Bas Teusink

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

163
papers8,042
citations48
h-index85
g-index182
ext. papers9,967
ext. citations7
avg, IF5.91
L-index

#	Paper	IF	Citations
163	Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies <i>Nature Communications</i> , 2022 , 13, 801	17.4	7
162	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
161	Metabolic Modeling of Wine Fermentation at Genome Scale. <i>Methods in Molecular Biology</i> , 2022 , 395-4	15 4 .4	
160	Serial propagation in water-in-oil emulsions selects for Saccharomyces cerevisiae strains with a reduced cell size or an increased biomass yield on glucose. <i>Metabolic Engineering</i> , 2021 , 64, 1-14	9.7	4
159	Understanding FBA Solutions under Multiple Nutrient Limitations. <i>Metabolites</i> , 2021 , 11,	5.6	2
158	Proteome constraints reveal targets for improving microbial fitness in nutrient-rich environments. <i>Molecular Systems Biology</i> , 2021 , 17, e10093	12.2	6
157	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
156	A yeast FRET biosensor enlightens cAMP signaling. <i>Molecular Biology of the Cell</i> , 2021 , 32, 1229-1240	3.5	2
155	Microbial competition reduces metabolic interaction distances to the low pm-range. <i>ISME Journal</i> , 2021 , 15, 688-701	11.9	16
154	Protein cost allocation explains metabolic strategies in Escherichia coli. <i>Journal of Biotechnology</i> , 2021 , 327, 54-63	3.7	5
153	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
152	Unlocking Elementary Conversion Modes: ecmtool Unveils All Capabilities of Metabolic Networks. <i>Patterns</i> , 2021 , 2, 100177	5.1	5
151	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
150	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
149	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. Nature Microbiology, 2021 , 6, 196-208	26.6	44
148	Metabolic Modeling of Fungi 2021 , 394-405		
147	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

146	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
145	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272	- 24746 5	121
144	An Improved ATP FRET Sensor For Yeast Shows Heterogeneity During Nutrient Transitions. <i>ACS Sensors</i> , 2020 , 5, 814-822	9.2	10
143	Elementary Growth Modes provide a molecular description of cellular self-fabrication. <i>PLoS Computational Biology</i> , 2020 , 16, e1007559	5	13
142	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
141	A proteome-integrated, carbon source dependent genetic regulatory network in Saccharomyces cerevisiae. <i>Molecular Omics</i> , 2020 , 16, 59-72	4.4	4
140	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
139	Microdroplet screening and selection for improved microbial production of extracellular compounds. <i>Current Opinion in Biotechnology</i> , 2020 , 61, 72-81	11.4	16
138	Lifestyle, metabolism and environmental adaptation in Lactococcus lactis. <i>FEMS Microbiology Reviews</i> , 2020 , 44, 804-820	15.1	4
137	Searching for principles of microbial physiology. FEMS Microbiology Reviews, 2020, 44, 821-844	15.1	14
136	A genome-scale metabolic network of the aroma bacterium Leuconostoc mesenteroides subsp. cremoris. <i>Applied Microbiology and Biotechnology</i> , 2019 , 103, 3153-3165	5.7	12
135	Ecophysiology of Acetoclastic Methanogens 2019 , 1-14		1
134	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
133	A systematic assessment of current genome-scale metabolic reconstruction tools. <i>Genome Biology</i> , 2019 , 20, 158	18.3	73
132	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
131	Ecophysiology of Acetoclastic Methanogens 2019 , 109-121		1
130	In vivo characterisation of fluorescent proteins in budding yeast. <i>Scientific Reports</i> , 2019 , 9, 2234	4.9	32
129	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

