

# Determination of confidence intervals of metabolic flux measurements

Metabolic Engineering

8, 324-337

DOI: [10.1016/j.ymben.2006.01.004](https://doi.org/10.1016/j.ymben.2006.01.004)

Citation Report

#	ARTICLE	IF	CITATIONS
3	Metabolic networks in motion: 13 C&E-based flux analysis. <i>Molecular Systems Biology</i> , 2006, 2, 62.	3.2	582
4	Gaining Insight into Microbial Physiology in the Large Intestine: A Special Role for Stable Isotopes. <i>Advances in Microbial Physiology</i> , 2007, 53, 73-314.	1.0	44
5	Accurate Assessment of Amino Acid Mass Isotopomer Distributions for Metabolic Flux Analysis. <i>Analytical Chemistry</i> , 2007, 79, 7554-7559.	3.2	247
6	Toward metabolome-based 13C flux analysis: a universal tool for measuring in vivo metabolic activity. <i>Topics in Current Genetics</i> , 2007, , 129-157.	0.7	4
7	Elementary metabolite units (EMU): A novel framework for modeling isotopic distributions. <i>Metabolic Engineering</i> , 2007, 9, 68-86.	3.6	514
8	Metabolic flux analysis in a nonstationary system: Fed-batch fermentation of a high yielding strain of <i>E. coli</i> producing 1,3-propanediol. <i>Metabolic Engineering</i> , 2007, 9, 277-292.	3.6	217
9	Metabolic flux elucidation for large-scale models using 13C labeled isotopes. <i>Metabolic Engineering</i> , 2007, 9, 387-405.	3.6	104
10	13C-Labeled metabolic flux analysis of a fed-batch culture of elutriated <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2007, 7, 511-526.	1.1	34
11	An elementary metabolite unit (EMU) based method of isotopically nonstationary flux analysis. <i>Biotechnology and Bioengineering</i> , 2008, 99, 686-699.	1.7	241
12	Identification of optimal measurement sets for complete flux elucidation in metabolic flux analysis experiments. <i>Biotechnology and Bioengineering</i> , 2008, 100, 1039-1049.	1.7	35
13	An analytic and systematic framework for estimating metabolic flux ratios from 13C tracer experiments. <i>BMC Bioinformatics</i> , 2008, 9, 266.	1.2	40
14	Oxygen dependence of metabolic fluxes and energy generation of <i>Saccharomyces cerevisiae</i> CEN.PK113-1A. <i>BMC Systems Biology</i> , 2008, 2, 60.	3.0	102
15	Ensemble Modeling of Metabolic Networks. <i>Biophysical Journal</i> , 2008, 95, 5606-5617.	0.2	233
16	Metabolic Flux Analysis in Plants: From Intelligent Design to Rational Engineering. <i>Annual Review of Plant Biology</i> , 2008, 59, 625-650.	8.6	92
17	Quantifying Reductive Carboxylation Flux of Glutamine to Lipid in a Brown Adipocyte Cell Line. <i>Journal of Biological Chemistry</i> , 2008, 283, 20621-20627.	1.6	265
18	Applications of possibilistic reasoning to intelligent system monitoring: a case study. , 2009, , .		0
19	Flux Balance Analysis Within Physiologically Feasible Region. , 2009, , .		0
20	Effect of Anaplerotic Fluxes and Amino Acid Availability on Hepatic Lipoapoptosis. <i>Journal of Biological Chemistry</i> , 2009, 284, 33425-33436.	1.6	60

#	ARTICLE	IF	CITATIONS
21	Analysis of Metabolic Flux Phenotypes for Two Arabidopsis Mutants with Severe Impairment in Seed Storage Lipid Synthesis. <i>Plant Physiology</i> , 2009, 151, 1617-1634.	2.3	139
22	Advances in analysis of microbial metabolic fluxes via <sup>13</sup> C isotopic labeling. <i>Mass Spectrometry Reviews</i> , 2009, 28, 362-375.	2.8	137
23	Analysis of metabolic pathways and fluxes in a newly discovered thermophilic and ethanol-tolerant <i>Geobacillus</i> strain. <i>Biotechnology and Bioengineering</i> , 2009, 102, 1377-1386.	1.7	61
24	Toward systematic metabolic engineering based on the analysis of metabolic regulation by the integration of different levels of information. <i>Biochemical Engineering Journal</i> , 2009, 46, 235-251.	1.8	44
25	Ensemble modeling for strain development of l-lysine-producing <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2009, 11, 221-233.	3.6	63
26	Quantification of statin effects on hepatic cholesterol synthesis by transient <sup>13</sup> C-flux analysis. <i>Metabolic Engineering</i> , 2009, 11, 292-309.	3.6	52
27	Evaluation of <sup>13</sup> C isotopic tracers for metabolic flux analysis in mammalian cells. <i>Journal of Biotechnology</i> , 2009, 144, 167-174.	1.9	257
28	Ensemble modeling and related mathematical modeling of metabolic networks. <i>Journal of the Taiwan Institute of Chemical Engineers</i> , 2009, 40, 595-601.	2.7	17
29	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 6477-6482.	3.3	154
30	Isotopic Steady-State Flux Analysis. , 2009, , 245-284.		4
31	OpenFLUX: efficient modelling software for <sup>13</sup> C-based metabolic flux analysis. <i>Microbial Cell Factories</i> , 2009, 8, 25.	1.9	218
32	Plant Metabolic Networks. , 2009, , .		7
33	Applications of metabolomics and proteomics to the mdx mouse model of Duchenne muscular dystrophy: lessons from downstream of the transcriptome. <i>Genome Medicine</i> , 2009, 1, 32.	3.6	38
34	Hyperpolarized [ <sup>13</sup> C]-Fructose: A Hemiketal DNP Substrate for In Vivo Metabolic Imaging. <i>Journal of the American Chemical Society</i> , 2009, 131, 17591-17596.	6.6	106
35	Metabolic Flux Analysis of CHO-320 Cells: Undetermined Network and Effect of Measurement Errors. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2010, 43, 437-442.	0.4	0
36	Current status of <sup>13</sup> C-metabolic flux analysis and future perspectives. <i>Process Biochemistry</i> , 2010, 45, 1873-1881.	1.8	23
37	A detailed metabolic flux analysis of an underdetermined network of CHO cells. <i>Journal of Biotechnology</i> , 2010, 150, 497-508.	1.9	60
38	Improved computational performance of MFA using elementary metabolite units and flux coupling. <i>Metabolic Engineering</i> , 2010, 12, 123-128.	3.6	27

