, 340-351.	7.0	32
674	Manipulation of malic enzyme in <i>Saccharomyces cerevisiae</i> for increasing NADPH production capacity aerobically in different cellular compartments. <i>Metabolic Engineering</i> , 2004, 6, 352-363.	7.0	73
675	Use of genome-scale microbial models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2004, 15, 64-69.	6.6	150
676	Use of laminar flow patterning for miniaturised biochemical assays. <i>Lab on A Chip</i> , 2004, 4, 654-657.	6.0	24
677	En Route for Systems Biology: In Silico Pathway Analysis and Metabolite Profiling. , 2004, , 47-58.		0
678	It Is All about Metabolic Fluxes. <i>Journal of Bacteriology</i> , 2003, 185, 7031-7035.	2.2	221
679	Large-Scale Evaluation of In Silico Gene Deletions in <i>Saccharomyces cerevisiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 193-202.	2.0	135
680	Production of the glycopeptide antibiotic A40926 by <i>Nonomuraea</i> sp. ATCC 39727: influence of medium composition in batch fermentation. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2003, 30, 150-156.	3.0	35
681	Morphology and physiology of the dimorphic fungus <i>Mucor circinelloides</i> (syn. <i>M. racemosus</i>) during anaerobic growth. <i>Mycological Research</i> , 2003, 107, 223-230.	2.5	25
682	Effect of deletion of chitin synthase genes on mycelial morphology and culture viscosity in <i>Aspergillus oryzae</i> . <i>Biotechnology and Bioengineering</i> , 2003, 81, 525-534.	3.3	18
683	Production of savinase and population viability of <i>Bacillus clausii</i> during high-cell-density fed-batch cultivations. <i>Biotechnology and Bioengineering</i> , 2003, 83, 344-352.	3.3	24
684	Continuous cultivations of a <i>Penicillium chrysogenum</i> strain expressing the expandase gene from <i>Streptomyces clavuligerus</i> : Growth yields and morphological characterization. <i>Biotechnology and Bioengineering</i> , 2003, 83, 361-368.	3.3	18

#	ARTICLE	IF	CITATIONS
685	Continuous cultivations of a <i>Penicillium chrysogenum</i> strain expressing the expandase gene from <i>Streptomyces clavuligerus</i> : Kinetics of adipoyl-7-aminodeacetoxycephalosporanic acid and byproduct formations. <i>Biotechnology and Bioengineering</i> , 2003, 83, 353-360.	3.3	8
686	Simultaneous analysis of amino and nonamino organic acids as methyl chloroformate derivatives using gas chromatography-mass spectrometry. <i>Analytical Biochemistry</i> , 2003, 322, 134-138.	2.4	177
687	Influence of the adipate and dissolved oxygen concentrations on the \hat{I}^2 -lactam production during continuous cultivations of a <i>Penicillium chrysogenum</i> strain expressing the expandase gene from <i>Streptomyces clavuligerus</i> . <i>Metabolic Engineering</i> , 2003, 5, 42-48.	7.0	14
688	Reconstruction of the central carbon metabolism of <i>Aspergillus niger</i> . <i>FEBS Journal</i> , 2003, 270, 4243-4253.	0.2	79
689	Characterization of the <i>Mucor circinelloides</i> life cycle by on-line image analysis. <i>Journal of Applied Microbiology</i> , 2003, 95, 1152-1160.	3.1	32
690	Surface Hydrophobicity of <i>Aspergillus nidulans</i> Conidiospores and Its Role in Pellet Formation. <i>Biotechnology Progress</i> , 2003, 19, 1049-1052.	2.6	62
691	Fungal genomics beyond <i>Saccharomyces cerevisiae</i> ?. <i>Current Opinion in Biotechnology</i> , 2003, 14, 226-231.	6.6	31
692	Metabolic engineering of \hat{I}^2 -lactam production. <i>Metabolic Engineering</i> , 2003, 5, 56-69.	7.0	104
693	Aerobic physiology of redox-engineered strains modified in the ammonium assimilation for increased NADPH availability. <i>FEMS Yeast Research</i> , 2003, 4, 59-68.	2.3	39
694	Bioreaction Engineering: From Bioprocess Design to Systems Biology. , 2003, , 1-8.		0
695	Biochemical Reactions – A First Look. , 2003, , 47-93.		2
696	Biochemical Reaction Networks. , 2003, , 119-188.		0
697	Enzyme Kinetics and Metabolic Control Analysis. , 2003, , 189-234.		0
698	Modeling of Growth Kinetics. , 2003, , 235-314.		4
699	Population Balance Equations. , 2003, , 315-338.		0
700	Genome-Scale Reconstruction of the <i>Saccharomyces cerevisiae</i> Metabolic Network. <i>Genome Research</i> , 2003, 13, 244-253.	5.5	931
701	Branching is coordinated with mitosis in growing hyphae of <i>Aspergillus nidulans</i> . <i>Fungal Genetics and Biology</i> , 2003, 40, 15-24.	2.1	57
