

Bas Teusink

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163
papers

8,042
citations

48
h-index

85
g-index

182
ext. papers

9,967
ext. citations

7
avg, IF

5.91
L-index

#	Paper	IF	Citations
163	A functional genomics strategy that uses metabolome data to reveal the phenotype of silent mutations. <i>Nature Biotechnology</i> , 2001 , 19, 45-50	44.5	839
162	Can yeast glycolysis be understood in terms of in vitro kinetics of the constituent enzymes? Testing biochemistry. <i>FEBS Journal</i> , 2000 , 267, 5313-29		498
161	Shifts in growth strategies reflect tradeoffs in cellular economics. <i>Molecular Systems Biology</i> , 2009 , 5, 323	12.2	373
160	Analysis of growth of <i>Lactobacillus plantarum</i> WCFS1 on a complex medium using a genome-scale metabolic model. <i>Journal of Biological Chemistry</i> , 2006 , 281, 40041-8	5.4	212
159	The danger of metabolic pathways with turbo design. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 162-9	10.3	198
158	Lost in transition: start-up of glycolysis yields subpopulations of nongrowing cells. <i>Science</i> , 2014 , 343, 1245114	33.3	193
157	Reconstructing the metabolic network of a bacterium from its genome. <i>Trends in Microbiology</i> , 2005 , 13, 550-8	12.4	165
156	Bet-hedging during bacterial diauxic shift. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 7427-32	11.5	158
155	Compartmentation protects trypanosomes from the dangerous design of glycolysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 2087-92	11.5	155
154	Acetaldehyde mediates the synchronization of sustained glycolytic oscillations in populations of yeast cells. <i>FEBS Journal</i> , 1996 , 235, 238-41		154
153	In silico reconstruction of the metabolic pathways of <i>Lactobacillus plantarum</i> : comparing predictions of nutrient requirements with those from growth experiments. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 7253-62	4.8	146
152	CD36 deficiency increases insulin sensitivity in muscle, but induces insulin resistance in the liver in mice. <i>Journal of Lipid Research</i> , 2003 , 44, 2270-7	6.3	128
151	Community flux balance analysis for microbial consortia at balanced growth. <i>PLoS ONE</i> , 2013 , 8, e64567	3.7	125
150	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-275	44.5	121
149	Availability of public goods shapes the evolution of competing metabolic strategies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 14302-7	11.5	120
148	Exploring metabolic pathway reconstruction and genome-wide expression profiling in <i>Lactobacillus reuteri</i> to define functional probiotic features. <i>PLoS ONE</i> , 2011 , 6, e18783	3.7	120
147	Contribution of fatty acids released from lipolysis of plasma triglycerides to total plasma fatty acid flux and tissue-specific fatty acid uptake. <i>Diabetes</i> , 2003 , 52, 614-20	0.9	118

