

Uwe Sauer

List of Publications by Year in descending order

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Version: 2024-02-01

184
papers

22,275
citations

5261

83
h-index

10441

139
g-index

204
all docs

204
docs citations

204
times ranked

21599
citing authors

#	ARTICLE	IF	CITATIONS
1	Glycolysis/gluconeogenesis specialization in microbes is driven by biochemical constraints of flux sensing. <i>Molecular Systems Biology</i> , 2022, 18, e10704.	3.2	21
2	High-Throughput Metabolomics and Diabetic Kidney Disease Progression: Evidence from the Chronic Renal Insufficiency (CRIC) Study. <i>American Journal of Nephrology</i> , 2022, 53, 215-225.	1.4	14
3	Metabolic cross-feeding structures the assembly of polysaccharide degrading communities. <i>Science Advances</i> , 2022, 8, eabk3076.	4.7	40
4	Metabolic reprogramming of <i>Pseudomonas aeruginosa</i> by phage-based quorum sensing modulation. <i>Cell Reports</i> , 2022, 38, 110372.	2.9	20
5	Distinct N and C Cross-Feeding Networks in a Synthetic Mouse Gut Consortium. <i>MSystems</i> , 2022, 7, e0148421.	1.7	9
6	High-throughput metabolomics predicts drug-target relationships for eukaryotic proteins. <i>Molecular Systems Biology</i> , 2022, 18, e10767.	3.2	16
7	Reconfiguration of metabolic fluxes in <i>Pseudomonas putida</i> as a response to sub-lethal oxidative stress. <i>ISME Journal</i> , 2021, 15, 1751-1766.	4.4	79
8	Long-term evolution and short-term adaptation of microbiota strains and sub-strains in mice. <i>Cell Host and Microbe</i> , 2021, 29, 650-663.e9.	5.1	58
9	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. <i>Molecular Systems Biology</i> , 2021, 17, e10064.	3.2	33
10	Salt-Tolerant Metabolomics for Exometabolomic Measurements of Marine Bacterial Isolates. <i>Analytical Chemistry</i> , 2021, 93, 7164-7171.	3.2	10
11	Conservation of metabolic regulation by phosphorylation and non-covalent small-molecule interactions. <i>Cell Systems</i> , 2021, 12, 538-546.	2.9	5
12	A distinct growth physiology enhances bacterial growth under rapid nutrient fluctuations. <i>Nature Communications</i> , 2021, 12, 3662.	5.8	40
13	Niche partitioning facilitates coexistence of closely related honey bee gut bacteria. <i>ELife</i> , 2021, 10, .	2.8	53
14	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	9.0	403
15	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	5.9	138
16	Extensive regulation of enzyme activity by phosphorylation in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2021, 12, 5650.	5.8	14
17	Reversible amyloids of pyruvate kinase couple cell metabolism and stress granule disassembly. <i>Nature Cell Biology</i> , 2021, 23, 1085-1094.	4.6	33
18	Metabolism as a signal generator in bacteria. <i>Current Opinion in Systems Biology</i> , 2021, 28, 100404.	1.3	6