702	Metabolic Engineering of Ammonium Assimilation in Xylose-Fermenting <i>Saccharomyces cerevisiae</i> Improves Ethanol Production. <i>Applied and Environmental Microbiology</i> , 2003, 69, 4732-4736.	3.1	92

#	ARTICLE	IF	CITATIONS
703	Identification of In Vivo Enzyme Activities in the Cometabolism of Glucose and Acetate by <i>Saccharomyces cerevisiae</i> by Using 13 C-Labeled Substrates. <i>Eukaryotic Cell</i> , 2003, 2, 599-608.	3.4	63
704	<i>Saccharomyces cerevisiae</i> phenotypes can be predicted by using constraint-based analysis of a genome-scale reconstructed metabolic network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13134-13139.	7.1	345
705	Metabolic Engineering. , 2003, , 391-406.		3
706	Transcriptional, Proteomic, and Metabolic Responses to Lithium in Galactose-grown Yeast Cells. <i>Journal of Biological Chemistry</i> , 2003, 278, 32141-32149.	3.4	83
707	Yeast functional genomics and metabolic engineering: past, present and future. <i>Topics in Current Genetics</i> , 2003, , 331-360.	0.7	2
708	Bioreaction Engineering Principles. , 2003, , .		132
709	From Cellular Function to Industrial Products. , 2003, , 9-45.		0
710	Metabolic Engineering of the Morphology of <i>Aspergillus oryzae</i> by Altering Chitin Synthesis. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1827-1836.	3.1	61
711	Reproducibility of Oligonucleotide Microarray Transcriptome Analyses. <i>Journal of Biological Chemistry</i> , 2002, 277, 37001-37008.	3.4	208
712	Altering the expression of two chitin synthase genes differentially affects the growth and morphology of <i>Aspergillus oryzae</i> The GenBank accession numbers for the chsB, chsC and chsA gene sequences reported in this paper are AY029261, AF410464 and AF429307, respectively.. <i>Microbiology (United Kingdom)</i> , 2002, 148, 4025-4033.	1.8	31
713	Physiological characterisation of recombinant <i>Aspergillus nidulans</i> strains with different creA genotypes expressing <i>A. oryzae</i> α -amylase. <i>Journal of Biotechnology</i> , 2002, 92, 279-285.	3.8	22
714	Production of extracellular protease and glucose uptake in <i>Bacillus clausii</i> in steady-state and transient continuous cultures. <i>Journal of Biotechnology</i> , 2002, 97, 265-273.	3.8	30
715	An expanded role for microbial physiology in metabolic engineering and functional genomics: moving towards systems biology. <i>FEMS Yeast Research</i> , 2002, 2, 175-181.	2.3	11
716	Steady-state and transient-state analyses of aerobic fermentation in. <i>FEMS Yeast Research</i> , 2002, 2, 233-244.	2.3	14
717	Aerobic glucose metabolism of <i>Saccharomyces kluyveri</i> : Growth, metabolite production, and quantification of metabolic fluxes. <i>Biotechnology and Bioengineering</i> , 2002, 77, 186-193.	3.3	40
718	Production of teicoplanin by <i>Actinoplanes teichomyceticus</i> in continuous fermentation. <i>Biotechnology and Bioengineering</i> , 2002, 77, 589-598.	3.3	10
719	The simultaneous biosynthesis and uptake of amino acids by <i>Lactococcus lactis</i> studied by ^{13}C -labeling experiments. <i>Biotechnology and Bioengineering</i> , 2002, 78, 11-16.	3.3	9
720	A functional genomics approach using metabolomics and in silico pathway analysis. <i>Biotechnology and Bioengineering</i> , 2002, 79, 703-712.	3.3	79

#	ARTICLE	IF	CITATIONS
721	Metabolic Network Analysis of an Adipoyl-7-ADCA-Producing Strain of <i>Penicillium chrysogenum</i> : Elucidation of Adipate Degradation. <i>Metabolic Engineering</i> , 2002, 4, 151-158.	7.0	37
722	Metabolic Network Analysis of <i>Bacillus clausii</i> on Minimal and Semirich Medium Using ¹³ C-Labeled Glucose. <i>Metabolic Engineering</i> , 2002, 4, 159-169.	7.0	42
723	Growth physiology and dimorphism of <i>Mucor circinelloides</i> (syn . <i>racemosus</i>) during submerged batch cultivation. <i>Applied Microbiology and Biotechnology</i> , 2002, 58, 495-502.	3.6	66
724	Fermentation performance and intracellular metabolite patterns in laboratory and industrial xylose-fermenting <i>Saccharomyces cerevisiae</i> . <i>Applied Microbiology and Biotechnology</i> , 2002, 59, 436-442.	3.6	98
725	Analysis of flux estimates based on ¹³ C-labelling experiments. <i>FEBS Journal</i> , 2002, 269, 2795-2800.	0.2	59
726	An expanded role for microbial physiology in metabolic engineering and functional genomics: moving towards systems biology. <i>FEMS Yeast Research</i> , 2002, 2, 175-181.	2.3	61
727	Steady-state and transient-state analyses of aerobic fermentation in <i>Saccharomyces kluyveri</i> . <i>FEMS Yeast Research</i> , 2002, 2, 233-244.	2.3	10
