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	Definitions and guidelines for research on antibiotic persistence. Nature Reviews Microbiology, 2019, 17, 441-448.	13.6	748
2	The quantitative and condition-dependent Escherichia coli proteome. Nature Biotechnology, 2016, 34, 104-110.	9.4	655
3	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. Nature Biotechnology, 2008, 26, 1155-1160.	9.4	530
4	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nature Methods, 2021, 18, 747-756.	9.0	403
5	Multidimensional Optimality of Microbial Metabolism. Science, 2012, 336, 601-604.	6.0	360
6	Synthetic biology--putting engineering into biology. Bioinformatics, 2006, 22, 2790-2799.	1.8	282
7	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
8	Putative regulatory sites unraveled by networkâ€embedded thermodynamic analysis of metabolome data. Molecular Systems Biology, 2006, 2, 2006.0034.	3.2	258
9	From good old biochemical analyses to high-throughput omics measurements and back. Current Opinion in Biotechnology, 2011, 22, 1-2.	3.3	233
10	Phenotypic bistability in <i>Escherichia coli</i>'s central carbon metabolism. Molecular Systems Biology, 2014, 10, 736.	3.2	230
11	Bacterial adaptation through distributed sensing of metabolic fluxes. Molecular Systems Biology, 2010, 6, 355.	3.2	224
12	GENETICS: Getting Closer to the Whole Picture. Science, 2007, 316, 550-551.	6.0	222
13	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
14	The Cost of Virulence: Retarded Growth of Salmonella Typhimurium Cells Expressing Type III Secretion System 1. PLoS Pathogens, 2011, 7, e1002143.	2.1	213
15	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
16	Functioning of a metabolic flux sensor in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 1130-1135.	3.3	177
17	Bacterial persistence is an active Ïƒ ^S stress response to metabolic flux limitation. Molecular Systems Biology, 2016, 12, 882.	3.2	158
18	Protein biogenesis machinery is a driver of replicative aging in yeast. ELife, 2015, 4, e08527.	2.8	151

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19	Autonomous Metabolic Oscillations Robustly Gate the Early and Late Cell Cycle. Molecular Cell, 2017, 65, 285-295.	4.5	150
20	Prediction of Microbial Growth Rate versus Biomass Yield by a Metabolic Network with Kinetic Parameters. PLoS Computational Biology, 2012, 8, e1002575.	1.5	148
21	Optimization of a blueprint for in vitro glycolysis by metabolic real-time analysis. Nature Chemical Biology, 2011, 7, 271-277.	3.9	139
22	Temporal systemâ€level organization of the switch from glycolytic to gluconeogenic operation in yeast. Molecular Systems Biology, 2013, 9, 651.	3.2	138
23	Physiology of Mycobacteria. Advances in Microbial Physiology, 2009, 55, 81-319.	1.0	135
24	Systematic assignment of thermodynamic constraints in metabolic network models. BMC Bioinformatics, 2006, 7, 512.	1.2	132
25	Mass Spectrometric Method for Analyzing Metabolites in Yeast with Single Cell Sensitivity. Angewandte Chemie - International Edition, 2008, 47, 5382-5385.	7.2	130
26	In silico genome-scale reconstruction and validation of theStaphylococcus aureusmetabolic network. Biotechnology and Bioengineering, 2005, 92, 850-864.	1.7	128
27	Dissecting specific and global transcriptional regulation of bacterial gene expression. Molecular Systems Biology, 2013, 9, 658.	3.2	115
28	An upper limit on Gibbs energy dissipation governs cellular metabolism. Nature Metabolism, 2019, 1, 125-132.	5.1	115
29	Single cell metabolomics. Current Opinion in Biotechnology, 2011, 22, 26-31.	3.3	114
30	Systems biology of microbial metabolism. Current Opinion in Microbiology, 2010, 13, 337-343.	2.3	111
31	Comprehensive quantitative analysis of central carbon and aminoâ€acid metabolism in <i>Saccharomyces cerevisiae</i> under multiple conditions by targeted proteomics. Molecular Systems Biology, 2011, 7, 464.	3.2	105
32	How bacteria recognise and respond to surface contact. FEMS Microbiology Reviews, 2020, 44, 106-122.	3.9	92
33	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
34	RNA polymerase III limits longevity downstream of TORC1. Nature, 2017, 552, 263-267.	13.7	83
35	Metabolic heterogeneity in clonal microbial populations. Current Opinion in Microbiology, 2018, 45, 30-38.	2.3	82
36	Exploiting cellâ€free systems: Implementation and debugging of a system of biotransformations. Biotechnology and Bioengineering, 2010, 106, 376-389.	1.7	81