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19	Membrane composition and organization of <i>Bacillus subtilis</i> 168 and its genome-reduced derivative mini <i>Bacillus</i> PG10. <i>Microbial Biotechnology</i> , 2021, , .	2.0	4
20	Cooperation and Cheating among Germinating Spores. <i>Current Biology</i> , 2020, 30, 4745-4752.e4.	1.8	15
21	A universal trade-off between growth and lag in fluctuating environments. <i>Nature</i> , 2020, 584, 470-474.	13.7	139
22	β -Oxidation and autophagy are critical energy providers during acute glucose depletion in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12239-12248.	3.3	27
23	Import of Aspartate and Malate by DcuABC Drives H ₂ /Fumarate Respiration to Promote Initial <i>Salmonella</i> Gut-Lumen Colonization in Mice. <i>Cell Host and Microbe</i> , 2020, 27, 922-936.e6.	5.1	58
24	Model-based integration of genomics and metabolomics reveals SNP functionality in <i>Mycobacterium tuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 8494-8502.	3.3	24
25	Bacterial Glycogen Provides Short-Term Benefits in Changing Environments. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	1.4	53
26	Co-catabolism of arginine and succinate drives symbiotic nitrogen fixation. <i>Molecular Systems Biology</i> , 2020, 16, e9419.	3.2	33
27	Implications of initial physiological conditions for bacterial adaptation to changing environments. <i>Molecular Systems Biology</i> , 2020, 16, e9965.	3.2	4
28	Regulatory mechanisms underlying coordination of amino acid and glucose catabolism in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 3354.	5.8	101
29	Reserve Flux Capacity in the Pentose Phosphate Pathway by NADPH Binding Is Conserved across Kingdoms. <i>IScience</i> , 2019, 19, 1133-1144.	1.9	44
30	<i>Escherichia coli</i> limits <i>Salmonella Typhimurium</i> infections after diet shifts and fat-mediated microbiota perturbation in mice. <i>Nature Microbiology</i> , 2019, 4, 2164-2174.	5.9	88
31	Biological insights through omics data integration. <i>Current Opinion in Systems Biology</i> , 2019, 15, 39-47.	1.3	59
32	Hidden resources in the <i>Escherichia coli</i> genome restore PLP synthesis and robust growth after deletion of the essential gene <i>pdxB</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24164-24173.	3.3	23
33	Systematic mapping of protein-metabolite interactions in central metabolism of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2019, 15, e9008.	3.2	45
34	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, .	5.8	102
35	A Map of Protein-Metabolite Interactions Reveals Principles of Chemical Communication. <i>Cell</i> , 2018, 172, 358-372.e23.	13.5	350
36	Synthesis and degradation of FtsZ quantitatively predict the first cell division in starved bacteria. <i>Molecular Systems Biology</i> , 2018, 14, e8623.	3.2	66

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37	Editorial overview: Current Opinion in Microbiology 2018 Special issue "Microbial systems biology, vol. 45". Current Opinion in Microbiology, 2018, 45, vi-viii.	2.3	0
38	Antibodies Set Boundaries Limiting Microbial Metabolite Penetration and the Resultant Mammalian Host Response. Immunity, 2018, 49, 545-559.e5.	6.6	121
39	Reserve Flux Capacity in the Pentose Phosphate Pathway Enables Escherichia coli's Rapid Response to Oxidative Stress. Cell Systems, 2018, 6, 569-578.e7.	2.9	162
40	Capacity for instantaneous catabolism of preferred and non-preferred carbon sources in Escherichia coli and Bacillus subtilis. Scientific Reports, 2018, 8, 11760.	1.6	26
41	Genomewide landscape of gene-metabolome associations in Escherichia coli. Molecular Systems Biology, 2017, 13, 907.	3.2	109
42	Spatiotemporal Analysis of a Glycolytic Activity Gradient Linked to Mouse Embryo Mesoderm Development. Developmental Cell, 2017, 40, 331-341.e4.	3.1	107
43	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. Cell Reports, 2017, 19, 1214-1228.	2.9	139
44	Glycolysis without pyruvate kinase in Clostridium thermocellum. Metabolic Engineering, 2017, 39, 169-180.	3.6	62
45	Metabolic constraints on the evolution of antibiotic resistance. Molecular Systems Biology, 2017, 13, 917.	3.2	151
46	Nontargeted in vitro metabolomics for high-throughput identification of novel enzymes in Escherichia coli. Nature Methods, 2017, 14, 187-194.	9.0	125
47	Few regulatory metabolites coordinate expression of central metabolic genes in Escherichia coli. Molecular Systems Biology, 2017, 13, 903.	3.2	129
48	Frontiers of high-throughput metabolomics. Current Opinion in Chemical Biology, 2017, 36, 15-23.	2.8	139
49	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. Cell Systems, 2017, 5, 345-357.e6.	2.9	247
50	Integration of Metabolomics and Transcriptomics Reveals a Complex Diet of Mycobacterium tuberculosis during Early Macrophage Infection. MSystems, 2017, 2, .	1.7	112
51	Genome-Scale Architecture of Small Molecule Regulatory Networks and the Fundamental Trade-Off between Regulation and Enzymatic Activity. Cell Reports, 2017, 20, 2666-2677.	2.9	70
52	Metabolomics-driven understanding of genotype-phenotype relations in model organisms. Current Opinion in Systems Biology, 2017, 6, 28-36.	1.3	17
53	Towards detecting regulatory protein-metabolite interactions. Current Opinion in Microbiology, 2017, 39, 16-23.	2.3	42
54	Systems Pharmacology Dissection of Cholesterol Regulation Reveals Determinants of Large Pharmacodynamic Variability between Cell Lines. Cell Systems, 2017, 5, 604-619.e7.	2.9	17