728	Reciprocal ¹³ C-Labeling: A Method for Investigating the Catabolism of Cosubstrates. <i>Biotechnology Progress</i> , 2002, 18, 163-166.	2.6	8
729	Growth energetics of an alkaline serine protease-producing strain of <i>Bacillus clausii</i> during continuous cultivation. <i>Bioprocess and Biosystems Engineering</i> , 2002, 24, 329-339.	3.4	8
730	GROWTH AND ENZYME PRODUCTION DURING CONTINUOUS CULTURES OF A HIGH AMYLASE-PRODUCING VARIANT OF <i>Aspergillus Oryzae</i> . <i>Brazilian Journal of Chemical Engineering</i> , 2002, 19, 55-68.	1.3	9
731	Metabolic Engineering of the Morphology of <i>Aspergillus</i> . <i>Advances in Biochemical Engineering/Biotechnology</i> , 2001, 73, 103-128.	1.1	46
732	The impact of , , and on glucose control of the system in. <i>FEMS Yeast Research</i> , 2001, 1, 47-55.	2.3	1
733	Î±-Amylase production in high cell density submerged cultivation of <i>Aspergillus oryzae</i> and <i>A. nidulans</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 55, 81-84.	3.6	20
734	Metabolic engineering. <i>Applied Microbiology and Biotechnology</i> , 2001, 55, 263-283.	3.6	285
735	Changes of in vivo fluxes through central metabolic pathways during the production of nystatin by <i>Streptomyces noursei</i> in batch culture. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 93-100.	3.6	33
736	Fuel ethanol production from lignocellulose: a challenge for metabolic engineering and process integration. <i>Applied Microbiology and Biotechnology</i> , 2001, 56, 17-34.	3.6	788
737	Production of a heterologous proteinase A by <i>Saccharomyces kluyveri</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 57, 216-219.	3.6	6
738	Influence of carbon source on Î±-amylase production by <i>Aspergillus oryzae</i> . <i>Applied Microbiology and Biotechnology</i> , 2001, 57, 346-349.	3.6	74

#	ARTICLE	IF	CITATIONS
739	Physiological characterisation of <i>Penicillium chrysogenum</i> strains expressing the expandase gene from <i>Streptomyces clavuligerus</i> during batch cultivations. Growth and adipoyl-7-aminodeacetoxycephalosporanic acid production.. <i>Applied Microbiology and Biotechnology</i> , 2001, 57, 357-362.	3.6	28
740	Quantitative analysis of <i>Penicillium chrysogenum</i> Wis54-1255 transformants overexpressing the penicillin biosynthetic genes. <i>Biotechnology and Bioengineering</i> , 2001, 72, 379-388.	3.3	42
741	Expression of a cytoplasmic transhydrogenase in <i>Saccharomyces cerevisiae</i> results in formation of 2-oxoglutarate due to depletion of the NADPH pool. <i>Yeast</i> , 2001, 18, 19-32.	1.7	115
742	In vivo dynamics of galactose metabolism in <i>Saccharomyces cerevisiae</i> : Metabolic fluxes and metabolite levels. <i>Biotechnology and Bioengineering</i> , 2001, 73, 412-425.	3.3	50
743	Simple and robust method for estimation of the split between the oxidative pentose phosphate pathway and the Embden-Meyerhof-Parnas pathway in microorganisms. <i>Biotechnology and Bioengineering</i> , 2001, 74, 517-523.	3.3	28
744	The impact of GAL6, GAL80, and MIG1 on glucose control of the GAL system in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2001, 1, 47-55.	2.3	39
745	Network Identification and Flux Quantification in the Central Metabolism of <i>Saccharomyces cerevisiae</i> under Different Conditions of Glucose Repression. <i>Journal of Bacteriology</i> , 2001, 183, 1441-1451.	2.2	334
746	Quantitative analysis of <i>Penicillium chrysogenum</i> Wis54-1255 transformants overexpressing the penicillin biosynthetic genes. , 2001, 72, 379.		1
747	Mathematical Modelling of Microbial Processes-Motivation and Means. , 2001, , 61-75.		2
748	Morphological characterization of <i>Aspergillus nidulans</i> : growth, septation and fragmentation. <i>Microbiology (United Kingdom)</i> , 2001, 147, 239-246.	1.8	20
749	Semi-on-line analysis for fast and precise monitoring of bioreaction processes. , 2000, 52, 237-247.		16
750	Physiological studies in aerobic batch cultivations of <i>Saccharomyces cerevisiae</i> strains harboring the MEL1 gene. <i>Biotechnology and Bioengineering</i> , 2000, 68, 252-259.	3.3	57
751	Metabolic network analysis of <i>penicillium chrysogenum</i> using ¹³ C-labeled glucose. , 2000, 68, 652-659.		105
752	Anaerobic and aerobic batch cultivations of <i>Saccharomyces cerevisiae</i> mutants impaired in glycerol synthesis. <i>Yeast</i> , 2000, 16, 463-474.	1.7	140
