Matthias Heinemann

List of Publications by Year
in descending order

84 papers	9,275 citations	57719 44 h-index	53190 85 g-index
102 all docs	102 docs citations	102 times ranked	10674 citing authors

#	Article	IF	Citations
1	Mutations in respiratory complex I promote antibiotic persistence through alterations in intracellular acidity and protein synthesis. Nature Communications, 2022, 13, 546.	5.8	21
2	Metabolic dynamics during the cell cycle. Current Opinion in Systems Biology, 2022, 30, 100415.	1.3	6
3	Perspective: a stirring role for metabolism in cells. Molecular Systems Biology, 2022, 18, e10822.	3.2	12
4	The timing of Start is determined primarily by increased synthesis of the Cln3 activator rather than dilution of the Whi5 inhibitor. Molecular Biology of the Cell, 2022, 33, rp2.	0.9	9
5	A Robust Method for Generating, Quantifying, and Testing Large Numbers of Escherichia coli Persisters. Methods in Molecular Biology, 2021, 2357, 41-62.	0.4	1
6	A synthetic RNA-based biosensor for fructose-1,6-bisphosphate that reports glycolytic flux. Cell Chemical Biology, 2021, 28, 1554-1568.e8.	2.5	17
7	Physical bioenergetics: Energy fluxes, budgets, and constraints in cells. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	52
8	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	9.0	403
9	A New Sugar for an Old Phage: a c-di-GMP-Dependent Polysaccharide Pathway Sensitizes *Escherichia coli* for Bacteriophage Infection. MBio, 2021, 12, e0324621.	1.8	15
10	How bacteria recognise and respond to surface contact. FEMS Microbiology Reviews, 2020, 44, 106-122.	3.9	92
11	Implications of initial physiological conditions for bacterial adaptation to changing environments. Molecular Systems Biology, 2020, 16, e9965.	3.2	4
12	Inference of the High-Level Interaction Topology between the Metabolic and Cell-Cycle Oscillators from Single-Cell Dynamics. Cell Systems, 2019, 9, 354-365.e6.	2.9	23
13	Differential scaling between G1 protein production and cell size dynamics promotes commitment to the cell division cycle in budding yeast. Nature Cell Biology, 2019, 21, 1382-1392.	4.6	61
14	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	13.6	748
15	Yeast Ataxin-2 Forms an Intracellular Condensate Required for the Inhibition of TORC1 Signaling during Respiratory Growth. Cell, 2019, 177, 697-710.e17.	13.5	73
16	Measuring glycolytic flux in single yeast cells with an orthogonal synthetic biosensor. Molecular Systems Biology, 2019, 15, e9071.	3.2	34
17	Manipulating rod-shaped bacteria with optical tweezers. Scientific Reports, 2019, 9, 19086.	1.6	24
18	An upper limit on Gibbs energy dissipation governs cellular metabolism. Nature Metabolism, 2019, 1, 125-132.	5.1	115

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19	Saccharomyces cerevisiae goes through distinct metabolic phases during its replicative lifespan. ELife, 2019, 8, .	2.8	36
20	Metabolic heterogeneity in clonal microbial populations. Current Opinion in Microbiology, 2018, 45, 30-38.	2.3	82
21	An engineered Calvin-Benson-Bassham cycle for carbon dioxide fixation in Methylobacterium extorquens AM1. Metabolic Engineering, 2018, 47, 423-433.	3.6	53
22	Dynamic single-cell NAD(P)H measurement reveals oscillatory metabolism throughout the E. coli cell division cycle. Scientific Reports, 2018, 8, 2162.	1.6	19
23	Metabolic-flux dependent regulation of microbial physiology. Current Opinion in Microbiology, 2018, 42, 71-78.	2.3	56
24	Reassessing the role of the Escherichia coli CpxAR system in sensing surface contact. PLoS ONE, 2018, 13, e0207181.	1.1	16
25	Assessment of the interaction between the flux‐signaling metabolite fructose‐1,6‐bisphosphate and the bacterial transcription factors CggR and Cra. Molecular Microbiology, 2018, 109, 278-290.	1.2	24
26	Bacterial persistence from a system-level perspective. Current Opinion in Biotechnology, 2017, 46, 98-105.	3.3	48
27	Autonomous Metabolic Oscillations Robustly Gate the Early and Late Cell Cycle. Molecular Cell, 2017, 65, 285-295.	4.5	150
28	Editorial overview: Systems biology for biotechnology. Current Opinion in Biotechnology, 2017, 46, iv-v.	3.3	0
29	RNA polymerase III limits longevity downstream of TORC1. Nature, 2017, 552, 263-267.	13.7	83
30	Quantitative characterization of the auxin-inducible degron: a guide for dynamic protein depletion in single yeast cells. Scientific Reports, 2017, 7, 4704.	1.6	32
31	Bacterial persistence is an active σ^S stress response to metabolic flux limitation. Molecular Systems Biology, 2016, 12, 882.	3.2	158
32	The quantitative and condition-dependent Escherichia coli proteome. Nature Biotechnology, 2016, 34, 104-110.	9.4	655
33	Distinct transcriptional regulation of the two Escherichia coli transhydrogenases PntAB and UdhA. Microbiology (United Kingdom), 2016, 162, 1672-1679.	0.7	20
34	Protein biogenesis machinery is a driver of replicative aging in yeast. ELife, 2015, 4, e08527.	2.8	151
35	Bacillus subtilis Biosensor Engineered To Assess Meat Spoilage. ACS Synthetic Biology, 2014, 3, 999-1002.	1.9	18
36	Phenotypic bistability in Escherichia coli's central carbon metabolism. Molecular Systems Biology, 2014, 10, 736.	3.2	230