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55	PknG senses amino acid availability to control metabolism and virulence of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006399.	2.1	81
56	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	1.5	51
57	Disentangling metabolic functions of bacteria in the honey bee gut. <i>PLoS Biology</i> , 2017, 15, e2003467.	2.6	270
58	Untargeted metabolomics unravels functionalities of phosphorylation sites in <i>Saccharomyces cerevisiae</i> . <i>BMC Systems Biology</i> , 2016, 10, 104.	3.0	15
59	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . <i>EMBO Reports</i> , 2016, 17, 455-469.	2.0	116
60	Systematic Identification of Protein-Metabolite Interactions in Complex Metabolite Mixtures by Ligand-Detected Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2016, 55, 2590-2600.	1.2	20
61	A rheostat mechanism governs the bifurcation of carbon flux in mycobacteria. <i>Nature Communications</i> , 2016, 7, 12527.	5.8	27
62	A dynamic pathway analysis approach reveals a limiting futile cycle in N-acetylglucosamine overproducing <i>Bacillus subtilis</i> . <i>Nature Communications</i> , 2016, 7, 11933.	5.8	45
63	The maternal microbiota drives early postnatal innate immune development. <i>Science</i> , 2016, 351, 1296-1302.	6.0	871
64	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. <i>ISME Journal</i> , 2016, 10, 1823-1835.	4.4	126
65	Distinct transcriptional regulation of the two <i>Escherichia coli</i> transhydrogenases PntAB and UdhA. <i>Microbiology (United Kingdom)</i> , 2016, 162, 1672-1679.	0.7	20
66	Elucidation of Genetic Interactions in the Yeast GATA-Factor Network Using Bayesian Model Selection. <i>PLoS Computational Biology</i> , 2016, 12, e1004784.	1.5	8
67	Global Metabolic Responses to Salt Stress in Fifteen Species. <i>PLoS ONE</i> , 2016, 11, e0148888.	1.1	61
68	Dynamic exometabolome analysis reveals active metabolic pathways in non-replicating mycobacteria. <i>Environmental Microbiology</i> , 2015, 17, 4802-4815.	1.8	40
69	Posttranslational regulation of microbial metabolism. <i>Current Opinion in Microbiology</i> , 2015, 27, 10-17.	2.3	45
70	The Neurometabolic Fingerprint of Excessive Alcohol Drinking. <i>Neuropsychopharmacology</i> , 2015, 40, 1259-1268.	2.8	24
71	A roadmap for interpreting ¹³ C metabolite labeling patterns from cells. <i>Current Opinion in Biotechnology</i> , 2015, 34, 189-201.	3.3	513
72	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. <i>Molecular Systems Biology</i> , 2015, 11, 802.	3.2	49

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73	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of Mycobacterium tuberculosis. <i>Cell Host and Microbe</i> , 2015, 18, 96-108.	5.1	229
74	Transhydrogenase Promotes the Robustness and Evolvability of <i>E. coli</i> Deficient in NADPH Production. <i>PLoS Genetics</i> , 2015, 11, e1005007.	1.5	42
75	Characterization of the Mycobacterial Acyl-CoA Carboxylase Holo Complexes Reveals Their Functional Expansion into Amino Acid Catabolism. <i>PLoS Pathogens</i> , 2015, 11, e1004623.	2.1	19
76	Bistability in a Metabolic Network Underpins the De Novo Evolution of Colony Switching in <i>Pseudomonas fluorescens</i> . <i>PLoS Biology</i> , 2015, 13, e1002109.	2.6	78
77	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015, 8, rs4.	1.6	64
78	<i>Pseudomonas putida</i> KT2440 Strain Metabolizes Glucose through a Cycle Formed by Enzymes of the Entner-Doudoroff, Embden-Meyerhof-Parnas, and Pentose Phosphate Pathways. <i>Journal of Biological Chemistry</i> , 2015, 290, 25920-25932.	1.6	269
79	The outer mucus layer hosts a distinct intestinal microbial niche. <i>Nature Communications</i> , 2015, 6, 8292.	5.8	390
80	Real-time metabolome profiling of the metabolic switch between starvation and growth. <i>Nature Methods</i> , 2015, 12, 1091-1097.	9.0	209
81	Pseudo-transition Analysis Identifies the Key Regulators of Dynamic Metabolic Adaptations from Steady-State Data. <i>Cell Systems</i> , 2015, 1, 270-282.	2.9	133
82	Biological insights through nontargeted metabolomics. <i>Current Opinion in Biotechnology</i> , 2015, 34, 1-8.	3.3	115
83	Nitrogen Source Activates TOR (Target of Rapamycin) Complex 1 via Glutamine and Independently of Ctr/Rag Proteins. <i>Journal of Biological Chemistry</i> , 2014, 289, 25010-25020.	1.6	172
84	Topological augmentation to infer hidden processes in biological systems. <i>Bioinformatics</i> , 2014, 30, 221-227.	1.8	12
85	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 762.	3.2	159
86	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. <i>Science Signaling</i> , 2014, 7, rs6.	1.6	32
87	Ubiquinone accumulation improves osmotic-stress tolerance in <i>Escherichia coli</i> . <i>Nature Chemical Biology</i> , 2014, 10, 266-272.	3.9	120
88	Coordination of microbial metabolism. <i>Nature Reviews Microbiology</i> , 2014, 12, 327-340.	13.6	439
89	Advancing metabolic models with kinetic information. <i>Current Opinion in Biotechnology</i> , 2014, 29, 8-14.	3.3	99
90	Identification of Transcriptional and Metabolic Programs Related to Mammalian Cell Size. <i>Current Biology</i> , 2014, 24, 598-608.	1.8	108