753	Simultaneous overexpression of enzymes of the lower part of glycolysis can enhance the fermentative capacity of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2000, 16, 1325-1334.	1.7	75
754	Construction and Characterization of an Oxalic Acid Nonproducing Strain of <i>Aspergillus niger</i> . <i>Metabolic Engineering</i> , 2000, 2, 34-41.	7.0	65
755	Optimization of Ethanol Production in <i>Saccharomyces cerevisiae</i> by Metabolic Engineering of the Ammonium Assimilation. <i>Metabolic Engineering</i> , 2000, 2, 69-77.	7.0	200
756	Structural and transcriptional analysis of the pyrABCN, pyrD and pyrF genes in <i>Aspergillus nidulans</i> and the evolutionary origin of fungal dihydroorotases. Erratum. <i>Molecular Microbiology</i> , 2000, 36, 995-995.	2.5	0

#	ARTICLE	IF	CITATIONS
757	An interlaboratory comparison of physiological and genetic properties of four <i>Saccharomyces cerevisiae</i> strains. <i>Enzyme and Microbial Technology</i> , 2000, 26, 706-714.	3.2	488
758	The role of metabolic engineering in the improvement of <i>Saccharomyces cerevisiae</i> : utilization of industrial media. <i>Enzyme and Microbial Technology</i> , 2000, 26, 785-792.	3.2	46
759	Mathematical modelling of metabolism. <i>Current Opinion in Biotechnology</i> , 2000, 11, 180-186.	6.6	165
760	Increasing galactose consumption by <i>Saccharomyces cerevisiae</i> through metabolic engineering of the GAL gene regulatory network. <i>Nature Biotechnology</i> , 2000, 18, 1283-1286.	17.5	168
761	Metabolic characterization of high- and low-yielding strains of <i>Penicillium chrysogenum</i> . <i>Applied Microbiology and Biotechnology</i> , 2000, 54, 212-217.	3.6	41
762	Glucoamylase production in batch, chemostat and fed-batch cultivations by an industrial strain of <i>Aspergillus niger</i> . <i>Applied Microbiology and Biotechnology</i> , 2000, 53, 272-277.	3.6	64
763	The influence of nitrogen sources on the α -amylase productivity of <i>Aspergillus oryzae</i> in continuous cultures. <i>Applied Microbiology and Biotechnology</i> , 2000, 53, 278-281.	3.6	74
764	Cloning and characterization of oah, the gene encoding oxaloacetate hydrolase in <i>Aspergillus niger</i> . <i>Molecular Genetics and Genomics</i> , 2000, 263, 281-286.	2.4	33
765	Antisense Silencing of the creA Gene in <i>Aspergillus nidulans</i> . <i>Applied and Environmental Microbiology</i> , 2000, 66, 4579-4581.	3.1	38
766	Biosynthetic Studies of the Glycopeptide Teicoplanin by ¹ H and ¹³ C NMR. <i>Journal of Biological Chemistry</i> , 2000, 275, 6201-6206.	3.4	6
767	Role of substrate concentration in mitosis and hyphal extension of <i>Aspergillus</i> . <i>Biotechnology and Bioengineering</i> , 2000, 67, 390-397.	3.3	33
768	Metabolic Engineering of <i>Saccharomyces cerevisiae</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2000, 64, 34-50.	6.6	369
769	Metabolic network analysis. A powerful tool in metabolic engineering. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2000, 66, 209-31.	1.1	20
770	Metabolic network analysis of <i>Penicillium chrysogenum</i> using (¹³ C)-labeled glucose. <i>Biotechnology and Bioengineering</i> , 2000, 68, 652-9.	3.3	21
771	Identification of Enzymes and Quantification of Metabolic Fluxes in the Wild Type and in a Recombinant <i>Aspergillus oryzae</i> Strain. <i>Applied and Environmental Microbiology</i> , 1999, 65, 11-19.	3.1	77
772	Study of the glucoamylase promoter in <i>Aspergillus niger</i> using green fluorescent protein. <i>Microbiology (United Kingdom)</i> , 1999, 145, 729-734.	1.8	30
773	Structural and transcriptional analysis of the pyrABCN, pyrD and pyrF genes in <i>Aspergillus nidulans</i> and the evolutionary origin of fungal dihydroorotases. <i>Molecular Microbiology</i> , 1999, 33, 599-611.	2.5	13
774	Metabolic control analysis of the penicillin biosynthetic pathway: the influence of the LLD-ACV:bisACV ratio on the flux control. <i>Antonie Van Leeuwenhoek</i> , 1999, 75, 145-154.	1.7	30

#	ARTICLE	IF	CITATIONS
775	Isotopomer Analysis Using GC-MS. <i>Metabolic Engineering</i> , 1999, 1, 282-290.	7.0	218
776	Genetically structured modeling of protein production in filamentous fungi. , 1999, 66, 164-170.		10
777	On-line study of growth kinetics of single hyphae of <i>Aspergillus oryzae</i> in a flow-through cell. , 1999, 63, 147-153.		29
778	Kinetics of α -amylase secretion in <i>Aspergillus oryzae</i> . , 1999, 65, 76-82.		4