#	ARTICLE	IF	CITATIONS
39	Metabolic flux analysis and pharmaceutical production. <i>Metabolic Engineering</i> , 2010, 12, 81-95.	3.6	101
40	A kinetic model describes metabolic response to perturbations and distribution of flux control in the benzenoid network of <i>Petunia hybrida</i> . <i>Plant Journal</i> , 2010, 62, 64-76.	2.8	59
41	Metabolic response of <i>Geobacter sulfurreducens</i> towards electron donor/acceptor variation. <i>Microbial Cell Factories</i> , 2010, 9, 90.	1.9	69
42	Metabolic Flux Analysis in the Cloud. , 2010, , .		12
43	Metabolism strikes back: metabolic flux regulates cell signaling: Figure 1.. <i>Genes and Development</i> , 2010, 24, 2717-2722.	2.7	118
44	Measuring Deuterium Enrichment of Glucose Hydrogen Atoms by Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 3211-3216.	3.2	111
45	Analysis of mammalian fatty acyl-coenzyme A species by mass spectrometry and tandem mass spectrometry. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2011, 1811, 663-668.	1.2	18
46	Erk regulation of pyruvate dehydrogenase flux through PDK4 modulates cell proliferation. <i>Genes and Development</i> , 2011, 25, 1716-1733.	2.7	162
47	Oncogenic Kâ€Ras decouples glucose and glutamine metabolism to support cancer cell growth. <i>Molecular Systems Biology</i> , 2011, 7, 523.	3.2	404
48	Elucidation of Cellular Metabolism Via Metabolomics and Stable-Isotope Assisted Metabolomics. <i>Current Pharmaceutical Biotechnology</i> , 2011, 12, 1075-1086.	0.9	43
49	Enhanced glycoprotein production in HEK-293 cells expressing pyruvate carboxylase. <i>Metabolic Engineering</i> , 2011, 13, 499-507.	3.6	48
50	Metabolic flux analysis of CHO cells at growth and non-growth phases using isotopic tracers and mass spectrometry. <i>Metabolic Engineering</i> , 2011, 13, 598-609.	3.6	222
51	Mapping photoautotrophic metabolism with isotopically nonstationary <sup>13</sup> C flux analysis. <i>Metabolic Engineering</i> , 2011, 13, 656-665.	3.6	307
52	Dynamic metabolic flux analysis (DMFA): A framework for determining fluxes at metabolic non-steady state. <i>Metabolic Engineering</i> , 2011, 13, 745-755.	3.6	102
53	Resolving the TCA cycle and pentoseâ€phosphate pathway of <i>Clostridium acetobutylicum</i> ATCC 824: Isotopomer analysis, <i>in vitro</i> activities and expression analysis. <i>Biotechnology Journal</i> , 2011, 6, 300-305.	1.8	82
54	Eukaryotic metabolism: Measuring compartment fluxes. <i>Biotechnology Journal</i> , 2011, 6, 1071-1085.	1.8	49
55	Unraveling the metabolism of HEK-293 cells using lactate isotopomer analysis. <i>Bioprocess and Biosystems Engineering</i> , 2011, 34, 263-273.	1.7	35
56	The benefits of being transient: isotope-based metabolic flux analysis at the short time scale. <i>Applied Microbiology and Biotechnology</i> , 2011, 91, 1247-1265.	1.7	69

#	ARTICLE	IF	CITATIONS
57	Fluxomers: a new approach for <sup>13</sup> C metabolic flux analysis. <i>BMC Systems Biology</i> , 2011, 5, 129.	3.0	45
58	Redox homeostasis phenotypes in RubisCO-deficient <i>Rhodobacter sphaeroides</i> via ensemble modeling. <i>Biotechnology Progress</i> , 2011, 27, 15-22.	1.3	13
59	Metabolic flux analysis of CHO cell metabolism in the late non-growth phase. <i>Biotechnology and Bioengineering</i> , 2011, 108, 82-92.	1.7	113
60	Construction of an <i>E. Coli</i> genome-scale atom mapping model for MFA calculations. <i>Biotechnology and Bioengineering</i> , 2011, 108, 1372-1382.	1.7	42
61	Tandem mass spectrometry: A novel approach for metabolic flux analysis. <i>Metabolic Engineering</i> , 2011, 13, 225-233.	3.6	90
62	Capturing Metabolite Channeling in Metabolic Flux Phenotypes. <i>Plant Physiology</i> , 2011, 157, 981-984.	2.3	40
63	Synthetic Biology and Metabolic Engineering. <i>ACS Synthetic Biology</i> , 2012, 1, 514-525.	1.9	212
64	Reductive glutamine metabolism by IDH1 mediates lipogenesis under hypoxia. <i>Nature</i> , 2012, 481, 380-384.	13.7	1,470
65	Expanding the concepts and tools of metabolic engineering to elucidate cancer metabolism. <i>Biotechnology Progress</i> , 2012, 28, 1409-1418.	1.3	18
66	Parallel labeling experiments with [U- <sup>13</sup> C]glucose validate <i>E. coli</i> metabolic network model for <sup>13</sup> C metabolic flux analysis. <i>Metabolic Engineering</i> , 2012, 14, 533-541.	3.6	86
67	Strategies for investigating the plant metabolic network with steady-state metabolic flux analysis: lessons from an <i>Arabidopsis</i> cell culture and other systems. <i>Journal of Experimental Botany</i> , 2012, 63, 2309-2323.	2.4	62
68	Metabolic cartography: experimental quantification of metabolic fluxes from isotopic labelling studies. <i>Journal of Experimental Botany</i> , 2012, 63, 2293-2308.	2.4	66
69	Measuring Complete Isotopomer Distribution of Aspartate Using Gas Chromatography/Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4628-4632.	3.2	78
70	Rational design of <sup>13</sup> C-labeling experiments for metabolic flux analysis in mammalian cells. <i>BMC Systems Biology</i> , 2012, 6, 43.	3.0	93
71	Systems Metabolic Engineering. , 2012, , .		11
72	Systems-Level Analysis of Cancer Metabolism. , 2012, , 349-381.		1
73	Stable isotope-resolved metabolomics and applications for drug development. , 2012, 133, 366-391.		186
74	Optimization of <sup>13</sup> C isotopic tracers for metabolic flux analysis in mammalian cells. <i>Metabolic Engineering</i> , 2012, 14, 162-171.	3.6	72

