

Uwe Sauer

List of Publications by Year in descending order

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Version: 2024-02-01

184
papers

22,275
citations

5268

83
h-index

10445

139
g-index

204
all docs

204
docs citations

204
times ranked

21599
citing authors

#	ARTICLE	IF	CITATIONS
1	The maternal microbiota drives early postnatal innate immune development. <i>Science</i> , 2016, 351, 1296-1302.	12.6	871
2	Systematic evaluation of objective functions for predicting intracellular fluxes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2007, 3, 119.	7.2	623
3	Metabolic networks in motion: ¹³ C-based flux analysis. <i>Molecular Systems Biology</i> , 2006, 2, 62.	7.2	582
4	¹³ C-based metabolic flux analysis. <i>Nature Protocols</i> , 2009, 4, 878-892.	12.0	520
5	A roadmap for interpreting ¹³ C metabolite labeling patterns from cells. <i>Current Opinion in Biotechnology</i> , 2015, 34, 189-201.	6.6	513
6	The Soluble and Membrane-bound Transhydrogenases UdhA and PntAB Have Divergent Functions in NADPH Metabolism of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 6613-6619.	3.4	501
7	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.	8.6	441
8	Coordination of microbial metabolism. <i>Nature Reviews Microbiology</i> , 2014, 12, 327-340.	28.6	439
9	Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. <i>Nature Methods</i> , 2021, 18, 747-756.	19.0	403
10	The outer mucus layer hosts a distinct intestinal microbial niche. <i>Nature Communications</i> , 2015, 6, 8292.	12.8	390
11	Metabolic Flux Ratio Analysis of Genetic and Environmental Modulations of <i>Escherichia coli</i> Central Carbon Metabolism. <i>Journal of Bacteriology</i> , 1999, 181, 6679-6688.	2.2	361
12	Multidimensional Optimality of Microbial Metabolism. <i>Science</i> , 2012, 336, 601-604.	12.6	360
13	A Map of Protein-Metabolite Interactions Reveals Principles of Chemical Communication. <i>Cell</i> , 2018, 172, 358-372.e23.	28.9	350
14	Experimental Identification and Quantification of Glucose Metabolism in Seven Bacterial Species. <i>Journal of Bacteriology</i> , 2005, 187, 1581-1590.	2.2	340
15	Metabolic flux profiling of <i>Escherichia coli</i> mutants in central carbon metabolism using GC-MS. <i>FEBS Journal</i> , 2003, 270, 880-891.	0.2	332
16	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.	6.5	317
17	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.	21.4	288
18	High-throughput metabolic flux analysis based on gas chromatography→mass spectrometry derived ¹³ C constraints. <i>Analytical Biochemistry</i> , 2004, 325, 308-316.	2.4	276