779	Metabolic Network Analysis. <i>Advances in Biochemical Engineering/Biotechnology</i> , 1999, , 209-231.	1.1	24
780	Investigation of the impact of 1 and 2 on the physiology of. <i>Journal of Biotechnology</i> , 1999, 68, 197-212.	3.8	65
781	Quantitative analysis of metabolic fluxes in <i>Escherichia coli</i> , using two-dimensional NMR spectroscopy and complete isotopomer models. <i>Journal of Biotechnology</i> , 1999, 71, 175-189.	3.8	154
782	Derepression of galactose metabolism in melibiase producing bakers' and distillers' yeast. <i>Journal of Biotechnology</i> , 1999, 72, 213-228.	3.8	30
783	Growth and Production Kinetics of a Teicoplanin Producing Strain of <i>Actinoplanes teichomyceticus</i> .. <i>Journal of Antibiotics</i> , 1999, 52, 40-44.	2.0	16
784	Expression of the <i>Escherichia coli</i> pntA and pntB Genes, Encoding Nicotinamide Nucleotide Transhydrogenase, in <i>Saccharomyces cerevisiae</i> and Its Effect on Product Formation during Anaerobic Glucose Fermentation. <i>Applied and Environmental Microbiology</i> , 1999, 65, 2333-2340.	3.1	52
785	α -Amylase production in recombinant <i>Aspergillus oryzae</i> during fed-batch and continuous cultivations. <i>Journal of Bioscience and Bioengineering</i> , 1998, 86, 49-56.	0.9	25
786	Cleanup and Analysis of Sugar Phosphates in Biological Extracts by Using Solid-Phase Extraction and Anion-Exchange Chromatography with Pulsed Amperometric Detection. <i>Analytical Biochemistry</i> , 1998, 261, 36-42.	2.4	79
787	Growth and product formation of <i>Aspergillus oryzae</i> during submerged cultivations: Verification of a morphologically structured model using fluorescent probes. , 1998, 57, 321-329.		66
788	Metabolic engineering: Techniques for analysis of targets for genetic manipulations. <i>Biotechnology and Bioengineering</i> , 1998, 58, 125-132.	3.3	130
789	^{13}C tracer experiments and metabolite balancing for metabolic flux analysis: Comparing two approaches. , 1998, 58, 254-257.		75
790	On-line study of fungal morphology during submerged growth in a small flow-through cell. , 1998, 58, 541-553.		61
791	Modelling of the protonophoric uncoupling by phenoxyacetic acid of the plasma membrane potential of <i>Penicillium chrysogenum</i> . , 1998, 60, 761-767.		17
792	Carbon catabolite repression of invertase during batch cultivations of <i>Saccharomyces cerevisiae</i> : the role of glucose, fructose, and mannose. <i>Applied Microbiology and Biotechnology</i> , 1998, 50, 579-582.	3.6	47

#	ARTICLE	IF	CITATIONS
793	Identification and purification of O-acetyl-L-serine sulphhydrylase in <i>Penicillium chrysogenum</i> . <i>Applied Microbiology and Biotechnology</i> , 1998, 50, 663-668.	3.6	8
794	Nitrogen-limited continuous cultivations as a tool to quantify glucose control in <i>Saccharomyces cerevisiae</i> . <i>Enzyme and Microbial Technology</i> , 1998, 23, 91-100.	3.2	8
795	The role of metabolic engineering in the production of secondary metabolites. <i>Current Opinion in Microbiology</i> , 1998, 1, 330-336.	5.1	38
796	Modeling the mycelium morphology of <i>Penicillium</i> species in submerged cultures. <i>Advances in Biochemical Engineering/Biotechnology</i> , 1998, , 125-152.	1.1	10
797	The Essence of Metabolic Engineering. , 1998, , 1-20.		214
798	Methods for the Experimental Determination of Metabolic Fluxes by Isotope Labeling. , 1998, , 353-410.		0
799	Applications of Metabolic Flux Analysis. , 1998, , 411-459.		2
800	Metabolic Control Analysis. , 1998, , 461-533.		3
801	Material Balances and Data Consistency. , 1998, , 115-146.		6
802	High exogenous concentrations of phenoxyacetic acid are crucial for a high penicillin V productivity in <i>Penicillium chrysogenum</i> . <i>Microbiology (United Kingdom)</i> , 1998, 144, 2001-2006.	1.8	8
803	Glucose control in <i>Saccharomyces cerevisiae</i> : the role of MIG1 in metabolic functions. <i>Microbiology (United Kingdom)</i> , 1998, 144, 13-24.	1.8	181
804	Thermodynamics of Cellular Processes. , 1998, , 629-694.		0
805	Review of Cellular Metabolism. , 1998, , 21-79.		11
806	On-line study of fungal morphology during submerged growth in a small flow-through cell. <i>Biotechnology and Bioengineering</i> , 1998, 58, 541-53.	3.3	11
807	Modelling of the protonophoric uncoupling by phenoxyacetic acid of the plasma membrane potential of <i>Penicillium chrysogenum</i> . <i>Biotechnology and Bioengineering</i> , 1998, 60, 761-7.	3.3	4