#	ARTICLE	IF	CITATIONS
75	Selection of tracers for <sup>13</sup> C-Metabolic Flux Analysis using Elementary Metabolite Units (EMU) basis vector methodology. <i>Metabolic Engineering</i> , 2012, 14, 150-161.	3.6	78
76	Towards dynamic metabolic flux analysis in CHO cell cultures. <i>Biotechnology Journal</i> , 2012, 7, 61-74.	1.8	107
77	Computational approaches for understanding energy metabolism. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2013, 5, 733-750.	6.6	12
78	Model-based design of synthetic, biological systems. <i>Chemical Engineering Science</i> , 2013, 103, 2-11.	1.9	18
79	Mechanistic analysis of multi-omics datasets to generate kinetic parameters for constraint-based metabolic models. <i>BMC Bioinformatics</i> , 2013, 14, 32.	1.2	37
80	The metabolic flux phenotype of heterotrophic <i>S. cerevisiae</i> cells reveals a complex response to changes in nitrogen supply. <i>Plant Journal</i> , 2013, 74, 569-582.	2.8	88
81	Isotopically nonstationary <sup>13</sup> C flux analysis of Myc-induced metabolic reprogramming in B-cells. <i>Metabolic Engineering</i> , 2013, 15, 206-217.	3.6	81
82	<sup>13</sup> C metabolic flux analysis: optimal design of isotopic labeling experiments. <i>Current Opinion in Biotechnology</i> , 2013, 24, 1116-1121.	3.3	100
83	The impact of the timing of induction on the metabolism and productivity of CHO cells in culture. <i>Biochemical Engineering Journal</i> , 2013, 79, 162-171.	1.8	10
84	Metformin Decreases Glucose Oxidation and Increases the Dependency of Prostate Cancer Cells on Reductive Glutamine Metabolism. <i>Cancer Research</i> , 2013, 73, 4429-4438.	0.4	178
85	Publishing <sup>13</sup> C metabolic flux analysis studies: A review and future perspectives. <i>Metabolic Engineering</i> , 2013, 20, 42-48.	3.6	91
86	Computational estimation of tricarboxylic acid cycle fluxes using noisy NMR data from cardiac biopsies. <i>BMC Systems Biology</i> , 2013, 7, 82.	3.0	5
87	Designer labels for plant metabolism: statistical design of isotope labeling experiments for improved quantification of flux in complex plant metabolic networks. <i>Molecular BioSystems</i> , 2013, 9, 99-112.	2.9	27
88	Cloud MapReduce for Monte Carlo bootstrap applied to Metabolic Flux Analysis. <i>Future Generation Computer Systems</i> , 2013, 29, 582-590.	4.9	12
89	COMPLETE-MFA: Complementary parallel labeling experiments technique for metabolic flux analysis. <i>Metabolic Engineering</i> , 2013, 20, 49-55.	3.6	121
90	Tandem mass spectrometry for measuring stable-isotope labeling. <i>Current Opinion in Biotechnology</i> , 2013, 24, 48-53.	3.3	56
91	Parallel labeling experiments with [ <sup>1,2-<sup>13</sup>C</sup> ]glucose and [ <sup>U-<sup>13</sup>C</sup> ]glutamine provide new insights into CHO cell metabolism. <i>Metabolic Engineering</i> , 2013, 15, 34-47.	3.6	132
92	Profiling metabolic networks to study cancer metabolism. <i>Current Opinion in Biotechnology</i> , 2013, 24, 60-68.	3.3	99

#	ARTICLE	IF	CITATIONS
93	13C-Based Metabolic Flux Analysis: Fundamentals and Practice. <i>Methods in Molecular Biology</i> , 2013, 985, 297-334.	0.4	13
94	Using Multiple Tracers for 13C Metabolic Flux Analysis. <i>Methods in Molecular Biology</i> , 2013, 985, 353-365.	0.4	15
95	Isotopically Nonstationary 13C Metabolic Flux Analysis. <i>Methods in Molecular Biology</i> , 2013, 985, 367-390.	0.4	36
96	Understanding Metabolic Regulation and Its Influence on Cell Physiology. <i>Molecular Cell</i> , 2013, 49, 388-398.	4.5	253
97	Probing the metabolism of an inducible mammalian expression system using extracellular isotopomer analysis. <i>Journal of Biotechnology</i> , 2013, 164, 469-478.	1.9	31
98	Peak antibody production is associated with increased oxidative metabolism in an industrially relevant fed-batch CHO cell culture. <i>Biotechnology and Bioengineering</i> , 2013, 110, 2013-2024.	1.7	175
99	Parallel labeling experiments and metabolic flux analysis: Past, present and future methodologies. <i>Metabolic Engineering</i> , 2013, 16, 21-32.	3.6	73
100	Isotopically non-stationary metabolic flux analysis: complex yet highly informative. <i>Current Opinion in Biotechnology</i> , 2013, 24, 979-986.	3.3	91
101	Dynamic metabolic flux analysis of plant cell wall synthesis. <i>Metabolic Engineering</i> , 2013, 18, 78-85.	3.6	39
102	ERROR ANALYSIS AND PROPAGATION IN METABOLOMICS DATA ANALYSIS. <i>Computational and Structural Biotechnology Journal</i> , 2013, 4, e201301006.	1.9	43
103	Carbon and Nitrogen Provisions Alter the Metabolic Flux in Developing Soybean Embryos. <i>Plant Physiology</i> , 2013, 161, 1458-1475.	2.3	87
104	An integrated computational approach for metabolic flux analysis coupled with inference of tandem-MS collisional fragments. <i>Bioinformatics</i> , 2013, 29, 3045-3052.	1.8	5
105	Glutamine-driven oxidative phosphorylation is a major ATP source in transformed mammalian cells in both normoxia and hypoxia. <i>Molecular Systems Biology</i> , 2013, 9, 712.	3.2	338
106	Kinetic isotope effects significantly influence intracellular metabolite <sup>13</sup> C labeling patterns and flux determination. <i>Biotechnology Journal</i> , 2013, 8, 1080-1089.	1.8	26
107	Metabolic Fluxes in an Illuminated <i>Arabidopsis</i> Rosette. <i>Plant Cell</i> , 2013, 25, 694-714.	3.1	303
108	Carbon-Flux Distribution within <i>Streptomyces coelicolor</i> Metabolism: A Comparison between the Actinorhodin-Producing Strain M145 and Its Non-Producing Derivative M1146. <i>PLoS ONE</i> , 2013, 8, e84151.	1.1	33
109	Reliable Metabolic Flux Estimation in <i>Escherichia coli</i> Central Carbon Metabolism Using Intracellular Free Amino Acids. <i>Metabolites</i> , 2014, 4, 408-420.	1.3	19
110	Metabolic flux analysis using <sup>13</sup> C peptide label measurements. <i>Plant Journal</i> , 2014, 77, 476-486.	2.8	25