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19	Disentangling metabolic functions of bacteria in the honey bee gut. PLoS Biology, 2017, 15, e2003467.	5.6	270
20	Pseudomonas putida KT2440 Strain Metabolizes Glucose through a Cycle Formed by Enzymes of the Entner-Doudoroff, Embden-Meyerhof-Parnas, and Pentose Phosphate Pathways. Journal of Biological Chemistry, 2015, 290, 25920-25932.	3.4	269
21	Impact of Global Transcriptional Regulation by ArcA, ArcB, Cra, Crp, Cya, Fnr, and Mlc on Glucose Catabolism in <i>Escherichia coli</i> . Journal of Bacteriology, 2005, 187, 3171-3179.	2.2	256
22	Global Network Reorganization During Dynamic Adaptations of <i>Bacillus subtilis</i> Metabolism. Science, 2012, 335, 1099-1103.	12.6	255
23	Yeast Creates a Niche for Symbiotic Lactic Acid Bacteria through Nitrogen Overflow. Cell Systems, 2017, 5, 345-357.e6.	6.2	247
24	Metabolic fluxes in riboflavin-producing <i>Bacillus subtilis</i> . Nature Biotechnology, 1997, 15, 448-452.	17.5	241
25	High-throughput phenomics: experimental methods for mapping fluxomes. Current Opinion in Biotechnology, 2004, 15, 58-63.	6.6	236
26	From good old biochemical analyses to high-throughput omics measurements and back. Current Opinion in Biotechnology, 2011, 22, 1-2.	6.6	233
27	Convergent Peripheral Pathways Catalyze Initial Glucose Catabolism in <i>Pseudomonas putida</i> : Genomic and Flux Analysis. Journal of Bacteriology, 2007, 189, 5142-5152.	2.2	231
28	Absolute Proteome Composition and Dynamics during Dormancy and Resuscitation of <i>Mycobacterium tuberculosis</i> . Cell Host and Microbe, 2015, 18, 96-108.	11.0	229
29	Identification of furfural as a key toxin in lignocellulosic hydrolysates and evolution of a tolerant yeast strain. Microbial Biotechnology, 2008, 1, 497-506.	4.2	227
30	Systematic identification of allosteric protein-metabolite interactions that control enzyme activity in vivo. Nature Biotechnology, 2013, 31, 357-361.	17.5	225
31	GENETICS: Getting Closer to the Whole Picture. Science, 2007, 316, 550-551.	12.6	222
32	Fumarate Reductase Activity Maintains an Energized Membrane in Anaerobic <i>Mycobacterium tuberculosis</i> . PLoS Pathogens, 2011, 7, e1002287.	4.7	221
33	FiatFlux—a software for metabolic flux analysis from ¹³ C-glucose experiments. BMC Bioinformatics, 2005, 6, 209.	2.6	216
34	Ensemble modeling for analysis of cell signaling dynamics. Nature Biotechnology, 2007, 25, 1001-1006.	17.5	214
35	GC-MS Analysis of Amino Acids Rapidly Provides Rich Information for Isotopomer Balancing. Biotechnology Progress, 2000, 16, 642-649.	2.6	211
36	Real-time metabolome profiling of the metabolic switch between starvation and growth. Nature Methods, 2015, 12, 1091-1097.	19.0	209

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37	Nitrogen Source Activates TOR (Target of Rapamycin) Complex 1 via Glutamine and Independently of Gtr/Rag Proteins. <i>Journal of Biological Chemistry</i> , 2014, 289, 25010-25020.	3.4	172
38	Metabolic flux analysis with a comprehensive isotopomer model in <i>Bacillus subtilis</i> . <i>Biotechnology and Bioengineering</i> , 2001, 76, 144-156.	3.3	170
39	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.	0.9	168
40	<i>Bacillus subtilis</i> Metabolism and Energetics in Carbon-Limited and Excess-Carbon Chemostat Culture. <i>Journal of Bacteriology</i> , 2001, 183, 7308-7317.	2.2	165
41	Reserve Flux Capacity in the Pentose Phosphate Pathway Enables <i>Escherichia coli</i> 's Rapid Response to Oxidative Stress. <i>Cell Systems</i> , 2018, 6, 569-578.e7.	6.2	162
42	Metabolic flux response to phosphoglucose isomerase knock-out in <i>Escherichia coli</i> and impact of overexpression of the soluble transhydrogenase UdhA. <i>FEMS Microbiology Letters</i> , 2001, 204, 247-252.	1.8	160
43	Tradeoff between enzyme and metabolite efficiency maintains metabolic homeostasis upon perturbations in enzyme capacity. <i>Molecular Systems Biology</i> , 2010, 6, 356.	7.2	159
44	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 762.	7.2	159
45	Regulation of yeast central metabolism by enzyme phosphorylation. <i>Molecular Systems Biology</i> , 2012, 8, 623.	7.2	154
46	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.	7.2	151
47	Metabolic constraints on the evolution of antibiotic resistance. <i>Molecular Systems Biology</i> , 2017, 13, 917.	7.2	151
48	Transcriptional regulation is insufficient to explain substrate-induced flux changes in <i>Bacillus subtilis</i> . <i>Molecular Systems Biology</i> , 2013, 9, 709.	7.2	149
49	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.	3.1	144
50	Regulation and control of metabolic fluxes in microbes. <i>Current Opinion in Biotechnology</i> , 2011, 22, 566-575.	6.6	142
51	Nontargeted Metabolomics Reveals the Multilevel Response to Antibiotic Perturbations. <i>Cell Reports</i> , 2017, 19, 1214-1228.	6.4	139
52	Frontiers of high-throughput metabolomics. <i>Current Opinion in Chemical Biology</i> , 2017, 36, 15-23.	6.1	139
53	A universal trade-off between growth and lag in fluctuating environments. <i>Nature</i> , 2020, 584, 470-474.	27.8	139
54	Temporal system-level organization of the switch from glycolytic to gluconeogenic operation in yeast. <i>Molecular Systems Biology</i> , 2013, 9, 651.	7.2	138