808	Flux Distributions in Anaerobic, Glucose-Limited Continuous Cultures of <i>Saccharomyces Cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 1997, 143, 203-218.	1.8	358
809	Metabolic control analysis of biochemical pathways based on a thermokinetic description of reaction rates. <i>Biochemical Journal</i> , 1997, 321, 133-138.	3.7	71
810	Purification and characterization of γ -(L- α -aminoadipyl)-L-cysteinyl-D-valine synthetase from <i>Penicillium chrysogenum</i> . <i>Biochemical Journal</i> , 1997, 327, 185-191.	3.7	51

#	ARTICLE	IF	CITATIONS
811	Thermodynamics of Metabolic Pathways for Penicillin Production: Analysis of Thermodynamic Feasibility and Free Energy Changes During Fed-Batch Cultivation. <i>Biotechnology Progress</i> , 1997, 13, 156-165.	2.6	20
812	Influence of the Dissolved Oxygen Concentration on the Penicillin Biosynthetic Pathway in Steady-State Cultures of <i>Penicillium chrysogenum</i> . <i>Biotechnology Progress</i> , 1997, 13, 776-782.	2.6	40
813	Kinetic studies on the carboxylation of 6-amino-penicillanic acid to 8-hydroxy-penicillic acid. <i>Process Biochemistry</i> , 1997, 32, 85-91.	3.7	14
814	On-line and in situ monitoring of biomass in submerged cultivations. <i>Trends in Biotechnology</i> , 1997, 15, 517-522.	9.3	131
815	Title is missing!. <i>Biotechnology Letters</i> , 1997, 19, 257-262.	2.2	31
816	Modeling the growth and proteinase A production in continuous cultures of recombinant <i>Saccharomyces cerevisiae</i> . , 1997, 55, 447-454.		20
817	Modeling isotopomer distributions in biochemical networks using isotopomer mapping matrices. , 1997, 55, 831-840.		282
818	Simulation of penicillin production in fed-batch cultivations using a morphologically structured model. , 1997, 56, 593-604.		33
819	Analysis of single hyphal growth and fragmentation in submerged cultures using a population model. <i>Chemical Engineering Science</i> , 1997, 52, 2641-2652.	3.8	12
820	Silencing MIG1 in <i>Saccharomyces cerevisiae</i> : effects of antisense MIG1 expression and MIG1 gene disruption. <i>Applied and Environmental Microbiology</i> , 1997, 63, 2366-2371.	3.1	22
821	Growth energetics and metabolic fluxes in continuous cultures of <i>Penicillium chrysogenum</i> . <i>Journal of Biotechnology</i> , 1996, 45, 149-164.	3.8	103
822	Modelling the morphology of filamentous microorganisms. <i>Trends in Biotechnology</i> , 1996, 14, 438-443.	9.3	76
823	Pathway kinetics and metabolic control analysis of a high-yielding strain of <i>Penicillium chrysogenum</i> during fed batch cultivations. , 1996, 51, 168-176.		49
824	On-line monitoring of glucose and penicillin by sequential injection analysis. <i>Analytica Chimica Acta</i> , 1996, 320, 199-205.	5.4	40
825	Kinetic studies of acid-inactivation of α -amylase from <i>Aspergillus oryzae</i> . <i>Chemical Engineering Science</i> , 1996, 51, 37-43.	3.8	16
826	A kinetic model for the penicillin biosynthetic pathway in <i>Penicillium chrysogenum</i> . <i>Control Engineering Practice</i> , 1996, 4, 765-771.	5.5	11
827	Morphology and physiology of an α -amylase producing strain of <i>Aspergillus oryzae</i> during batch cultivations. <i>Biotechnology and Bioengineering</i> , 1996, 49, 266-276.	3.3	134
828	Alleviation of glucose repression of maltose metabolism by MIG1 disruption in <i>Saccharomyces cerevisiae</i> . <i>Applied and Environmental Microbiology</i> , 1996, 62, 4441-4449.	3.1	63

#	ARTICLE	IF	CITATIONS
829	Pellet formation and fragmentation in submerged cultures of <i>Penicillium chrysogenum</i> and its relation to penicillin production. <i>Biotechnology Progress</i> , 1995, 11, 93-98.	2.6	118
830	Metabolic control analysis of the penicillin biosynthetic pathway in a high-yielding strain of <i>Penicillium chrysogenum</i> . <i>Biotechnology Progress</i> , 1995, 11, 299-305.	2.6	80
831	Metabolic flux distributions in <i>Penicillium chrysogenum</i> during fed-batch cultivations. <i>Biotechnology and Bioengineering</i> , 1995, 46, 117-131.	3.3	170
832	Hyphal growth and fragmentation of <i>Penicillium chrysogenum</i> in submerged cultures. <i>Biotechnology and Bioengineering</i> , 1995, 46, 588-598.	3.3	84
833	Morphology of <i>Trichoderma reesei</i> QM 9414 in submerged cultures. <i>Biotechnology and Bioengineering</i> , 1995, 47, 609-615.	3.3	33