#	ARTICLE	IF	CITATIONS
112	Isotopic Studies of Metabolic Systems by Mass Spectrometry: Using Pascal's Triangle To Produce Biological Standards with Fully Controlled Labeling Patterns. <i>Analytical Chemistry</i> , 2014, 86, 10288-10295.	3.2	27
113	Isotopically nonstationary <sup>13</sup> C flux analysis of changes in <i>Arabidopsis thaliana</i> leaf metabolism due to high light acclimation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16967-16972.	3.3	189
114	OpenFLUX2: <sup>13</sup> C-MFA modeling software package adjusted for the comprehensive analysis of single and parallel labeling experiments. <i>Microbial Cell Factories</i> , 2014, 13, 152.	1.9	29
115	OpenMebius: An Open Source Software for Isotopically Nonstationary <sup>13</sup> C-Based Metabolic Flux Analysis. <i>BioMed Research International</i> , 2014, 2014, 1-10.	0.9	87
116	IsoDesign: A software for optimizing the design of <sup>13</sup> C metabolic flux analysis experiments. <i>Biotechnology and Bioengineering</i> , 2014, 111, 202-208.	1.7	35
117	<sup>13</sup> C-metabolic flux analysis in heterologous cellulase production by <i>Bacillus subtilis</i> genome-reduced strain. <i>Journal of Biotechnology</i> , 2014, 179, 42-49.	1.9	35
118	INCA: a computational platform for isotopically non-stationary metabolic flux analysis. <i>Bioinformatics</i> , 2014, 30, 1333-1335.	1.8	351
119	Mathematical Modeling of Isotope Labeling Experiments for Metabolic Flux Analysis. <i>Methods in Molecular Biology</i> , 2014, 1083, 109-131.	0.4	5
120	A Systems Biology Approach to Study Metabolic Syndrome. , 2014, , .		5
121	Regulation of Substrate Utilization by the Mitochondrial Pyruvate Carrier. <i>Molecular Cell</i> , 2014, 56, 425-435.	4.5	243
122	<sup>13</sup> C metabolic flux analysis of recombinant expression hosts. <i>Current Opinion in Biotechnology</i> , 2014, 30, 238-245.	3.3	28
123	Parallel labeling experiments validate <i>Clostridium acetobutylicum</i> metabolic network model for <sup>13</sup> C metabolic flux analysis. <i>Metabolic Engineering</i> , 2014, 26, 23-33.	3.6	57
124	The impact of anti-apoptotic gene Bcl-2 expression on CHO central metabolism. <i>Metabolic Engineering</i> , 2014, 25, 92-102.	3.6	48
125	Central metabolic responses to the overproduction of fatty acids in <i>Escherichia coli</i> based on <sup>13</sup> C metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2014, 111, 575-585.	1.7	112
126	IDH1 Mutations Alter Citric Acid Cycle Metabolism and Increase Dependence on Oxidative Mitochondrial Metabolism. <i>Cancer Research</i> , 2014, 74, 3317-3331.	0.4	224
127	<sup>13</sup> C Isotope-Assisted Methods for Quantifying Glutamine Metabolism in Cancer Cells. <i>Methods in Enzymology</i> , 2014, 542, 369-389.	0.4	41
128	Non-stationary <sup>13</sup> C metabolic flux analysis of Chinese hamster ovary cells in batch culture using extracellular labeling highlights metabolic reversibility and compartmentation. <i>BMC Systems Biology</i> , 2014, 8, 50.	3.0	57
129	Integrated Metabolic Flux and Omics Analysis of <i>Synechocystis</i> sp. PCC 6803 under Mixotrophic and Photoheterotrophic Conditions. <i>Plant and Cell Physiology</i> , 2014, 55, 1605-1612.	1.5	86