128	Adaption to glucose limitation is modulated by the pleotropic regulator CcpA, independent of selection pressure strength. <i>BMC Evolutionary Biology</i> , 2019 , 19, 15	3	10
127	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	O
126	Low affinity uniporter carrier proteins can increase net substrate uptake rate by reducing efflux. <i>Scientific Reports</i> , 2018 , 8, 5576	4.9	14
125	Metabolite Depletion Affects Flux Profiling of Cell Lines. <i>Trends in Biochemical Sciences</i> , 2018 , 43, 395-3	97 6.3	4
124	Understanding start-up problems in yeast glycolysis. <i>Mathematical Biosciences</i> , 2018 , 299, 117-126	3.9	1
123	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
122	Dynamic elementary mode modelling of non-steady state flux data. <i>BMC Systems Biology</i> , 2018 , 12, 71	3.5	7
121	Further Elucidation of Galactose Utilization in MG1363. Frontiers in Microbiology, 2018, 9, 1803	5.7	3
120	Maintaining maximal metabolic flux by gene expression control. <i>PLoS Computational Biology</i> , 2018 , 14, e1006412	5	10
119	Training for translation between disciplines: a philosophy for life and data sciences curricula. <i>Bioinformatics</i> , 2018 , 34, i4-i12	7.2	2
118	Experimental evolution and the adjustment of metabolic strategies in lactic acid bacteria. <i>FEMS Microbiology Reviews</i> , 2017 , 41, S201-S219	15.1	43
117	Probing the Genome-Scale Metabolic Landscape of Bordetella pertussis, the Causative Agent of Whooping Cough. <i>Applied and Environmental Microbiology</i> , 2017 , 83,	4.8	14
116	Systems biology of lactic acid bacteria: For food and thought. <i>Current Opinion in Systems Biology</i> , 2017 , 6, 7-13	3.2	37
115	Model-based quantification of metabolic interactions from dynamic microbial-community data. <i>PLoS ONE</i> , 2017 , 12, e0173183	3.7	32
114	Evolutionary pressures on microbial metabolic strategies in the chemostat. <i>Scientific Reports</i> , 2016 , 6, 29503	4.9	25
113	Genome-scale reconstruction of the Streptococcus pyogenes M49 metabolic network reveals growth requirements and indicates potential drug targets. <i>Journal of Biotechnology</i> , 2016 , 232, 25-37	3.7	13
112	Strategies for structuring interdisciplinary education in Systems Biology: an European perspective. <i>Npj Systems Biology and Applications</i> , 2016 , 2, 16011	5	14
111	Constraint-based stoichiometric modelling from single organisms to microbial communities. Journal of the Royal Society Interface, 2016 , 13,	4.1	55

110	Public goods and metabolic strategies. Current Opinion in Microbiology, 2016, 31, 109-115	7.9	30
109	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
108	Interplay between constraints, objectives, and optimality for genome-scale stoichiometric models. <i>PLoS Computational Biology</i> , 2015 , 11, e1004166	5	18
107	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
106	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
105	Using a genome-scale metabolic model of Enterococcus faecalis 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
104	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
103	Evolutionary engineering to enhance starter culture performance in food fermentations. <i>Current Opinion in Biotechnology</i> , 2015 , 32, 1-7	11.4	51
102	Binding proteins enhance specific uptake rate by increasing the substrate-transporter encounter rate. <i>FEBS Journal</i> , 2015 , 282, 2394-407	5.7	11
101	Metabolism at evolutionary optimal States. <i>Metabolites</i> , 2015 , 5, 311-43	5.6	9
101	Metabolism at evolutionary optimal States. <i>Metabolites</i> , 2015 , 5, 311-43 A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195	5.6 6.4	9
	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased		
100	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195 MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance		48
100	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195 MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. <i>Molecular BioSystems</i> , 2015 , 11, 137-45 Lost in transition: start-up of glycolysis yields subpopulations of nongrowing cells. <i>Science</i> , 2014 ,	6.4	48
100 99 98	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195 MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. <i>Molecular BioSystems</i> , 2015 , 11, 137-45 Lost in transition: start-up of glycolysis yields subpopulations of nongrowing cells. <i>Science</i> , 2014 , 343, 1245114 Bet-hedging during bacterial diauxic shift. <i>Proceedings of the National Academy of Sciences of the</i>	6.4	48 25 193
100999897	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195 MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. <i>Molecular BioSystems</i> , 2015 , 11, 137-45 Lost in transition: start-up of glycolysis yields subpopulations of nongrowing cells. <i>Science</i> , 2014 , 343, 1245114 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 Understanding bistability in yeast glycolysis using general properties of metabolic pathways.	6.4 33·3 11.5	48 25 193 158
10099989796	A novel consortium of Lactobacillus rhamnosus and Streptococcus thermophilus for increased access to functional fermented foods. <i>Microbial Cell Factories</i> , 2015 , 14, 195 MetDFBA: incorporating time-resolved metabolomics measurements into dynamic flux balance analysis. <i>Molecular BioSystems</i> , 2015 , 11, 137-45 Lost in transition: start-up of glycolysis yields subpopulations of nongrowing cells. <i>Science</i> , 2014 , 343, 1245114 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 Understanding bistability in yeast glycolysis using general properties of metabolic pathways. <i>Mathematical Biosciences</i> , 2014 , 255, 33-42 A data integration and visualization resource for the metabolic network of Synechocystis sp. PCC	6.4 33·3 11.5	48 25 193 158