146	Accelerating the reconstruction of genome-scale metabolic networks. <i>BMC Bioinformatics</i> , 2006 , 7, 296	3.6	116
145	How fast-growing bacteria robustly tune their ribosome concentration to approximate growth-rate maximization. <i>FEBS Journal</i> , 2015 , 282, 2029-44	5.7	114
144	Modelling strategies for the industrial exploitation of lactic acid bacteria. <i>Nature Reviews Microbiology</i> , 2006 , 4, 46-56	22.2	113
143	PAPD5-mediated 3Qdenylation and subsequent degradation of miR-21 is disrupted in proliferative disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 11467-72	11.5	106
142	Understanding the adaptive growth strategy of <i>Lactobacillus plantarum</i> by in silico optimisation. <i>PLoS Computational Biology</i> , 2009 , 5, e1000410	5	101
141	Intracellular glucose concentration in derepressed yeast cells consuming glucose is high enough to reduce the glucose transport rate by 50%. <i>Journal of Bacteriology</i> , 1998 , 180, 556-62	3.5	100
140	Increased hepatic insulin sensitivity together with decreased hepatic triglyceride stores in hormone-sensitive lipase-deficient mice. <i>Endocrinology</i> , 2003 , 144, 3456-62	4.8	95
139	Genome-scale model of <i>Streptococcus thermophilus</i> LMG18311 for metabolic comparison of lactic acid bacteria. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3627-33	4.8	93
138	Apolipoprotein C3 deficiency results in diet-induced obesity and aggravated insulin resistance in mice. <i>Diabetes</i> , 2005 , 54, 664-71	0.9	87
137	Thioredoxin reductase is a key factor in the oxidative stress response of <i>Lactobacillus plantarum</i> WCFS1. <i>Microbial Cell Factories</i> , 2007 , 6, 29	6.4	83
136	Sustained oscillations in free-energy state and hexose phosphates in yeast 1996 , 12, 731-740		77
135	A systematic assessment of current genome-scale metabolic reconstruction tools. <i>Genome Biology</i> , 2019 , 20, 158	18.3	73
134	Around the growth phase transition <i>S. cerevisiae</i> Q make-up favours sustained oscillations of intracellular metabolites. <i>FEBS Letters</i> , 1993 , 318, 80-2	3.8	71
133	Co-regulation of metabolic genes is better explained by flux coupling than by network distance. <i>PLoS Computational Biology</i> , 2008 , 4, e26	5	70
132	Control of glycolytic dynamics by hexose transport in <i>Saccharomyces cerevisiae</i> . <i>Biophysical Journal</i> , 2001 , 80, 626-34	2.9	70
131	The VLDL receptor plays a major role in chylomicron metabolism by enhancing LPL-mediated triglyceride hydrolysis. <i>Journal of Lipid Research</i> , 2004 , 45, 1475-81	6.3	66
130	Development of a minimal growth medium for <i>Lactobacillus plantarum</i> . <i>Letters in Applied Microbiology</i> , 2010 , 50, 57-64	2.9	65
129	SBML Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020 , 16, e9110	12.2	65

128	FAME, the Flux Analysis and Modeling Environment. <i>BMC Systems Biology</i> , 2012 , 6, 8	3.5	62
127	Constraint-based stoichiometric modelling from single organisms to microbial communities. <i>Journal of the Royal Society Interface</i> , 2016 , 13,	4.1	55
126	A critical view of metabolic network adaptations. <i>HFSP Journal</i> , 2009 , 3, 24-35		53
125	Genome data mining of lactic acid bacteria: the impact of bioinformatics. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 105-15	11.4	53
124	Finding Functional Differences Between Species in a Microbial Community: Case Studies in Wine Fermentation and Kefir Culture. <i>Frontiers in Microbiology</i> , 2019 , 10, 1347	5.7	52
123	Response of apolipoprotein E*3-Leiden transgenic mice to dietary fatty acids: combining liver proteomics with physiological data. <i>FASEB Journal</i> , 2005 , 19, 813-5	0.9	52
122	LDL receptor deficiency unmasks altered VLDL triglyceride metabolism in VLDL receptor transgenic and knockout mice. <i>Journal of Lipid Research</i> , 2000 , 41, 2055-2062	6.3	52
121	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015 , 32, 1-7	11.4	51
120	Metabolic shifts: a fitness perspective for microbial cell factories. <i>Biotechnology Letters</i> , 2012 , 34, 2147-60		51
119	Understanding the physiology of <i>Lactobacillus plantarum</i> at zero growth. <i>Molecular Systems Biology</i> , 2010 , 6, 413	12.2	51
118	Intestinal lipid absorption is not affected in CD36 deficient mice. <i>Molecular and Cellular Biochemistry</i> , 2002 , 239, 199-202	4.2	51
117	Yeast cells with a specific cellular make-up and an environment that removes acetaldehyde are prone to sustained glycolytic oscillations. <i>FEBS Letters</i> , 1994 , 341, 223-6	3.8	49
116	A novel consortium of <i>Lactobacillus rhamnosus</i> and <i>Streptococcus thermophilus</i> for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195	6.4	48
115	Control analysis of glycolytic oscillations. <i>Biophysical Chemistry</i> , 1996 , 62, 15-24	3.5	48
114	Metabolic states with maximal specific rate carry flux through an elementary flux mode. <i>FEBS Journal</i> , 2014 , 281, 1547-55	5.7	46
113	Role of phosphate in the central metabolism of two lactic acid bacteria—a comparative systems biology approach. <i>FEBS Journal</i> , 2012 , 279, 1274-90	5.7	45
112	Predicting metabolic fluxes using gene expression differences as constraints. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 206-16	3	45
111	Systems biology of lactic acid bacteria: a critical review. <i>Microbial Cell Factories</i> , 2011 , 10 Suppl 1, S11	6.4	45