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55	Metabolic cooperation and spatiotemporal niche partitioning in a kefir microbial community. <i>Nature Microbiology</i> , 2021, 6, 196-208.	13.3	138
56	Different Biochemical Mechanisms Ensure Network-Wide Balancing of Reducing Equivalents in Microbial Metabolism. <i>Journal of Bacteriology</i> , 2009, 191, 2112-2121.	2.2	136
57	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.	3.1	135
58	Pseudo-transition Analysis Identifies the Key Regulators of Dynamic Metabolic Adaptations from Steady-State Data. <i>Cell Systems</i> , 2015, 1, 270-282.	6.2	133
59	TCA cycle activity in <i>Saccharomyces cerevisiae</i> is a function of the environmentally determined specific growth and glucose uptake rates. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1085-1093.	1.8	130
60	Few regulatory metabolites coordinate expression of central metabolic genes in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2017, 13, 903.	7.2	129
61	Stoichiometric growth model for riboflavin-producing <i>Bacillus subtilis</i> . <i>Biotechnology and Bioengineering</i> , 2001, 76, 132-143.	3.3	126
62	High coverage metabolomics analysis reveals phage-specific alterations to <i>Pseudomonas aeruginosa</i> physiology during infection. <i>ISME Journal</i> , 2016, 10, 1823-1835.	9.8	126
63	Nontargeted in vitro metabolomics for high-throughput identification of novel enzymes in <i>Escherichia coli</i> . <i>Nature Methods</i> , 2017, 14, 187-194.	19.0	125
64	Fermentation performance of engineered and evolved xylose-fermenting <i>Saccharomyces cerevisiae</i> strains. <i>Biotechnology and Bioengineering</i> , 2004, 87, 90-98.	3.3	123
65	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.	2.3	123
66	Antibodies Set Boundaries Limiting Microbial Metabolite Penetration and the Resultant Mammalian Host Response. <i>Immunity</i> , 2018, 49, 545-559.e5.	14.3	121
67	Novel biological insights through metabolomics and ¹³ C-flux analysis. <i>Current Opinion in Microbiology</i> , 2009, 12, 553-558.	5.1	120
68	Ubiquinone accumulation improves osmotic-stress tolerance in <i>Escherichia coli</i> . <i>Nature Chemical Biology</i> , 2014, 10, 266-272.	8.0	120
69	Life span extension by targeting a link between metabolism and histone acetylation in <i>Drosophila</i> . <i>EMBO Reports</i> , 2016, 17, 455-469.	4.5	116
70	Dissecting specific and global transcriptional regulation of bacterial gene expression. <i>Molecular Systems Biology</i> , 2013, 9, 658.	7.2	115
71	Biological insights through nontargeted metabolomics. <i>Current Opinion in Biotechnology</i> , 2015, 34, 1-8.	6.6	115
72	Integration of Metabolomics and Transcriptomics Reveals a Complex Diet of <i>Mycobacterium tuberculosis</i> during Early Macrophage Infection. <i>MSystems</i> , 2017, 2, .	3.8	112