834	Acoustic off-gas analyser for bioreactors: Precision, accuracy and dynamics of detection. <i>Chemical Engineering Science</i> , 1995, 50, 2601-2610.	3.8	65
835	Simultaneous monitoring of glucose, lactic acid and penicillin by sequential injection analysis. <i>Analytica Chimica Acta</i> , 1995, 312, 149-156.	5.4	45
836	Influence of pH on the morphology of <i>Trichoderma reesei</i> qm 9414 in submerged culture.. <i>Biotechnology Letters</i> , 1995, 17, 341-344.	2.2	7
837	Measurement of α -amylase activity by Sequential Injection Analysis. <i>Biotechnology Letters</i> , 1995, 9, 763-766.	0.5	3
838	Continuous cultivation of <i>Penicillium chrysogenum</i> . Growth on glucose and penicillin production. <i>Journal of Biotechnology</i> , 1995, 42, 95-107.	3.8	54
839	Analysis of penicillin V biosynthesis during fed-batch cultivations with a high-yielding strain of <i>Penicillium chrysogenum</i> . <i>Applied Microbiology and Biotechnology</i> , 1995, 43, 123-130.	3.6	47
840	Induction and repression of α -amylase production in batch and continuous cultures of <i>Aspergillus oryzae</i> . <i>Microbiology (United Kingdom)</i> , 1995, 141, 2449-2454.	1.8	67
841	Analysis of Penicillin V biosynthesis during fed-batch cultivations with a high-yielding strain of <i>Penicillium chrysogenum</i> . <i>Applied Microbiology and Biotechnology</i> , 1995, 43, 123-130.	3.6	1
842	A novel technique based on 85Kr for quantification of gas-liquid mass transfer in bioreactors. <i>Chemical Engineering Science</i> , 1994, 49, 803-810.	3.8	27
843	An improved FIA-system for measuring α -amylase in cultivation media. <i>Biotechnology Letters</i> , 1994, 8, 479.	0.5	15
844	A robust liquid chromatographic method for measurement of medium components during penicillin fermentations. <i>Analytica Chimica Acta</i> , 1994, 296, 51-62.	5.4	41
845	Growth energetics of <i>Lactococcus cremoris</i> FD1 during energy-, carbon-, and nitrogen-limitation in steady state and transient cultures. <i>Chemical Engineering Science</i> , 1994, 49, 589-609.	3.8	54
846	Degradation of penicillin-V in fermentation media. <i>Biotechnology and Bioengineering</i> , 1994, 44, 165-169.	3.3	22

#	ARTICLE	IF	CITATIONS
847	Characterization of mixing in stirred tank bioreactors equipped with rushton turbines. Biotechnology and Bioengineering, 1994, 44, 1013-1017.	3.3	18
848	Simulation of Bioreactions. Computers and Chemical Engineering, 1994, 18, S615-S620.	3.8	2
849	Culture fluorescence measurements during batch and fed-batch cultivations with <i>Penicillium chrysogenum</i> . Journal of Biotechnology, 1994, 38, 51-62.	3.8	41
850	Modeling of Reaction Kinetics. , 1994, , 163-227.		2
851	Bioreactor Modeling. , 1994, , 415-440.		2
852	Growth and Protein Formation of Recombinant <i>Aspergillus</i> : Utility of Morphological Characterization by Image Analysis. , 1994, , 197-202.		7
853	Galactose Expulsion during Lactose Metabolism in <i>Lactococcus lactis</i> subsp. <i>cremoris</i> FD1 Due to Dephosphorylation of Intracellular Galactose 6-Phosphate. Applied and Environmental Microbiology, 1994, 60, 1254-1259.	3.1	39
854	Population Balances Based on Cell Number. , 1994, , 271-294.		1
855	Flow-injection analysis for the measurement of penicillin V in fermentation media. Analytica Chimica Acta, 1993, 274, 117-123.	5.4	16
856	On-line monitoring of penicillin V during penicillin fermentations: a comparison of two different methods based on flow-injection analysis. Analytica Chimica Acta, 1993, 279, 51-58.	5.4	29
857	Rheological characterization of media containing <i>Penicillium chrysogenum</i> . Biotechnology and Bioengineering, 1993, 41, 162-164.	3.3	49
858	A Simple morphologically structured model describing the growth of filamentous microorganisms. Biotechnology and Bioengineering, 1993, 41, 715-727.	3.3	89
859	Transport of sugars via two anomer-specific sites on mannose-phosphotransferase system in <i>Lactococcus cremoris</i> : In vivo study of mechanism, kinetics, and adaptation. Biotechnology and Bioengineering, 1993, 42, 440-448.	3.3	8
860	Two Uptake Systems for Fructose in <i>Lactococcus lactis</i> subsp. <i>cremoris</i> FD1 Produce Glycolytic and Gluconeogenic Fructose Phosphates and Induce Oscillations in Growth and Lactic Acid Formation. Applied and Environmental Microbiology, 1993, 59, 3206-3211.	3.1	21
861	On-line monitoring of penicillin V during penicillin fermentations: a comparison of two different methods based on flow-injection analysis. , 1993, , 51-58.		0