110	LDL receptor deficiency unmasks altered VLDL triglyceride metabolism in VLDL receptor transgenic and knockout mice. <i>Journal of Lipid Research</i> , 2000 , 41, 2055-62	6.3	45
109	Systems modeling approaches for microbial community studies: from metagenomics to inference of the community structure. <i>Frontiers in Microbiology</i> , 2015 , 6, 213	5.7	44
108	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021 , 6, 196-208	26.6	44
107	Experimental evolution and the adjustment of metabolic strategies in lactic acid bacteria. <i>FEMS Microbiology Reviews</i> , 2017 , 41, S201-S219	15.1	43
106	The number of active metabolic pathways is bounded by the number of cellular constraints at maximal metabolic rates. <i>PLoS Computational Biology</i> , 2019 , 15, e1006858	5	43
105	Protein costs do not explain evolution of metabolic strategies and regulation of ribosomal content: does protein investment explain an anaerobic bacterial Crabtree effect?. <i>Molecular Microbiology</i> , 2015 , 97, 77-92	4.1	43
104	Standardized assay medium to measure <i>Lactococcus lactis</i> enzyme activities while mimicking intracellular conditions. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 134-43	4.8	40
103	A practical guide to genome-scale metabolic models and their analysis. <i>Methods in Enzymology</i> , 2011 , 500, 509-32	1.7	39
102	The transport of triglycerides through the secretory pathway of hepatocytes is impaired in apolipoprotein E deficient mice. <i>Journal of Hepatology</i> , 2004 , 40, 599-606	13.4	39
101	Towards metagenome-scale models for industrial applications--the case of Lactic Acid Bacteria. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 200-6	11.4	38
100	Systems biology of lactic acid bacteria: For food and thought. <i>Current Opinion in Systems Biology</i> , 2017 , 6, 7-13	3.2	37
99	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005 , 33, 6164-71	20.1	37
98	Basic concepts and principles of stoichiometric modeling of metabolic networks. <i>Biotechnology Journal</i> , 2013 , 8, 997-1008	5.6	36
97	Control of frequency and amplitudes is shared by all enzymes in three models for yeast glycolytic oscillations. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1996 , 1275, 204-12	4.6	35
96	Functional identification in <i>Lactobacillus reuteri</i> of a PoxR-like transcription factor regulating glycerol utilization and vitamin B12 synthesis. <i>Microbial Cell Factories</i> , 2011 , 10, 55	6.4	33
95	Functional ingredient production: application of global metabolic models. <i>Current Opinion in Biotechnology</i> , 2005 , 16, 190-7	11.4	32
94	Model-based quantification of metabolic interactions from dynamic microbial-community data. <i>PLoS ONE</i> , 2017 , 12, e0173183	3.7	32
93	In vivo characterisation of fluorescent proteins in budding yeast. <i>Scientific Reports</i> , 2019 , 9, 2234	4.9	32