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73	Systems biology of microbial metabolism. <i>Current Opinion in Microbiology</i> , 2010, 13, 337-343.	5.1	111
74	Genomewide landscape of gene–metabolome associations in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2017, 13, 907.	7.2	109
75	Identification of Transcriptional and Metabolic Programs Related to Mammalian Cell Size. <i>Current Biology</i> , 2014, 24, 598-608.	3.9	108
76	A prototrophic deletion mutant collection for yeast metabolomics and systems biology. <i>Nature Biotechnology</i> , 2012, 30, 1176-1178.	17.5	107
77	Spatiotemporal Analysis of a Glycolytic Activity Gradient Linked to Mouse Embryo Mesoderm Development. <i>Developmental Cell</i> , 2017, 40, 331-341.e4.	7.0	107
78	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.	7.2	105
79	High-throughput metabolomic analysis predicts mode of action of uncharacterized antimicrobial compounds. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	102
80	Regulatory mechanisms underlying coordination of amino acid and glucose catabolism in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2019, 10, 3354.	12.8	101
81	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. <i>Nature Communications</i> , 2010, 1, 145.	12.8	100
82	Metabolic Fluxes during Strong Carbon Catabolite Repression by Malate in <i>Bacillus subtilis</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 1587-1596.	3.4	100
83	Advancing metabolic models with kinetic information. <i>Current Opinion in Biotechnology</i> , 2014, 29, 8-14.	6.6	99
84	Transcriptional regulation of respiration in yeast metabolizing differently repressive carbon substrates. <i>BMC Systems Biology</i> , 2010, 4, 12.	3.0	96
85	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.	3.3	93
86	<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.	13.3	88
87	Metabolic capacity of <i>Bacillus subtilis</i> for the production of purine nucleosides, riboflavin, and folic acid. , 1998, 59, 227-238.		85
88	PknG senses amino acid availability to control metabolism and virulence of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2017, 13, e1006399.	4.7	81
89	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.	9.8	79
90	Regulatory Tasks of the Phosphoenolpyruvate-Phosphotransferase System of <i>Pseudomonas putida</i> in Central Carbon Metabolism. <i>MBio</i> , 2012, 3, .	4.1	78

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91	The importance of post-translational modifications in regulating <i>Saccharomyces cerevisiae</i> metabolism. <i>FEMS Yeast Research</i> , 2012, 12, 104-117.	2.3	78
92	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.	5.6	78
93	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.	3.6	71
94	Intracellular Carbon Fluxes in Riboflavin-Producing <i>Bacillus subtilis</i> during Growth on Two-Carbon Substrate Mixtures. <i>Applied and Environmental Microbiology</i> , 2002, 68, 1760-1771.	3.1	70
95	Genome-Scale Architecture of Small Molecule Regulatory Networks and the Fundamental Trade-Off between Regulation and Enzymatic Activity. <i>Cell Reports</i> , 2017, 20, 2666-2677.	6.4	70
96	Maintenance metabolism and carbon fluxes in <i>Bacillus</i> species. <i>Microbial Cell Factories</i> , 2008, 7, 19.	4.0	67
97	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.	2.2	67
98	Synthesis and degradation of FtsZ quantitatively predict the first cell division in starved bacteria. <i>Molecular Systems Biology</i> , 2018, 14, e8623.	7.2	66
99	Dynamic phosphoproteomics reveals TORC1-dependent regulation of yeast nucleotide and amino acid biosynthesis. <i>Science Signaling</i> , 2015, 8, rs4.	3.6	64
100	Reducing maintenance metabolism by metabolic engineering of respiration improves riboflavin production by <i>Bacillus subtilis</i> . <i>Metabolic Engineering</i> , 2003, 5, 49-55.	7.0	63
101	Application of mathematical tools for metabolic design of microbial ethanol production. , 1998, 58, 154-161.		62
102	Glycolysis without pyruvate kinase in <i>Clostridium thermocellum</i> . <i>Metabolic Engineering</i> , 2017, 39, 169-180.	7.0	62
103	Global Metabolic Responses to Salt Stress in Fifteen Species. <i>PLoS ONE</i> , 2016, 11, e0148888.	2.5	61
104	Use of a glycerol-limited, long-term chemostat for isolation of <i>Escherichia coli</i> mutants with improved physiological properties. <i>Microbiology (United Kingdom)</i> , 1997, 143, 1567-1574.	1.8	60
105	Quantification and Mass Isotopomer Profiling of \pm -Keto Acids in Central Carbon Metabolism. <i>Analytical Chemistry</i> , 2014, 86, 3232-3237.	6.5	60
106	Unraveling condition-dependent networks of transcription factors that control metabolic pathway activity in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 432.	7.2	59
107	Biological insights through omics data integration. <i>Current Opinion in Systems Biology</i> , 2019, 15, 39-47.	2.6	59
108	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.	11.0	58