#	ARTICLE	IF	CITATIONS
130	Metabolic flux pattern of glucose utilization by <i>Xanthomonas campestris</i> pv. <i>campestris</i> : prevalent role of the Entner-Doudoroff pathway and minor fluxes through the pentose phosphate pathway and glycolysis. <i>Molecular BioSystems</i> , 2014, 10, 2663-2676.	2.9	28
131	The metabolic flux phenotype of heterotrophic <i>Arabidopsis</i> cells reveals a flexible balance between the cytosolic and plastidic contributions to carbohydrate oxidation in response to phosphate limitation. <i>Plant Journal</i> , 2014, 78, 964-977.	2.8	58
132	Palmitate-induced Activation of Mitochondrial Metabolism Promotes Oxidative Stress and Apoptosis in H4IIEC3 Rat Hepatocytes. <i>Metabolism: Clinical and Experimental</i> , 2014, 63, 283-295.	1.5	123
133	Metabolic flux analysis of <i>Escherichia coli</i> knockouts: lessons from the Keio collection and future outlook. <i>Current Opinion in Biotechnology</i> , 2014, 28, 127-133.	3.3	49
134	Elucidating the effects of postinduction glutamine feeding on the growth and productivity of CHO cells. <i>Biotechnology Progress</i> , 2014, 30, 535-546.	1.3	35
135	Tracing Compartmentalized NADPH Metabolism in the Cytosol and Mitochondria of Mammalian Cells. <i>Molecular Cell</i> , 2014, 55, 253-263.	4.5	477
136	Metabolic network reconstruction, growth characterization and <sup>13</sup> C-metabolic flux analysis of the extremophile <i>Thermus thermophilus</i> HB8. <i>Metabolic Engineering</i> , 2014, 24, 173-180.	3.6	41
137	ER calcium release promotes mitochondrial dysfunction and hepatic cell lipotoxicity in response to palmitate overload. <i>Molecular Metabolism</i> , 2014, 3, 544-553.	3.0	133
138	Reducing Recon 2 for steady-state flux analysis of HEK cell culture. <i>Journal of Biotechnology</i> , 2014, 184, 172-178.	1.9	54
139	Mass spectrometry-based microassay of <sup>2</sup> H and <sup>13</sup> C plasma glucose labeling to quantify liver metabolic fluxes in vivo. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 309, E191-E203.	1.8	75
140	Integrated isotope-assisted metabolomics and <sup>13</sup> C metabolic flux analysis reveals metabolic flux redistribution for high glucoamylase production by <i>Aspergillus niger</i> . <i>Microbial Cell Factories</i> , 2015, 14, 147.	1.9	34
141	Metabolic plasticity maintains proliferation in pyruvate dehydrogenase deficient cells. <i>Cancer &amp; Metabolism</i> , 2015, 3, 7.	2.4	56
142	Enzymatic passaging of human embryonic stem cells alters central carbon metabolism and glycan abundance. <i>Biotechnology Journal</i> , 2015, 10, 1600-1611.	1.8	20
143	Effect of Error Propagation in Stable Isotope Tracer Studies. <i>Methods in Enzymology</i> , 2015, 561, 331-358.	0.4	9
144	Achieving Metabolic Flux Analysis for <i>S. cerevisiae</i> at a Genome-Scale: Challenges, Requirements, and Considerations. <i>Metabolites</i> , 2015, 5, 521-535.	1.3	15
145	Metformin Antagonizes Cancer Cell Proliferation by Suppressing Mitochondrial-Dependent Biosynthesis. <i>PLoS Biology</i> , 2015, 13, e1002309.	2.6	176
146	Catabolism of Branched Chain Amino Acids Contributes Significantly to Synthesis of Odd-Chain and Even-Chain Fatty Acids in 3T3-L1 Adipocytes. <i>PLoS ONE</i> , 2015, 10, e0145850.	1.1	153
147	<sup>13</sup> C flux analysis of cyanobacterial metabolism. <i>Photosynthesis Research</i> , 2015, 126, 19-32.	1.6	38

#	ARTICLE	IF	CITATIONS
148	Quantifying Protein Synthesis and Degradation in Arabidopsis by Dynamic <sup>13</sup> C-CO <sub>2</sub> Labeling and Analysis of Enrichment in Individual Amino Acids in Their Free Pools and in Protein. <i>Plant Physiology</i> , 2015, 168, 74-93.	2.3	132
149	Redistribution of metabolic fluxes in <i>Chlorella protothecoides</i> by variation of media nitrogen concentration. <i>Metabolic Engineering Communications</i> , 2015, 2, 124-131.	1.9	18
150	<sup>13</sup> C-based metabolic flux analysis of <i>Saccharomyces cerevisiae</i> with a reduced Crabtree effect. <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 140-144.	1.1	18
151	Methods and advances in metabolic flux analysis: a mini-review. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015, 42, 317-325.	1.4	192
152	Hierarchy in Pentose Sugar Metabolism in <i>Clostridium acetobutylicum</i> . <i>Applied and Environmental Microbiology</i> , 2015, 81, 1452-1462.	1.4	38
153	Integrated <sup>13</sup> C-metabolic flux analysis of 14 parallel labeling experiments in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2015, 28, 151-158.	3.6	94
154	<sup>13</sup> C-metabolic flux analysis of co-cultures: A novel approach. <i>Metabolic Engineering</i> , 2015, 31, 132-139.	3.6	79
155	<sup>13</sup> C-metabolic flux analysis in S-adenosyl-L-methionine production by <i>Saccharomyces cerevisiae</i> . <i>Journal of Bioscience and Bioengineering</i> , 2015, 120, 532-538.	1.1	30
156	Tracking the metabolic pulse of plant lipid production with isotopic labeling and flux analyses: Past, present and future. <i>Progress in Lipid Research</i> , 2015, 58, 97-120.	5.3	88
157	The oxidative pentose phosphate pathway is the primary source of NADPH for lipid overproduction from glucose in <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2015, 30, 27-39.	3.6	249
158	Metabolic network capacity of <i>Escherichia coli</i> for Krebs cycle-dependent proline hydroxylation. <i>Microbial Cell Factories</i> , 2015, 14, 108.	1.9	25
159	<sup>13</sup> C metabolic flux analysis at a genome-scale. <i>Metabolic Engineering</i> , 2015, 32, 12-22.	3.6	82
160	Metabolomic and <sup>13</sup> C-metabolic flux analysis of a xylose-consuming <i>Saccharomyces cerevisiae</i> strain expressing xylose isomerase. <i>Biotechnology and Bioengineering</i> , 2015, 112, 470-483.	1.7	73
161	GC-MS/MS survey of collision-induced dissociation of tert-butyl dimethylsilyl-derivatized amino acids and its application to <sup>13</sup> C-metabolic flux analysis of <i>Escherichia coli</i> central metabolism. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 6133-6140.	1.9	15
162	<sup>13</sup> C Metabolic Flux Analysis of acetate conversion to lipids by <i>Yarrowia lipolytica</i> . <i>Metabolic Engineering</i> , 2016, 38, 86-97.	3.6	68
163	Metabolic flux profiling of MDCK cells during growth and canine adenovirus vector production. <i>Scientific Reports</i> , 2016, 6, 23529.	1.6	15
164	Comprehensive metabolic modeling of multiple <sup>13</sup> C-isotopomer data sets to study metabolism in perfused working hearts. <i>American Journal of Physiology - Heart and Circulatory Physiology</i> , 2016, 311, H881-H891.	1.5	20
165	Metabolite concentrations, fluxes and free energies imply efficient enzyme usage. <i>Nature Chemical Biology</i> , 2016, 12, 482-489.	3.9	332