92	Strategies to determine the extent of control exerted by glucose transport on glycolytic flux in the yeast <i>Saccharomyces bayanus</i> . <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 12), 3447-3454	2.9	31
91	A specific mutation in the promoter region of the silent <i>cel</i> cluster accounts for the appearance of lactose-utilizing <i>Lactococcus lactis</i> MG1363. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5612-21	4.8	30
90	Public goods and metabolic strategies. <i>Current Opinion in Microbiology</i> , 2016 , 31, 109-115	7.9	30
89	Metabolic models for rational improvement of lactic acid bacteria as cell factories. <i>Journal of Applied Microbiology</i> , 2005 , 98, 1326-31	4.7	29
88	How biochemical constraints of cellular growth shape evolutionary adaptations in metabolism. <i>Genetics</i> , 2013 , 194, 505-12	4	28
87	Leptin deficiency per se dictates body composition and insulin action in <i>ob/ob</i> mice. <i>Journal of Neuroendocrinology</i> , 2008 , 20, 120-7	3.8	28
86	Analysis of the structure and function relationship of the human apolipoprotein E in vivo, using adenovirus-mediated gene transfer. <i>FASEB Journal</i> , 2001 , 15, 1598-600	0.9	28
85	Sustained oscillations in free-energy state and hexose phosphates in yeast. <i>Yeast</i> , 1996 , 12, 731-40	3.4	28
84	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
83	Evolutionary pressures on microbial metabolic strategies in the chemostat. <i>Scientific Reports</i> , 2016 , 6, 29503	4.9	25
82	MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. <i>Molecular BioSystems</i> , 2015 , 11, 137-45		25
81	Synchronized heat flux oscillations in yeast cell populations. <i>Journal of Biological Chemistry</i> , 1996 , 271, 24442-8	5.4	25
80	17 Metabolic Control Analysis as a Tool in the Elucidation of the Function of Novel Genes. <i>Methods in Microbiology</i> , 1998 , 297-336	2.8	25
79	Effect of amino acid availability on vitamin B12 production in <i>Lactobacillus reuteri</i> . <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3930-6	4.8	24
78	The common message of constraint-based optimization approaches: overflow metabolism is caused by two growth-limiting constraints. <i>Cellular and Molecular Life Sciences</i> , 2020 , 77, 441-453	10.3	24
77	A data integration and visualization resource for the metabolic network of <i>Synechocystis</i> sp. PCC 6803. <i>Plant Physiology</i> , 2014 , 164, 1111-21	6.6	23
76	Using a genome-scale metabolic model of <i>Enterococcus faecalis</i> V583 to assess amino acid uptake and its impact on central metabolism. <i>Applied and Environmental Microbiology</i> , 2015 , 81, 1622-33	4.8	20
75	Quantitative analysis of amino acid metabolism in liver cancer links glutamate excretion to nucleotide synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 10294-10304	11.5	19

74	Interplay between constraints, objectives, and optimality for genome-scale stoichiometric models. <i>PLoS Computational Biology</i> , 2015 , 11, e1004166	5	18
73	Monte-Carlo modeling of the central carbon metabolism of <i>Lactococcus lactis</i> : insights into metabolic regulation. <i>PLoS ONE</i> , 2014 , 9, e106453	3.7	18
72	Genomics and high-throughput screening approaches for optimal flavour production in dairy fermentation. <i>International Dairy Journal</i> , 2008 , 18, 781-789	3.5	18
71	Stimulation of the in vivo production of very low density lipoproteins by apolipoprotein E is independent of the presence of the low density lipoprotein receptor. <i>Journal of Biological Chemistry</i> , 2001 , 276, 40693-7	5.4	18
70	Glucose metabolites and enzymes. A rapid way of delineating metabolic control. <i>FEBS Journal</i> , 2000 , 267, 1889-93		18
69	Multi-tasking of biosynthetic and energetic functions of glycolysis explained by supply and demand logic. <i>BioEssays</i> , 2015 , 37, 34-45	4.1	17
68	Systems biology from micro-organisms to human metabolic diseases: the role of detailed kinetic models. <i>Biochemical Society Transactions</i> , 2010 , 38, 1294-301	5.1	17
67	Microdroplet screening and selection for improved microbial production of extracellular compounds. <i>Current Opinion in Biotechnology</i> , 2020 , 61, 72-81	11.4	16
66	Microbial competition reduces metabolic interaction distances to the low μm -range. <i>ISME Journal</i> , 2021 , 15, 688-701	11.9	16
65	Mice expressing only the mutant APOE3Leiden gene show impaired VLDL secretion. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2001 , 21, 1366-72	9.4	15
64	Control and regulation of metabolic fluxes in microbes by substrates and enzymes. <i>Antonie Van Leeuwenhoek</i> , 1993 , 63, 315-21	2.1	15
63	Low affinity uniporter carrier proteins can increase net substrate uptake rate by reducing efflux. <i>Scientific Reports</i> , 2018 , 8, 5576	4.9	14
62	Probing the Genome-Scale Metabolic Landscape of <i>Bordetella pertussis</i> , the Causative Agent of Whooping Cough. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	14
61	Multi-way analysis of flux distributions across multiple conditions. <i>Journal of Chemometrics</i> , 2009 , 23, 406-420	1.6	14
60	Comparative systems biology: from bacteria to man. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 518-532	6.6	14
59	Searching for principles of microbial physiology. <i>FEMS Microbiology Reviews</i> , 2020 , 44, 821-844	15.1	14
58	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016 , 2, 16011	5	14
57	Genome-scale reconstruction of the <i>Streptococcus pyogenes</i> M49 metabolic network reveals growth requirements and indicates potential drug targets. <i>Journal of Biotechnology</i> , 2016 , 232, 25-37	3.7	13