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91	Quantification and Mass Isotopomer Profiling of $\hat{\pm}$ -Keto Acids in Central Carbon Metabolism. <i>Analytical Chemistry</i> , 2014, 86, 3232-3237.	3.2	60
92	Non-stationary ¹³ C metabolic flux ratio analysis. <i>Biotechnology and Bioengineering</i> , 2013, 110, 3164-3176.	1.7	41
93	Nontargeted Profiling of Coenzyme A thioesters in biological samples by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 8284-8290.	3.2	24
94	Temporal system-level organization of the switch from glycolytic to gluconeogenic operation in yeast. <i>Molecular Systems Biology</i> , 2013, 9, 651.	3.2	138
95	A role for EIIA Ntr in controlling fluxes in the central metabolism of E. coli K12. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 2879-2889.	1.9	21
96	Local requirement of the Drosophila insulin binding protein imp-L2 in coordinating developmental progression with nutritional conditions. <i>Developmental Biology</i> , 2013, 381, 97-106.	0.9	28
97	Systematic identification of allosteric protein-metabolite interactions that control enzyme activity in vivo. <i>Nature Biotechnology</i> , 2013, 31, 357-361.	9.4	225
98	Somewhat in control – the role of transcription in regulating microbial metabolic fluxes. <i>Current Opinion in Biotechnology</i> , 2013, 24, 987-993.	3.3	54
99	Dissecting specific and global transcriptional regulation of bacterial gene expression. <i>Molecular Systems Biology</i> , 2013, 9, 658.	3.2	115
100	Transcriptional regulation is insufficient to explain substrate-induced flux changes in <i>Bacillus subtilis</i> . <i>Molecular Systems Biology</i> , 2013, 9, 709.	3.2	149
101	How do microbes control their metabolic operation. <i>FASEB Journal</i> , 2013, 27, 87.1.	0.2	0
102	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of <i>Pseudomonas putida</i> in Central Carbon Metabolism. <i>MBio</i> , 2012, 3, .	1.8	78
103	¹³ C-flux Analysis Reveals NADPH-balancing Transhydrogenation Cycles in Stationary Phase of Nitrogen-starving <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 27959-27970.	1.6	53
104	Targeted and quantitative metabolomics in bacteria. <i>Methods in Microbiology</i> , 2012, , 127-150.	0.4	14
105	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	9.4	107
106	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. <i>Science</i> , 2012, 335, 1099-1103.	6.0	255
107	Global probabilistic annotation of metabolic networks enables enzyme discovery. <i>Nature Chemical Biology</i> , 2012, 8, 848-854.	3.9	53
108	Dynamic metabolomics differentiates between carbon and energy starvation in recombinant <i>Saccharomyces cerevisiae</i> fermenting xylose. <i>Biotechnology for Biofuels</i> , 2012, 5, 34.	6.2	52