#	ARTICLE	IF	CITATIONS
166	Co-utilization of glucose and xylose by evolved <i>Thermus thermophilus</i> LC113 strain elucidated by <sup>13</sup> C metabolic flux analysis and whole genome sequencing. <i>Metabolic Engineering</i> , 2016, 37, 63-71.	3.6	27
167	Investigation of useful carbon tracers for <sup>13</sup> C-metabolic flux analysis of <i>Escherichia coli</i> by considering five experimentally determined flux distributions. <i>Metabolic Engineering Communications</i> , 2016, 3, 187-195.	1.9	15
168	Distinct Metabolic States Can Support Self-Renewal and Lipogenesis in Human Pluripotent Stem Cells under Different Culture Conditions. <i>Cell Reports</i> , 2016, 16, 1536-1547.	2.9	112
170	Metabolic flux analyses of <i>Pseudomonas aeruginosa</i> cystic fibrosis isolates. <i>Metabolic Engineering</i> , 2016, 38, 251-263.	3.6	9
171	Tracing insights into human metabolism using chemical engineering approaches. <i>Current Opinion in Chemical Engineering</i> , 2016, 14, 72-81.	3.8	11
172	LKB1 loss links serine metabolism to DNA methylation and tumorigenesis. <i>Nature</i> , 2016, 539, 390-395.	13.7	248
173	Identifying model error in metabolic flux analysis – a generalized least squares approach. <i>BMC Systems Biology</i> , 2016, 10, 91.	3.0	3
174	Fast exchange fluxes around the pyruvate node: a leaky cell model to explain the gain and loss of unlabelled and labelled metabolites in a tracer experiment. <i>Cancer &amp; Metabolism</i> , 2016, 4, 13.	2.4	14
175	Bridging the gap between non-targeted stable isotope labeling and metabolic flux analysis. <i>Cancer &amp; Metabolism</i> , 2016, 4, 10.	2.4	28
176	Evidence for transketolase-like TKTL1 flux in CHO cells based on parallel labeling experiments and <sup>13</sup> C-metabolic flux analysis. <i>Metabolic Engineering</i> , 2016, 37, 72-78.	3.6	37
177	Optimal tracers for parallel labeling experiments and <sup>13</sup> C metabolic flux analysis: A new precision and synergy scoring system. <i>Metabolic Engineering</i> , 2016, 38, 10-18.	3.6	68
178	Impacts of proline on the central metabolism of an industrial erythromycin-producing strain <i>Saccharopolyspora erythraea</i> via <sup>13</sup> C labeling experiments. <i>Journal of Biotechnology</i> , 2016, 231, 1-8.	1.9	15
179	<sup>13</sup> C metabolic flux analysis of microbial and mammalian systems is enhanced with GC-MS measurements of glycogen and RNA labeling. <i>Metabolic Engineering</i> , 2016, 38, 65-72.	3.6	49
180	Mannose metabolism in recombinant CHO cells and its effect on IgG glycosylation. <i>Biotechnology and Bioengineering</i> , 2016, 113, 1468-1480.	1.7	33
181	Malic enzyme tracers reveal hypoxia-induced switch in adipocyte NADPH pathway usage. <i>Nature Chemical Biology</i> , 2016, 12, 345-352.	3.9	103
182	Modeling Method for Increased Precision and Scope of Directly Measurable Fluxes at a Genome-Scale. <i>Analytical Chemistry</i> , 2016, 88, 3844-3852.	3.2	34
183	Assessing compartmentalized flux in lipid metabolism with isotopes. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2016, 1861, 1226-1242.	1.2	30
184	Identification of a small molecule inhibitor of 3-phosphoglycerate dehydrogenase to target serine biosynthesis in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 1778-1783.	3.3	239

#	ARTICLE	IF	CITATIONS
185	Green pathways: Metabolic network analysis of plant systems. <i>Metabolic Engineering</i> , 2016, 34, 1-24.	3.6	24
186	MID Max: LC-MS/MS Method for Measuring the Precursor and Product Mass Isotopomer Distributions of Metabolic Intermediates and Cofactors for Metabolic Flux Analysis Applications. <i>Analytical Chemistry</i> , 2016, 88, 1362-1370.	3.2	48
187	<sup>13</sup> C metabolic flux analysis of the extremely thermophilic, fast growing, xylose-utilizing <i>Geobacillus</i> strain LC300. <i>Metabolic Engineering</i> , 2016, 33, 148-157.	3.6	40
188	Quantification of Metabolic Rearrangements During Neural Stem Cells Differentiation into Astrocytes by Metabolic Flux Analysis. <i>Neurochemical Research</i> , 2017, 42, 244-253.	1.6	28
189	Overexpression of a diacylglycerol acyltransferase gene in <i>Phaeodactylum tricornutum</i> directs carbon towards lipid biosynthesis. <i>Journal of Phycology</i> , 2017, 53, 405-414.	1.0	46
190	The importance of accurately correcting for the natural abundance of stable isotopes. <i>Analytical Biochemistry</i> , 2017, 520, 27-43.	1.1	42
191	Estimation of flux ratios without uptake or release data: Application to serine and methionine metabolism. <i>Metabolic Engineering</i> , 2017, 43, 137-146.	3.6	6
192	Metabolomics: A Primer. <i>Trends in Biochemical Sciences</i> , 2017, 42, 274-284.	3.7	273
193	Metabolic impact of nutrient starvation in mevalonate-producing <i>Escherichia coli</i> . <i>Bioresource Technology</i> , 2017, 245, 1634-1640.	4.8	21
194	Metabolite Spectral Accuracy on Orbitraps. <i>Analytical Chemistry</i> , 2017, 89, 5940-5948.	3.2	201
195	Isotopically nonstationary <sup>13</sup> C flux analysis of cyanobacterial isobutyraldehyde production. <i>Metabolic Engineering</i> , 2017, 42, 9-18.	3.6	73
196	The metabolic function of cyclin D3-CDK6 kinase in cancer cell survival. <i>Nature</i> , 2017, 546, 426-430.	13.7	276
197	Rerouting of carbon flux in a glycogen mutant of cyanobacteria assessed via isotopically nonstationary <sup>13</sup> C metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2298-2308.	1.7	66
199	LKB1 promotes metabolic flexibility in response to energy stress. <i>Metabolic Engineering</i> , 2017, 43, 208-217.	3.6	42
200	Fast growth phenotype of <i>E. coli</i> K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. <i>Metabolic Engineering</i> , 2017, 44, 100-107.	3.6	59
201	Metabolism of the fast-growing bacterium <i>Vibrio natriegens</i> elucidated by <sup>13</sup> C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017, 44, 191-197.	3.6	63
202	<sup>13</sup> C metabolic flux analysis of three divergent extremely thermophilic bacteria: <i>Geobacillus</i> sp. LC300, <i>Thermus thermophilus</i> HB8, and <i>Rhodothermus marinus</i> DSM 4252. <i>Metabolic Engineering</i> , 2017, 44, 182-190.	3.6	37
203	Loss of hepatic AMP-activated protein kinase impedes the rate of glycogenolysis but not gluconeogenic fluxes in exercising mice. <i>Journal of Biological Chemistry</i> , 2017, 292, 20125-20140.	1.6	46