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109	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.	11.0	58
110	The <i>Bacillus subtilis</i> yqj Gene Encodes the NADP ⁺ -Dependent 6-P-Gluconate Dehydrogenase in the Pentose Phosphate Pathway. <i>Journal of Bacteriology</i> , 2004, 186, 4528-4534.	2.2	56
111	Somewhat in control—the role of transcription in regulating microbial metabolic fluxes. <i>Current Opinion in Biotechnology</i> , 2013, 24, 987-993.	6.6	54
112	Screening of <i>Bacillus subtilis</i> transposon mutants with altered riboflavin production. <i>Metabolic Engineering</i> , 2008, 10, 216-226.	7.0	53
113	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.	3.4	53
114	Global probabilistic annotation of metabolic networks enables enzyme discovery. <i>Nature Chemical Biology</i> , 2012, 8, 848-854.	8.0	53
115	Bacterial Glycogen Provides Short-Term Benefits in Changing Environments. <i>Applied and Environmental Microbiology</i> , 2020, 86, .	3.1	53
116	Niche partitioning facilitates coexistence of closely related honey bee gut bacteria. <i>ELife</i> , 2021, 10, .	6.0	53
117	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.	2.2	52
118	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
119	Systematic Analysis of Transcriptional and Post-transcriptional Regulation of Metabolism in Yeast. <i>PLoS Computational Biology</i> , 2017, 13, e1005297.	3.2	51
120	Standard reporting requirements for biological samples in metabolomics experiments: microbial and in vitro biology experiments. <i>Metabolomics</i> , 2007, 3, 189-194.	3.0	50
121	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.	7.0	49
122	Inferring causal metabolic signals that regulate the dynamic TORC1-dependent transcriptome. <i>Molecular Systems Biology</i> , 2015, 11, 802.	7.2	49
123	Posttranslational regulation of microbial metabolism. <i>Current Opinion in Microbiology</i> , 2015, 27, 10-17.	5.1	45
124	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.	12.8	45
125	Systematic mapping of protein-metabolite interactions in central metabolism of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2019, 15, e9008.	7.2	45
126	Reserve Flux Capacity in the Pentose Phosphate Pathway by NADPH Binding Is Conserved across Kingdoms. <i>IScience</i> , 2019, 19, 1133-1144.	4.1	44