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109	Regulation of yeast central metabolism by enzyme phosphorylation. <i>Molecular Systems Biology</i> , 2012, 8, 623.	3.2	154
110	Multidimensional Optimality of Microbial Metabolism. <i>Science</i> , 2012, 336, 601-604.	6.0	360
111	A high-throughput metabolomics method to predict high concentration cytotoxicity of drugs from low concentration profiles. <i>Metabolomics</i> , 2012, 8, 433-443.	1.4	10
112	The importance of post-translational modifications in regulating <i>Saccharomyces cerevisiae</i> metabolism. <i>FEMS Yeast Research</i> , 2012, 12, 104-117.	1.1	78
113	Collisional fragmentation of central carbon metabolites in LC-MS/MS increases precision of ¹³ C metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2012, 109, 763-771.	1.7	93
114	Acetate scavenging activity in <i>Escherichia coli</i> : interplay of acetyl-CoA synthetase and the PEP-glyoxylate cycle in chemostat cultures. <i>Applied Microbiology and Biotechnology</i> , 2012, 93, 2109-2124.	1.7	71
115	Large-scale ¹³ C flux analysis reveals distinct transcriptional control of respiratory and fermentative metabolism in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2011, 7, 477.	3.2	151
116	Comprehensive quantitative analysis of central carbon and amino acid metabolism in <i>Saccharomyces cerevisiae</i> under multiple conditions by targeted proteomics. <i>Molecular Systems Biology</i> , 2011, 7, 464.	3.2	105
117	Intracellular characterization of aerobic glucose metabolism in seven yeast species by ¹³ C flux analysis and metabolomics. <i>FEMS Yeast Research</i> , 2011, 11, 263-272.	1.1	123
118	Regulation and control of metabolic fluxes in microbes. <i>Current Opinion in Biotechnology</i> , 2011, 22, 566-575.	3.3	142
119	From good old biochemical analyses to high-throughput omics measurements and back. <i>Current Opinion in Biotechnology</i> , 2011, 22, 1-2.	3.3	233
120	Fumarate Reductase Activity Maintains an Energized Membrane in Anaerobic <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2011, 7, e1002287.	2.1	221
121	Dynamic flux responses in riboflavin overproducing <i>Bacillus subtilis</i> to increasing glucose limitation in fed-batch culture. <i>Biotechnology and Bioengineering</i> , 2010, 105, 795-804.	1.7	29
122	Tradeoff between enzyme and metabolite efficiency maintains metabolic homeostasis upon perturbations in enzyme capacity. <i>Molecular Systems Biology</i> , 2010, 6, 356.	3.2	159
123	Unraveling condition-dependent networks of transcription factors that control metabolic pathway activity in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 432.	3.2	59
124	Ultrahigh Performance Liquid Chromatography-Tandem Mass Spectrometry Method for Fast and Robust Quantification of Anionic and Aromatic Metabolites. <i>Analytical Chemistry</i> , 2010, 82, 4403-4412.	3.2	317
125	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	5.8	100
126	Transcriptional regulation of respiration in yeast metabolizing differently repressive carbon substrates. <i>BMC Systems Biology</i> , 2010, 4, 12.	3.0	96

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127	Metabolic Fluxes during Strong Carbon Catabolite Repression by Malate in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 1587-1596.	1.6	100
128	Systems biology of microbial metabolism. <i>Current Opinion in Microbiology</i> , 2010, 13, 337-343.	2.3	111
129	Resistance of <i>Saccharomyces cerevisiae</i> to High Concentrations of Furfural Is Based on NADPH-Dependent Reduction by at Least Two Oxireductases. <i>Applied and Environmental Microbiology</i> , 2009, 75, 7631-7638.	1.4	144
130	Different Biochemical Mechanisms Ensure Network-Wide Balancing of Reducing Equivalents in Microbial Metabolism. <i>Journal of Bacteriology</i> , 2009, 191, 2112-2121.	1.0	136
131	Measurements versus understanding: the (metabol)omics dilemma. <i>Microbial Biotechnology</i> , 2009, 2, 147-149.	2.0	1
132	¹³ C-based metabolic flux analysis. <i>Nature Protocols</i> , 2009, 4, 878-892.	5.5	520
133	Novel biological insights through metabolomics and ¹³ C-flux analysis. <i>Current Opinion in Microbiology</i> , 2009, 12, 553-558.	2.3	120
134	Screening of <i>Bacillus subtilis</i> transposon mutants with altered riboflavin production. <i>Metabolic Engineering</i> , 2008, 10, 216-226.	3.6	53
135	From biomarkers to integrated network responses. <i>Nature Biotechnology</i> , 2008, 26, 1090-1092.	9.4	12
136	Identification of furfural as a key toxin in lignocellulosic hydrolysates and evolution of a tolerant yeast strain. <i>Microbial Biotechnology</i> , 2008, 1, 497-506.	2.0	227
137	Maintenance metabolism and carbon fluxes in <i>Bacillus</i> species. <i>Microbial Cell Factories</i> , 2008, 7, 19.	1.9	67
138	Cyclic AMP-Dependent Catabolite Repression Is the Dominant Control Mechanism of Metabolic Fluxes under Glucose Limitation in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2008, 190, 2323-2330.	1.0	67
139	CcpN Controls Central Carbon Fluxes in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2008, 190, 6178-6187.	1.0	42
140	Convergent Peripheral Pathways Catalyze Initial Glucose Catabolism in <i>Pseudomonas putida</i> : Genomic and Flux Analysis. <i>Journal of Bacteriology</i> , 2007, 189, 5142-5152.	1.0	231
141	GENETICS: Getting Closer to the Whole Picture. <i>Science</i> , 2007, 316, 550-551.	6.0	222
142	Systematic evaluation of objective functions for predicting intracellular fluxes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2007, 3, 119.	3.2	623
143	Determination of Metabolic Flux Ratios From ¹³ C-Experiments and Gas Chromatography-Mass Spectrometry Data. <i>Methods in Molecular Biology</i> , 2007, 358, 177-197.	0.4	168
144	Ensemble modeling for analysis of cell signaling dynamics. <i>Nature Biotechnology</i> , 2007, 25, 1001-1006.	9.4	214