#	ARTICLE	IF	CITATIONS
204	Isotopically Nonstationary Metabolic Flux Analysis (INST-MFA) of Photosynthesis and Photorespiration in Plants. <i>Methods in Molecular Biology</i> , 2017, 1653, 167-194.	0.4	21
205	Learning from quantitative data to understand central carbon metabolism. <i>Biotechnology Advances</i> , 2017, 35, 971-980.	6.0	23
206	Distinct carbon sources affect structural and functional maturation of cardiomyocytes derived from human pluripotent stem cells. <i>Scientific Reports</i> , 2017, 7, 8590.	1.6	173
207	To be certain about the uncertainty: Bayesian statistics for <sup>13</sup> C metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2668-2684.	1.7	27
208	A comprehensive evaluation of constraining amino acid biosynthesis in compartmented models for metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2017, 5, 34-44.	1.9	12
209	Metabolic engineering of isopropyl alcohol-producing <i>Escherichia coli</i> strains with <sup>13</sup> C metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2017, 114, 2782-2793.	1.7	26
210	Metabolic flux analysis of <i>Synechocystis</i> sp. PCC 6803 $\Delta$ nrtABCD mutant reveals a mechanism for metabolic adaptation to nitrogen-limited conditions. <i>Plant and Cell Physiology</i> , 2017, 58, pcw233.	1.5	31
211	Temporal fluxomics reveals oscillations in TCA cycle flux throughout the mammalian cell cycle. <i>Molecular Systems Biology</i> , 2017, 13, 953.	3.2	72
212	Comprehensive analysis of glucose and xylose metabolism in <i>Escherichia coli</i> under aerobic and anaerobic conditions by <sup>13</sup> C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017, 39, 9-18.	3.6	99
213	Recent advances in high-throughput <sup>13</sup> C-fluxomics. <i>Current Opinion in Biotechnology</i> , 2017, 43, 104-109.	3.3	59
214	Metabolite pools and carbon flow during C <sub>4</sub> photosynthesis in maize: <sup>13</sup> CO <sub>2</sub> labeling kinetics and cell type fractionation. <i>Journal of Experimental Botany</i> , 2017, 68, 283-298.	2.4	104
215	Integration of parallel <sup>13</sup> C labeling experiments and in silico pathway analysis for enhanced production of ascomycin. <i>Biotechnology and Bioengineering</i> , 2017, 114, 1036-1044.	1.7	14
216	<sup>13</sup> C metabolic flux analysis of human adenovirus infection: Implications for viral vector production. <i>Biotechnology and Bioengineering</i> , 2017, 114, 195-207.	1.7	19
217	<sup>13</sup> C-metabolic flux analysis for mevalonate-producing strain of <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2017, 123, 177-182.	1.1	48
218	Understanding metabolism with flux analysis: From theory to application. <i>Metabolic Engineering</i> , 2017, 43, 94-102.	3.6	73
219	Metabolic Flux Analysis using <sup>13</sup> C Isotopes: III. Significance for Systems Biology and Metabolic Engineering. <i>Applied Biochemistry and Microbiology</i> , 2017, 53, 827-841.	0.3	0
220	Flux-Enabled Exploration of the Role of Sip1 in Galactose Yeast Metabolism. <i>Frontiers in Bioengineering and Biotechnology</i> , 2017, 5, 31.	2.0	4
221	Metabolic flux analysis of heterotrophic growth in <i>Chlamydomonas reinhardtii</i> . <i>PLoS ONE</i> , 2017, 12, e0177292.	1.1	40