92	Metabolic states with maximal specific rate carry flux through an elementary flux mode. <i>FEBS Journal</i> , 2014 , 281, 1547-55	5.7	46
91	Fatal attraction in glycolysis: how manages sudden transitions to high glucose. <i>Microbial Cell</i> , 2014 , 1, 103-106	3.9	4
90	Basic concepts and principles of stoichiometric modeling of metabolic networks. <i>Biotechnology Journal</i> , 2013 , 8, 997-1008	5.6	36
89	Towards metagenome-scale models for industrial applicationsthe case of Lactic Acid Bacteria. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 200-6	11.4	38
88	How biochemical constraints of cellular growth shape evolutionary adaptations in metabolism. <i>Genetics</i> , 2013 , 194, 505-12	4	28
87	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
86	Bioinformatics and systems biology: bridging the gap between heterogeneous student backgrounds. <i>Briefings in Bioinformatics</i> , 2013 , 14, 589-98	13.4	11
85	Gene network requirements for regulation of metabolic gene expression to a desired state. <i>Scientific Reports</i> , 2013 , 3, 1417	4.9	11
84	Community flux balance analysis for microbial consortia at balanced growth. <i>PLoS ONE</i> , 2013 , 8, e64567	3.7	125
83	Role of phosphate in the central metabolism of two lactic acid bacteriaa comparative systems biology approach. <i>FEBS Journal</i> , 2012 , 279, 1274-90	5.7	45
82	Metabolic shifts: a fitness perspective for microbial cell factories. <i>Biotechnology Letters</i> , 2012 , 34, 2147-	-690	51
81	Inferring differences in the distribution of reaction rates across conditions. <i>Molecular BioSystems</i> , 2012 , 8, 2415-23		
80	FAME, the Flux Analysis and Modeling Environment. <i>BMC Systems Biology</i> , 2012 , 6, 8	3.5	62
79	Understanding regulation of metabolism through feasibility analysis. <i>PLoS ONE</i> , 2012 , 7, e39396	3.7	8
78	Optimality principles in the regulation of metabolic networks. <i>Metabolites</i> , 2012 , 2, 529-52	5.6	10
77	Standardized assay medium to measure Lactococcus lactis enzyme activities while mimicking intracellular conditions. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 134-43	4.8	40
76	A specific mutation in the promoter region of the silent cel cluster accounts for the appearance of lactose-utilizing Lactococcus lactis MG1363. <i>Applied and Environmental Microbiology</i> , 2012 , 78, 5612-21	4.8	30
75	Exploring metabolic pathway reconstruction and genome-wide expression profiling in Lactobacillus reuteri to define functional probiotic features. <i>PLoS ONE</i> , 2011 , 6, e18783	3.7	120

(2008-2011)

74	A practical guide to genome-scale metabolic models and their analysis. <i>Methods in Enzymology</i> , 2011 , 500, 509-32	1.7	39
73	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
72	Functional identification in Lactobacillus reuteri of a PocR-like transcription factor regulating glycerol utilization and vitamin B12 synthesis. <i>Microbial Cell Factories</i> , 2011 , 10, 55	6.4	33
71	Systems biology of lactic acid bacteria: a critical review. <i>Microbial Cell Factories</i> , 2011 , 10 Suppl 1, S11	6.4	45
70	Development of a minimal growth medium for Lactobacillus plantarum. <i>Letters in Applied Microbiology</i> , 2010 , 50, 57-64	2.9	65
69	Understanding the physiology of Lactobacillus plantarum at zero growth. <i>Molecular Systems Biology</i> , 2010 , 6, 413	12.2	51
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	Comparative systems biology: from bacteria to man. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2010 , 2, 518-532	6.6	14
66	Understanding the adaptive growth strategy of Lactobacillus plantarum by in silico optimisation. <i>PLoS Computational Biology</i> , 2009 , 5, e1000410	5	101
65	Genome-scale model of Streptococcus thermophilus LMG18311 for metabolic comparison of lactic acid bacteria. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3627-33	4.8	93
64	Shifts in growth strategies reflect tradeoffs in cellular economics. <i>Molecular Systems Biology</i> , 2009 , 5, 323	12.2	373
63	Effect of amino acid availability on vitamin B12 production in Lactobacillus reuteri. <i>Applied and Environmental Microbiology</i> , 2009 , 75, 3930-6	4.8	24
62	Multi-way analysis of flux distributions across multiple conditions. <i>Journal of Chemometrics</i> , 2009 , 23, 406-420	1.6	14
61	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
60	A critical view of metabolic network adaptations. HFSP Journal, 2009, 3, 24-35		53
59	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
58	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
57	Leptin deficiency per se dictates body composition and insulin action in ob/ob mice. <i>Journal of Neuroendocrinology</i> , 2008 , 20, 120-7	3.8	28