56	Elementary Growth Modes provide a molecular description of cellular self-fabrication. <i>PLoS Computational Biology</i> , 2020 , 16, e1007559	5	13
55	A genome-scale metabolic network of the aroma bacterium <i>Leuconostoc mesenteroides</i> subsp. <i>cremoris</i> . <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 3153-3165	5.7	12
54	Living with noise: On the propagation of noise from molecules to phenotype and fitness. <i>Current Opinion in Systems Biology</i> , 2018 , 8, 144-150	3.2	12
53	Acute inhibition of hepatic beta-oxidation in APOE*3Leiden mice does not affect hepatic VLDL secretion or insulin sensitivity. <i>Journal of Lipid Research</i> , 2005 , 46, 988-93	6.3	12
52	Energy, control and DNA structure in the living cell. <i>Biophysical Chemistry</i> , 1995 , 55, 153-65	3.5	12
51	Genome-Scale Metabolic Reconstruction of 386B, a Candidate Functional Starter Culture for Cocoa Bean Fermentation. <i>Frontiers in Microbiology</i> , 2019 , 10, 2801	5.7	12
50	Binding proteins enhance specific uptake rate by increasing the substrate-transporter encounter rate. <i>FEBS Journal</i> , 2015 , 282, 2394-407	5.7	11
49	Bioinformatics and systems biology: bridging the gap between heterogeneous student backgrounds. <i>Briefings in Bioinformatics</i> , 2013 , 14, 589-98	13.4	11
48	Gene network requirements for regulation of metabolic gene expression to a desired state. <i>Scientific Reports</i> , 2013 , 3, 1417	4.9	11
47	An Improved ATP FRET Sensor For Yeast Shows Heterogeneity During Nutrient Transitions. <i>ACS Sensors</i> , 2020 , 5, 814-822	9.2	10
46	Optimality principles in the regulation of metabolic networks. <i>Metabolites</i> , 2012 , 2, 529-52	5.6	10
45	Adaption to glucose limitation is modulated by the pleiotropic regulator CcpA, independent of selection pressure strength. <i>BMC Evolutionary Biology</i> , 2019 , 19, 15	3	10
44	Maintaining maximal metabolic flux by gene expression control. <i>PLoS Computational Biology</i> , 2018 , 14, e1006412	5	10
43	Metabolism at evolutionary optimal States. <i>Metabolites</i> , 2015 , 5, 311-43	5.6	9
42	Enhancement of amino acid production and secretion by using a droplet-based biosensing and selection system. <i>Metabolic Engineering Communications</i> , 2020 , 11, e00133	6.5	8
41	Understanding regulation of metabolism through feasibility analysis. <i>PLoS ONE</i> , 2012 , 7, e39396	3.7	8
40	Hyperlipidemia in APOE2 transgenic mice is ameliorated by a truncated apoE variant lacking the C-terminal domain. <i>Journal of Lipid Research</i> , 2003 , 44, 408-14	6.3	8
39	Emergence of stable coexistence in a complex microbial community through metabolic cooperation and spatio-temporal niche partitioning		8