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37	Calorie restriction does not elicit a robust extension of replicative lifespan in *Saccharomyces cerevisiae*. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11727-11731.	3.3	44
38	Temporal system-level organization of the switch from glycolytic to gluconeogenic operation in yeast. Molecular Systems Biology, 2013, 9, 651.	3.2	138
39	Construction and use of a microfluidic dissection platform for long-term imaging of cellular processes in budding yeast. Nature Protocols, 2013, 8, 1019-1027.	5.5	35
40	Mass spectrometry-based metabolomics of single yeast cells. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8790-8794.	3.3	214
41	Dissecting specific and global transcriptional regulation of bacterial gene expression. Molecular Systems Biology, 2013, 9, 658.	3.2	115
42	Functioning of a metabolic flux sensor in *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1130-1135.	3.3	177
43	Continuous High-resolution Microscopic Observation of Replicative Aging in Budding Yeast. Journal of Visualized Experiments, 2013, , e50143.	0.2	7
44	System-Level Insights into Yeast Metabolism by Thermodynamic Analysis of Elementary Flux Modes. PLoS Computational Biology, 2012, 8, e1002415.	1.5	61
45	Prediction of Microbial Growth Rate versus Biomass Yield by a Metabolic Network with Kinetic Parameters. PLoS Computational Biology, 2012, 8, e1002575.	1.5	148
46	Whole lifespan microscopic observation of budding yeast aging through a microfluidic dissection platform. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 4916-4920.	3.3	192
47	Multidimensional Optimality of Microbial Metabolism. Science, 2012, 336, 601-604.	6.0	360
48	A flux-sensing mechanism could regulate the switch between respiration and fermentation. FEMS Yeast Research, 2012, 12, 118-128.	1.1	80
49	Carbon-13 labelling strategy for studying the ATP metabolism in individual yeast cells by micro-arrays for mass spectrometry. Molecular BioSystems, 2011, 7, 2837.	2.9	35
50	Comprehensive quantitative analysis of central carbon and amino-acid metabolism in *Saccharomyces cerevisiae* under multiple conditions by targeted proteomics. Molecular Systems Biology, 2011, 7, 464.	3.2	105
51	Optimization of a blueprint for in vitro glycolysis by metabolic real-time analysis. Nature Chemical Biology, 2011, 7, 271-277.	3.9	139
52	Single cell metabolomics. Current Opinion in Biotechnology, 2011, 22, 26-31.	3.3	114
53	From good old biochemical analyses to high-throughput omics measurements and back. Current Opinion in Biotechnology, 2011, 22, 1-2.	3.3	233
54	The Cost of Virulence: Retarded Growth of Salmonella Typhimurium Cells Expressing Type III Secretion System 1. PLoS Pathogens, 2011, 7, e1002143.	2.1	213