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37	A flux-sensing mechanism could regulate the switch between respiration and fermentation. FEMS Yeast Research, 2012, 12, 118-128.	1.1	80
38	Nutritional Systems Biology Modeling: From Molecular Mechanisms to Physiology. PLoS Computational Biology, 2009, 5, e1000554.	1.5	76
39	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
40	anNET: a tool for network-embedded thermodynamic analysis of quantitative metabolome data. BMC Bioinformatics, 2008, 9, 199.	1.2	70
41	System-Level Insights into Yeast Metabolism by Thermodynamic Analysis of Elementary Flux Modes. PLoS Computational Biology, 2012, 8, e1002415.	1.5	61
42	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
43	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
44	Metabolic-flux dependent regulation of microbial physiology. Current Opinion in Microbiology, 2018, 42, 71-78.	2.3	56
45	An engineered Calvin-Benson-Bassham cycle for carbon dioxide fixation in Methylobacterium extorquens AM1. Metabolic Engineering, 2018, 47, 423-433.	3.6	53
46	Differential glucose repression in common yeast strains in response to HXK2 deletion. FEMS Yeast Research, 2010, 10, 322-332.	1.1	52
47	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
48	Bacterial persistence from a system-level perspective. Current Opinion in Biotechnology, 2017, 46, 98-105.	3.3	48
49	Calorie restriction does not elicit a robust extension of replicative lifespan in <i>Saccharomyces cerevisiae</i>. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11727-11731.	3.3	44
50	Optimization of adsorptive immobilization of alcohol dehydrogenases. Journal of Bioscience and Bioengineering, 2005, 99, 340-347.	1.1	42
51	Saccharomyces cerevisiae goes through distinct metabolic phases during its replicative lifespan. ELife, 2019, 8, .	2.8	36
52	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
53	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
54	Living with an imperfect cell wall: compensation of femAB inactivation in Staphylococcus aureus. BMC Genomics, 2007, 8, 307.	1.2	34

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55	Measuring glycolytic flux in single yeast cells with an orthogonal synthetic biosensor. Molecular Systems Biology, 2019, 15, e9071.	3.2	34
56	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
57	Optimization of Enzymatic Gas-Phase Reactions by Increasing the Long-Term Stability of the Catalyst. Biotechnology Progress, 2004, 20, 975-978.	1.3	30
58	Thermodynamic Calculations for Biochemical Transport and Reaction Processes in Metabolic Networks. Biophysical Journal, 2010, 99, 3139-3144.	0.2	30
59	A divide-and-conquer approach to analyze underdetermined biochemical models. Bioinformatics, 2009, 25, 519-525.	1.8	25
60	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
61	Title is missing!. Biotechnology Letters, 2002, 24, 845-850.	1.1	24
62	Method for Quantitative Determination of Spatial Polymer Distribution in Alginate Beads Using Raman Spectroscopy. Applied Spectroscopy, 2005, 59, 280-285.	1.2	24
63	Manipulating rod-shaped bacteria with optical tweezers. Scientific Reports, 2019, 9, 19086.	1.6	24
64	Assessment of the interaction between the fluxâ€signaling metabolite fructoseâ€1,6â€bisphosphate and the bacterial transcription factors CggR and Cra. Molecular Microbiology, 2018, 109, 278-290.	1.2	24
65	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
66	Mutations in respiratory complex I promote antibiotic persistence through alterations in intracellular acidity and protein synthesis. Nature Communications, 2022, 13, 546.	5.8	21
67	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
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	Distinct transcriptional regulation of the two Escherichia coli transhydrogenases PntAB and UdhA. Microbiology (United Kingdom), 2016, 162, 1672-1679.	0.7	20
70	pH-optima in lipase-catalysed esterification. Biocatalysis and Biotransformation, 2005, 23, 307-314.	1.1	19
71	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
72	<i>Bacillus subtilis</i> Biosensor Engineered To Assess Meat Spoilage. ACS Synthetic Biology, 2014, 3, 999-1002.	1.9	18

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73	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
74	Reassessing the role of the Escherichia coli CpxAR system in sensing surface contact. PLoS ONE, 2018, 13, e0207181.	1.1	16
75	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
76	A New Sugar for an Old Phage: a c-di-GMP-Dependent Polysaccharide Pathway Sensitizes <i>Escherichia coli</i> for Bacteriophage Infection. MBio, 2021, 12, e0324621.	1.8	15
77	Suitability of teicoplaninâ€“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
78	Perspective: a stirring role for metabolism in cells. Molecular Systems Biology, 2022, 18, e10822.	3.2	12
79	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
80	Continuous High-resolution Microscopic Observation of Replicative Aging in Budding Yeast. Journal of Visualized Experiments, 2013, , e50143.	0.2	7
81	Metabolic dynamics during the cell cycle. Current Opinion in Systems Biology, 2022, 30, 100415.	1.3	6
82	Implications of initial physiological conditions for bacterial adaptation to changing environments. Molecular Systems Biology, 2020, 16, e9965.	3.2	4
83	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
84	Editorial overview: Systems biology for biotechnology. Current Opinion in Biotechnology, 2017, 46, iv-v.	3.3	0