56	Thioredoxin reductase is a key factor in the oxidative stress response of Lactobacillus plantarum WCFS1. <i>Microbial Cell Factories</i> , 2007 , 6, 29	6.4	83
55	Accelerating the reconstruction of genome-scale metabolic networks. <i>BMC Bioinformatics</i> , 2006 , 7, 296	3.6	116
54	Analysis of growth of Lactobacillus plantarum WCFS1 on a complex medium using a genome-scale metabolic model. <i>Journal of Biological Chemistry</i> , 2006 , 281, 40041-8	5.4	212
53	Modelling strategies for the industrial exploitation of lactic acid bacteria. <i>Nature Reviews Microbiology</i> , 2006 , 4, 46-56	22.2	113
52	Correlation between sequence conservation and the genomic context after gene duplication. <i>Nucleic Acids Research</i> , 2005 , 33, 6164-71	20.1	37
51	Reconstructing the metabolic network of a bacterium from its genome. <i>Trends in Microbiology</i> , 2005 , 13, 550-8	12.4	165
50	In silico reconstruction of the metabolic pathways of Lactobacillus plantarum: comparing predictions of nutrient requirements with those from growth experiments. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 7253-62	4.8	146
49	Functional ingredient production: application of global metabolic models. <i>Current Opinion in Biotechnology</i> , 2005 , 16, 190-7	11.4	32
48	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
47	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
46	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
45	Apolipoprotein C3 deficiency results in diet-induced obesity and aggravated insulin resistance in mice. <i>Diabetes</i> , 2005 , 54, 664-71	0.9	87
44	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
43	Genome data mining of lactic acid bacteria: the impact of bioinformatics. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 105-15	11.4	53
42	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
41	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
40	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
39	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

[1996-2003]

38	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
37	Intestinal lipid absorption is not affected in CD36 deficient mice. <i>Molecular and Cellular Biochemistry</i> , 2002 , 239, 199-202	4.2	51
36	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
35	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
34	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
33	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
32	Control of glycolytic dynamics by hexose transport in Saccharomyces cerevisiae. <i>Biophysical Journal</i> , 2001 , 80, 626-34	2.9	70
31	Q laveQmetabolites and enzymes. A rapid way of delineating metabolic control. <i>FEBS Journal</i> , 2000 , 267, 1889-93		18
30	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
29	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
28	Metabolic Control From The Back Benches: Biochemistry Towards Biocomplexity 2000 , 235-242		1
27	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
26	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
25	Strategies to determine the extent of control exerted by glucose transport on glycolytic flux in the yeast Saccharomyces bayanus. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 12), 3447-3454	2.9	31
24	The danger of metabolic pathways with turbo design. <i>Trends in Biochemical Sciences</i> , 1998 , 23, 162-9	10.3	198
23	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
22	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
21	Synchronized heat flux oscillations in yeast cell populations. <i>Journal of Biological Chemistry</i> , 1996 , 271, 24442-8	5.4	25

20	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
19	Acetaldehyde mediates the synchronization of sustained glycolytic oscillations in populations of yeast cells. <i>FEBS Journal</i> , 1996 , 235, 238-41		154
18	Sustained oscillations in free-energy state and hexose phosphates in yeast 1996 , 12, 731-740		77
17	Control analysis of glycolytic oscillations. <i>Biophysical Chemistry</i> , 1996 , 62, 15-24	3.5	48
16	Sustained oscillations in free-energy state and hexose phosphates in yeast. <i>Yeast</i> , 1996 , 12, 731-40	3.4	28
15	Energy, control and DNA structure in the living cell. <i>Biophysical Chemistry</i> , 1995 , 55, 153-65	3.5	12
14	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
13	Control and regulation of metabolic fluxes in microbes by substrates and enzymes. <i>Antonie Van Leeuwenhoek</i> , 1993 , 63, 315-21	2.1	15
12	Around the growth phase transition S. cerevisiae@ make-up favours sustained oscillations of intracellular metabolites. <i>FEBS Letters</i> , 1993 , 318, 80-2	3.8	71
11	Synchronization of Glycolytic Oscillations in Intact Yeast Cells 1993 , 413-416		3
10	Maintaining maximal metabolic flux by gene expression control		1
9	Glucose limitation inLactococcusshapes a single-peaked fitness landscape exposing membrane occupancy as a constraint		1
8	The number of active metabolic pathways is bounded by the number of cellular constraints at maximal metabolic rates		3
7	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
6	Emergence of stable coexistence in a complex microbial community through metabolic cooperation and spatio-temporal niche partitioning		8
5	A Systematic Assessment Of Current Genome-Scale Metabolic Reconstruction Tools		7
4	Elementary Growth Modes provide a molecular description of cellular self-fabrication		2
3	A yeast FRET biosensor enlightens cAMP signalling		2

2 Selection for cell yield does not reduce overflow metabolism in E. coli

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Whole-cell modeling in yeast predicts compartment-specific proteome constraints that drive metabolic strategies

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