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145	Standard reporting requirements for biological samples in metabolomics experiments: microbial and in vitro biology experiments. <i>Metabolomics</i> , 2007, 3, 189-194.	1.4	50
146	Metabolic networks in motion: 13 C-based flux analysis. <i>Molecular Systems Biology</i> , 2006, 2, 62.	3.2	582
147	YtsJ Has the Major Physiological Role of the Four Paralogous Malic Enzyme Isoforms in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2006, 188, 4727-4736.	1.0	52
148	Nonlinear Dependency of Intracellular Fluxes on Growth Rate in Miniaturized Continuous Cultures of <i>Escherichia coli</i> . <i>Applied and Environmental Microbiology</i> , 2006, 72, 1164-1172.	1.4	135
149	The PEP "pyruvate" oxaloacetate node as the switch point for carbon flux distribution in bacteria: We dedicate this paper to Rudolf K. Thauer, Director of the Max-Planck-Institute for Terrestrial Microbiology in Marburg, Germany, on the occasion of his 65th birthday. <i>FEMS Microbiology Reviews</i> , 2005, 29, 765-794.	3.9	441
150	Large-scale in vivo flux analysis shows rigidity and suboptimal performance of <i>Bacillus subtilis</i> metabolism. <i>Nature Genetics</i> , 2005, 37, 636-640.	9.4	288
151	FiatFlux—a software for metabolic flux analysis from 13C-glucose experiments. <i>BMC Bioinformatics</i> , 2005, 6, 209.	1.2	216
152	Transient expression and flux changes during a shift from high to low riboflavin production in continuous cultures of <i>Bacillus subtilis</i> . <i>Biotechnology and Bioengineering</i> , 2005, 89, 219-232.	1.7	32
153	Impact of Global Transcriptional Regulation by ArcA, ArcB, Cra, Crp, Cya, Fnr, and Mlc on Glucose Catabolism in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 3171-3179.	1.0	256
154	Experimental Identification and Quantification of Glucose Metabolism in Seven Bacterial Species. <i>Journal of Bacteriology</i> , 2005, 187, 1581-1590.	1.0	340
155	The <i>Bacillus subtilis</i> yqjI Gene Encodes the NADP+-Dependent 6-P-Gluconate Dehydrogenase in the Pentose Phosphate Pathway. <i>Journal of Bacteriology</i> , 2004, 186, 4528-4534.	1.0	56
156	Fermentation performance of engineered and evolved xylose-fermenting <i>Saccharomyces cerevisiae</i> strains. <i>Biotechnology and Bioengineering</i> , 2004, 87, 90-98.	1.7	123
157	The phosphoenolpyruvate carboxykinase also catalyzes C3 carboxylation at the interface of glycolysis and the TCA cycle of <i>Bacillus subtilis</i> . <i>Metabolic Engineering</i> , 2004, 6, 277-284.	3.6	49
158	High-throughput metabolic flux analysis based on gas chromatography-mass spectrometry derived 13C constraints. <i>Analytical Biochemistry</i> , 2004, 325, 308-316.	1.1	276
159	High-throughput phenomics: experimental methods for mapping fluxomes. <i>Current Opinion in Biotechnology</i> , 2004, 15, 58-63.	3.3	236
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