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55	Condition-Dependent Cell Volume and Concentration of Escherichia coli to Facilitate Data Conversion for Systems Biology Modeling. PLoS ONE, 2011, 6, e23126.	1.1	275
56	Exploiting cell–free systems: Implementation and debugging of a system of biotransformations. Biotechnology and Bioengineering, 2010, 106, 376-389.	1.7	81
57	Differential glucose repression in common yeast strains in response to HXK2 deletion. FEMS Yeast Research, 2010, 10, 322-332.	1.1	52
58	Bacterial adaptation through distributed sensing of metabolic fluxes. Molecular Systems Biology, 2010, 6, 355.	3.2	224
59	Thermodynamic Calculations for Biochemical Transport and Reaction Processes in Metabolic Networks. Biophysical Journal, 2010, 99, 3139-3144.	0.2	30
60	Systems biology of microbial metabolism. Current Opinion in Microbiology, 2010, 13, 337-343.	2.3	111
61	A divide-and-conquer approach to analyze underdetermined biochemical models. Bioinformatics, 2009, 25, 519-525.	1.8	25
62	Nutritional Systems Biology Modeling: From Molecular Mechanisms to Physiology. PLoS Computational Biology, 2009, 5, e1000554.	1.5	76
63	Physiology of Mycobacteria. Advances in Microbial Physiology, 2009, 55, 81-319.	1.0	135
64	Mass Spectrometric Method for Analyzing Metabolites in Yeast with Single Cell Sensitivity. Angewandte Chemie - International Edition, 2008, 47, 5382-5385.	7.2	130
65	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	9.4	530
66	anNET: a tool for network-embedded thermodynamic analysis of quantitative metabolome data. BMC Bioinformatics, 2008, 9, 199.	1.2	70
67	GENETICS: Getting Closer to the Whole Picture. Science, 2007, 316, 550-551.	6.0	222
68	Characterization of the AlkS/PalkB-expression system as an efficient tool for the production of recombinant proteins inEscherichia coli fed-batch fermentations. Biotechnology and Bioengineering, 2007, 96, 326-336.	1.7	20
69	Living with an imperfect cell wall: compensation of femAB inactivation in Staphylococcus aureus. BMC Genomics, 2007, 8, 307.	1.2	34
70	Integrated operation of continuous chromatography and biotransformations for the generic high yield production of fine chemicals. Journal of Biotechnology, 2006, 124, 146-162.	1.9	57
71	Synthetic biology--putting engineering into biology. Bioinformatics, 2006, 22, 2790-2799.	1.8	282
72	Suitability of teicoplanin–aglycone bonded stationary phase for simulated moving bed enantioseparation of racemic amino acids employing composition-constrained eluents. Journal of Chromatography A, 2006, 1113, 167-176.	1.8	14

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73	Systematic assignment of thermodynamic constraints in metabolic network models. BMC Bioinformatics, 2006, 7, 512.	1.2	132
74	Putative regulatory sites unraveled by network-embedded thermodynamic analysis of metabolome data. Molecular Systems Biology, 2006, 2, 2006.0034.	3.2	258
75	Reporter Metabolite Analysis of Transcriptional Profiles of a Staphylococcus aureus Strain with Normal Phenotype and Its Isogenic hemB Mutant Displaying the Small-Colony-Variant Phenotype. Journal of Bacteriology, 2006, 188, 7765-7777.	1.0	84
76	In silico genome-scale reconstruction and validation of theStaphylococcus aureusmetabolic network. Biotechnology and Bioengineering, 2005, 92, 850-864.	1.7	128
77	pH-optima in lipase-catalysed esterification. Biocatalysis and Biotransformation, 2005, 23, 307-314.	1.1	19
78	Optimization of adsorptive immobilization of alcohol dehydrogenases. Journal of Bioscience and Bioengineering, 2005, 99, 340-347.	1.1	42
79	Method for Quantitative Determination of Spatial Polymer Distribution in Alginate Beads Using Raman Spectroscopy. Applied Spectroscopy, 2005, 59, 280-285.	1.2	24
80	Optimization of Enzymatic Gas-Phase Reactions by Increasing the Long-Term Stability of the Catalyst. Biotechnology Progress, 2004, 20, 975-978.	1.3	30
81	New insights in the spatially resolved dynamic pH measurement in macroscopic large absorbent particles by confocal laser scanning microscopy. Journal of Chromatography A, 2004, 1024, 45-53.	1.8	20
82	Experimental and Theoretical Analysis of Phase Equilibria in a Two-phase System Used for Biocatalytic Esterifications. Biocatalysis and Biotransformation, 2003, 21, 115-121.	1.1	15
83	Enzymatic catalysis in gel-stabilized two-phase systems: improvement of the solvent phase. Journal of Molecular Catalysis B: Enzymatic, 2002, 18, 19-27.	1.8	24
84	Title is missing!. Biotechnology Letters, 2002, 24, 845-850.	1.1	24