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127	CcpN Controls Central Carbon Fluxes in <i>Bacillus subtilis</i> . Journal of Bacteriology, 2008, 190, 6178-6187.	2.2	42
128	Transhydrogenase Promotes the Robustness and Evolvability of E. coli Deficient in NADPH Production. PLoS Genetics, 2015, 11, e1005007.	3.5	42
129	Towards detecting regulatory protein-metabolite interactions. Current Opinion in Microbiology, 2017, 39, 16-23.	5.1	42
130	Non-stationary ¹³ C-metabolic flux ratio analysis. Biotechnology and Bioengineering, 2013, 110, 3164-3176.	3.3	41
131	Dynamic exometabolome analysis reveals active metabolic pathways in non-replicating mycobacteria. Environmental Microbiology, 2015, 17, 4802-4815.	3.8	40
132	A distinct growth physiology enhances bacterial growth under rapid nutrient fluctuations. Nature Communications, 2021, 12, 3662.	12.8	40
133	Metabolic cross-feeding structures the assembly of polysaccharide degrading communities. Science Advances, 2022, 8, eabk3076.	10.3	40
134	Estimation of P-to-O ratio in <i>Bacillus subtilis</i> and its influence on maximum riboflavin yield. , 1999, 64, 750-754.		39
135	Knockout of the high-coupling cytochrome aa ₃ oxidase reduces TCA cycle fluxes in <i>Bacillus subtilis</i> . FEMS Microbiology Letters, 2003, 226, 121-126.	1.8	39
136	Metabolic engineering of yeast: the perils of auxotrophic hosts. Biotechnology Letters, 1999, 21, 611-616.	2.2	38
137	Acetate-Specific Stress Response in Acetate-Resistant Bacteria: An Analysis of Protein Patterns. Biotechnology Progress, 1997, 13, 519-523.	2.6	36
138	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. Molecular Systems Biology, 2021, 17, e10064.	7.2	33
139	Co-catabolism of arginine and succinate drives symbiotic nitrogen fixation. Molecular Systems Biology, 2020, 16, e9419.	7.2	33
140	Reversible amyloids of pyruvate kinase couple cell metabolism and stress granule disassembly. Nature Cell Biology, 2021, 23, 1085-1094.	10.3	33
141	Transient expression and flux changes during a shift from high to low riboflavin production in continuous cultures of <i>Bacillus subtilis</i> . Biotechnology and Bioengineering, 2005, 89, 219-232.	3.3	32
142	Large-scale functional analysis of the roles of phosphorylation in yeast metabolic pathways. Science Signaling, 2014, 7, rs6.	3.6	32
143	Altered regulation of pyruvate kinase or co-overexpression of phosphofructokinase increases glycolytic fluxes in resting <i>Escherichia coli</i> . Biotechnology and Bioengineering, 2000, 67, 623-627.	3.3	30
144	Dynamic flux responses in riboflavin overproducing <i>Bacillus subtilis</i> to increasing glucose limitation in fed-batch culture. Biotechnology and Bioengineering, 2010, 105, 795-804.	3.3	29

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145	Local requirement of the <i>Drosophila</i> insulin binding protein imp-L2 in coordinating developmental progression with nutritional conditions. <i>Developmental Biology</i> , 2013, 381, 97-106.	2.0	28
146	A rheostat mechanism governs the bifurcation of carbon flux in mycobacteria. <i>Nature Communications</i> , 2016, 7, 12527.	12.8	27
147	$\hat{1}^2$ -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.	7.1	27
148	Capacity for instantaneous catabolism of preferred and non-preferred carbon sources in <i>Escherichia coli</i> and <i>Bacillus subtilis</i> . <i>Scientific Reports</i> , 2018, 8, 11760.	3.3	26
149	Nontargeted Profiling of Coenzyme A thioesters in biological samples by tandem mass spectrometry. <i>Analytical Chemistry</i> , 2013, 85, 8284-8290.	6.5	24
150	The Neurometabolic Fingerprint of Excessive Alcohol Drinking. <i>Neuropsychopharmacology</i> , 2015, 40, 1259-1268.	5.4	24
151	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.	7.1	24
152	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.	7.1	23
153	A role for EIIA Ntr in controlling fluxes in the central metabolism of <i>E. coli</i> K12. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2013, 1833, 2879-2889.	4.1	21
154	Glycolysis/gluconeogenesis specialization in microbes is driven by biochemical constraints of flux sensing. <i>Molecular Systems Biology</i> , 2022, 18, e10704.	7.2	21
155	Increased Phenylalanine Production by Growing and Nongrowing <i>Escherichia coli</i> Strain CWML2. <i>Biotechnology Progress</i> , 1998, 14, 420-424.	2.6	20
156	Systematic Identification of Protein-Metabolite Interactions in Complex Metabolite Mixtures by Ligand-Detected Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2016, 55, 2590-2600.	2.5	20
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