38	Dynamic elementary mode modelling of non-steady state flux data. <i>BMC Systems Biology</i> , 2018 , 12, 71	3.5	7
37	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies.. <i>Nature Communications</i> , 2022 , 13, 801	17.4	7
36	A Systematic Assessment Of Current Genome-Scale Metabolic Reconstruction Tools		7
35	Proteome constraints reveal targets for improving microbial fitness in nutrient-rich environments. <i>Molecular Systems Biology</i> , 2021 , 17, e10093	12.2	6
34	Dynamic co-culture metabolic models reveal the fermentation dynamics, metabolic capacities and interplays of cheese starter cultures. <i>Biotechnology and Bioengineering</i> , 2021 , 118, 223-237	4.9	6
33	Understanding bistability in yeast glycolysis using general properties of metabolic pathways. <i>Mathematical Biosciences</i> , 2014 , 255, 33-42	3.9	5
32	Protein cost allocation explains metabolic strategies in Escherichia coli. <i>Journal of Biotechnology</i> , 2021 , 327, 54-63	3.7	5
31	Unlocking Elementary Conversion Modes: ecmtool Unveils All Capabilities of Metabolic Networks. <i>Patterns</i> , 2021 , 2, 100177	5.1	5
30	A Multiphase Multiobjective Dynamic Genome-Scale Model Shows Different Redox Balancing among Yeast Species of the Genus in Fermentation. <i>MSystems</i> , 2021 , 6, e0026021	7.6	5
29	Metabolite Depletion Affects Flux Profiling of Cell Lines. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 395-397	7.3	4
28	Fatal attraction in glycolysis: how manages sudden transitions to high glucose. <i>Microbial Cell</i> , 2014 , 1, 103-106	3.9	4
27	A proteome-integrated, carbon source dependent genetic regulatory network in <i>Saccharomyces cerevisiae</i> . <i>Molecular Omics</i> , 2020 , 16, 59-72	4.4	4
26	Lifestyle, metabolism and environmental adaptation in <i>Lactococcus lactis</i> . <i>FEMS Microbiology Reviews</i> , 2020 , 44, 804-820	15.1	4
25	Serial propagation in water-in-oil emulsions selects for <i>Saccharomyces cerevisiae</i> strains with a reduced cell size or an increased biomass yield on glucose. <i>Metabolic Engineering</i> , 2021 , 64, 1-14	9.7	4
24	Population dynamics of microbial cross-feeding are determined by co-localization probabilities and cooperation-independent cheater growth. <i>ISME Journal</i> , 2021 , 15, 3050-3061	11.9	4
23	Further Elucidation of Galactose Utilization in MG1363. <i>Frontiers in Microbiology</i> , 2018 , 9, 1803	5.7	3
22	The evidence that pseudovitamin B(12) is biologically active in mammals is still lacking - a comment on Molina et al. (2009) experimental design. <i>Journal of Applied Microbiology</i> , 2009 , 107, 1763; author reply 1764	4.7	3
21	The number of active metabolic pathways is bounded by the number of cellular constraints at maximal metabolic rates		3

20	Synchronization of Glycolytic Oscillations in Intact Yeast Cells 1993 , 413-416		3
19	Elementary Growth Modes provide a molecular description of cellular self-fabrication		2
18	A yeast FRET biosensor enlightens cAMP signalling		2
17	Understanding FBA Solutions under Multiple Nutrient Limitations. <i>Metabolites</i> , 2021 , 11,	5.6	2
16	A yeast FRET biosensor enlightens cAMP signaling. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1229-1240	3.5	2
15	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies		2
14	Training for translation between disciplines: a philosophy for life and data sciences curricula. <i>Bioinformatics</i> , 2018 , 34, i4-i12	7.2	2
13	Ecophysiology of Acetoclastic Methanogens 2019 , 1-14		1
12	Understanding start-up problems in yeast glycolysis. <i>Mathematical Biosciences</i> , 2018 , 299, 117-126	3.9	1
11	Ecophysiology of Acetoclastic Methanogens 2019 , 109-121		1
10	Metabolic Control From The Back Benches: Biochemistry Towards Biocomplexity 2000 , 235-242		1
9	Maintaining maximal metabolic flux by gene expression control		1
8	Glucose limitation in <i>Lactococcus</i> shapes a single-peaked fitness landscape exposing membrane occupancy as a constraint		1
7	Selection for cell yield does not reduce overflow metabolism in <i>E. coli</i>		1
6	A centrifugation-based clearing method allows high-throughput acidification and growth-rate measurements in milk. <i>Journal of Dairy Science</i> , 2021 , 104, 8530-8540	4	1
5	An Integrated Model Quantitatively Describing Metabolism, Growth and Cell Cycle in Budding Yeast. <i>Communications in Computer and Information Science</i> , 2018 , 165-180	0.3	0
4	Use and limitations of genome-scale metabolic models in food microbiology. <i>Current Opinion in Food Science</i> , 2022 , 43, 225-231	9.8	0
3	Inferring differences in the distribution of reaction rates across conditions. <i>Molecular BioSystems</i> , 2012 , 8, 2415-23		

2 Metabolic Modeling of Fungi **2021**, 394-405

1 Metabolic Modeling of Wine Fermentation at Genome Scale. *Methods in Molecular Biology*, **2022**, 395-454.4