862	Modelling the growth of filamentous fungi. , 1992, 46, 187-223.		32
863	Modelling of Filamentous Microorganisms. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1992, 25, 45-51.	0.4	1
864	Identification of Rate Controlling Enzymes in the Biosynthetic Pathway to Penicillin in a High Yielding Strain of <i>Penicillium Chrysogenum</i> . IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 1992, 25, 251-254.	0.4	1

#	ARTICLE	IF	CITATIONS
865	Monitoring and control of fed-batch penicillin fermentation. Computers and Chemical Engineering, 1992, 16, S297-S304.	3.8	10
866	Product formation during batch fermentation with recombinant Escherichia coli containing a runaway plasmid. Bioprocess and Biosystems Engineering, 1992, 8, 173-181.	0.5	5
867	Anomeric specificity of glucose uptake systems in Lactococcus cremoris, Escherichia coli, and Saccharomyces cerevisiae: Mechanism, kinetics, and Implications. Biotechnology and Bioengineering, 1992, 40, 137-146.	3.3	19
868	Modelling of microbial kinetics. Chemical Engineering Science, 1992, 47, 4225-4270.	3.8	174
869	Flow-injection analysis of micromolar concentrations of glucose and lactate in fermentation media. Analytica Chimica Acta, 1992, 261, 145-153.	5.4	37
870	Characterization and application of precise and robust flow-injection analysers for on-line measurement during fermentations. Analytica Chimica Acta, 1991, 247, 45-50.	5.4	59
871	Delay and dispersion in an in situ membrane probe for bioreactors. Chemical Engineering Science, 1991, 46, 3304-3307.	3.8	32
872	Monitoring of substrates and products during fed-batch penicillin fermentations on complex media. Analytica Chimica Acta, 1991, 249, 123-136.	5.4	49
873	Modeling fermentations with recombinant microorganisms: Formulation of a structured model. Biotechnology and Bioengineering, 1991, 37, 802-808.	3.3	51
874	Structured modeling of a microbial system: I. A theoretical study of lactic acid fermentation. Biotechnology and Bioengineering, 1991, 38, 1-10.	3.3	77
875	Structured modeling of a microbial system: II. Experimental verification of a structured lactic acid fermentation model. Biotechnology and Bioengineering, 1991, 38, 11-23.	3.3	63
876	Structured modeling of a microbial system: III. Growth on mixed substrates. Biotechnology and Bioengineering, 1991, 38, 24-29.	3.3	37
877	A simple and reliable method for the determination of cellular RNA content. Biotechnology Letters, 1991, 5, 39-42.	0.5	91
878	Application of flow-injection analysis in the on-line monitoring of sugars, lactic acid, protein and biomass during lactic acid fermentations. Analytica Chimica Acta, 1990, 237, 165-175.	5.4	64
879	FIA for on-line monitoring of important lactic acid fermentation variables. Biotechnology and Bioengineering, 1989, 33, 1127-1134.	3.3	42
880	Compartment model concept used in the design of fermentation with recombinant microorganisms. Biotechnology and Bioengineering, 1989, 34, 478-486.	3.3	17
881	In-line flow injection analysis for monitoring lactic acid fermentations. Analytica Chimica Acta, 1988, 214, 137-145.	5.4	39
882	Purification and properties of a cellulase from Aspergillus niger. Biochemical Journal, 1977, 165, 33-41.	3.7	120

#	ARTICLE	IF	CITATIONS
883	Sampling and Sample Preparation. , 0, , 39-82.		14
884	Metabolomics in Humans and Other Mammals. , 0, , 253-288.		9
885	Metabolomics in Functional Genomics and Systems Biology. , 0, , 1-14.		1
886	The Chemical Challenge of the Metabolome. , 0, , 15-38.		3
887	Plant Metabolomics. , 0, , 215-238.		1
888	Yeast Metabolomics: The Discovery of New Metabolic Pathways in <i>Saccharomyces Cerevisiae</i> . , 0, , 189-202.		2
889	Microbial Metabolomics: Rapid Sampling Techniques to Investigate Intracellular Metabolite Dynamics—An Overview. , 0, , 203-214.		2
890	Wiley-Interscience Series in Mass Spectrometry. , 0, , 312-312.		0
891	Mass Profiling of Fungal Extract from <i>Penicillium</i> Species. , 0, , 239-252.		0
892	Analytical Tools. , 0, , 83-145.		1
893	New insight into the gut microbiome through metagenomics. <i>Advances in Genomics and Genetics</i> , 0, , 77.	0.8	10
894	From Research to Industry. <i>ChemistryViews</i> , 0, , .	0.0	0
895	Network Analysis Reveals Heterogeneous Response of Redox Metabolism in Hepatocellular Carcinoma Patients. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0