#	ARTICLE	IF	CITATIONS
222	Isotopically nonstationary metabolic flux analysis (INST-MFA): putting theory into practice. <i>Current Opinion in Biotechnology</i> , 2018, 54, 80-87.	3.3	59
223	Metabolic flux of the oxidative pentose phosphate pathway under low light conditions in <i>Synechocystis</i> sp. PCC 6803. <i>Journal of Bioscience and Bioengineering</i> , 2018, 126, 38-43.	1.1	21
224	Comprehensive assessment of measurement uncertainty in <sup>13</sup> C-based metabolic flux experiments. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 3337-3348.	1.9	18
225	A guide to <sup>13</sup> C metabolic flux analysis for the cancer biologist. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-13.	3.2	165
226	Elucidation of photoautotrophic carbon flux topology in <i>Synechocystis</i> PCC 6803 using genome-scale carbon mapping models. <i>Metabolic Engineering</i> , 2018, 47, 190-199.	3.6	52
227	Rerouting of Metabolism into Desired Cellular Products by Nutrient Stress: Fluxes Reveal the Selected Pathways in Cyanobacterial Photosynthesis. <i>ACS Synthetic Biology</i> , 2018, 7, 1465-1476.	1.9	27
228	<sup>13</sup> C Flux Analysis Reveals that Rebalancing Medium Amino Acid Composition can Reduce Ammonia Production while Preserving Central Carbon Metabolism of CHO Cell Cultures. <i>Biotechnology Journal</i> , 2018, 13, e1700518.	1.8	25
229	Hexokinase-2 depletion inhibits glycolysis and induces oxidative phosphorylation in hepatocellular carcinoma and sensitizes to metformin. <i>Nature Communications</i> , 2018, 9, 446.	5.8	311
230	Quantitative Analysis of NAD Synthesis-Breakdown Fluxes. <i>Cell Metabolism</i> , 2018, 27, 1067-1080.e5.	7.2	363
231	Targeting hepatic glutaminase activity to ameliorate hyperglycemia. <i>Nature Medicine</i> , 2018, 24, 518-524.	15.2	50
232	Reverse engineering the cancer metabolic network using flux analysis to understand drivers of human disease. <i>Metabolic Engineering</i> , 2018, 45, 95-108.	3.6	36
233	Expression of heterologous non-oxidative pentose phosphate pathway from <i>Bacillus methanolicus</i> and phosphoglucose isomerase deletion improves methanol assimilation and metabolite production by a synthetic <i>Escherichia coli</i> methylotroph. <i>Metabolic Engineering</i> , 2018, 45, 75-85.	3.6	74
234	Optimal <sup>13</sup> C-labeling of glycerol carbon source for precise flux estimation in <i>Escherichia coli</i> . <i>Journal of Bioscience and Bioengineering</i> , 2018, 125, 301-305.	1.1	4
235	DMFA-based operation model for fermentation processes. <i>Computers and Chemical Engineering</i> , 2018, 109, 138-150.	2.0	4
236	Mass Spectrometry-Based Method to Study Inhibitor-Induced Metabolic Redirection in the Central Metabolism of Cancer Cells. <i>Mass Spectrometry</i> , 2018, 7, A0067-A0067.	0.2	11
237	Advances in metabolic flux analysis toward genome-scale profiling of higher organisms. <i>Bioscience Reports</i> , 2018, 38, .	1.1	36
238	Serine synthesis through PHGDH coordinates nucleotide levels by maintaining central carbon metabolism. <i>Nature Communications</i> , 2018, 9, 5442.	5.8	143
239	<sup>13</sup> C-metabolic flux analysis of ethanol-assimilating <i>Saccharomyces cerevisiae</i> for S-adenosyl-l-methionine production. <i>Microbial Cell Factories</i> , 2018, 17, 82.	1.9	12

#	ARTICLE	IF	CITATIONS
240	Metabolism in dense microbial colonies: <sup>13</sup> C metabolic flux analysis of <i>E. coli</i> grown on agar identifies two distinct cell populations with acetate cross-feeding. <i>Metabolic Engineering</i> , 2018, 49, 242-247.	3.6	40
241	On structural identifiability analysis of the cascaded linear dynamic systems in isotopically non-stationary <sup>13</sup> C labelling experiments. <i>Mathematical Biosciences</i> , 2018, 300, 122-129.	0.9	3
242	Metformin reduces liver glucose production by inhibition of fructose-1-6-bisphosphatase. <i>Nature Medicine</i> , 2018, 24, 1395-1406.	15.2	212
243	Metabolic network-based predictions of toxicant-induced metabolite changes in the laboratory rat. <i>Scientific Reports</i> , 2018, 8, 11678.	1.6	37
244	Dissecting metabolic flux in C4 plants: experimental and theoretical approaches. <i>Phytochemistry Reviews</i> , 2018, 17, 1253-1274.	3.1	6
245	Metabolic flux responses to deletion of 20 core enzymes reveal flexibility and limits of <i>E. coli</i> metabolism. <i>Metabolic Engineering</i> , 2019, 55, 249-257.	3.6	40
246	Studying metabolic flux adaptations in cancer through integrated experimental-computational approaches. <i>BMC Biology</i> , 2019, 17, 51.	1.7	20
247	p13CMFA: Parsimonious <sup>13</sup> C metabolic flux analysis. <i>PLoS Computational Biology</i> , 2019, 15, e1007310.	1.5	9
248	Metabolic perturbations in mutants of glucose transporters and their applications in metabolite production in <i>Escherichia coli</i> . <i>Microbial Cell Factories</i> , 2019, 18, 170.	1.9	17
249	Glycerol induces G6pc in primary mouse hepatocytes and is the preferred substrate for gluconeogenesis both in vitro and in vivo. <i>Journal of Biological Chemistry</i> , 2019, 294, 18017-18028.	1.6	27
250	Repression of mitochondrial metabolism for cytosolic pyruvate-derived chemical production in <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2019, 18, 177.	1.9	11
251	High-resolution <sup>13</sup> C metabolic flux analysis. <i>Nature Protocols</i> , 2019, 14, 2856-2877.	5.5	132
252	Fluxomic Analysis Reveals Central Carbon Metabolism Adaptation for Diazotroph <i>Azotobacter vinelandii</i> Ammonium Excretion. <i>Scientific Reports</i> , 2019, 9, 13209.	1.6	13
253	<sup>13</sup> C metabolic flux analysis on roles of malate transporter in lipid accumulation of <i>Mucor circinelloides</i> . <i>Microbial Cell Factories</i> , 2019, 18, 154.	1.9	9
254	Near-equilibrium glycolysis supports metabolic homeostasis and energy yield. <i>Nature Chemical Biology</i> , 2019, 15, 1001-1008.	3.9	60
255	High extracellular lactate causes reductive carboxylation in breast tissue cell lines grown under normoxic conditions. <i>PLoS ONE</i> , 2019, 14, e0213419.	1.1	18
256	Synergistic substrate cofeeding stimulates reductive metabolism. <i>Nature Metabolism</i> , 2019, 1, 643-651.	5.1	71
257	<sup>2</sup> H and <sup>13</sup> C metabolic flux analysis elucidates in vivo thermodynamics of the ED pathway in <i>Zymomonas mobilis</i> . <i>Metabolic Engineering</i> , 2019, 54, 301-316.	3.6	51

#	ARTICLE	IF	CITATIONS
258	<sup>13</sup> C-Metabolic Flux Analysis Reveals Effect of Phenol on Central Carbon Metabolism in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1010.	1.5	10
259	EMUlator: An Elementary Metabolite Unit (EMU) Based Isotope Simulator Enabled by Adjacency Matrix. <i>Frontiers in Microbiology</i> , 2019, 10, 922.	1.5	4
260	Spatial-fluxomics provides a subcellular-compartmentalized view of reductive glutamine metabolism in cancer cells. <i>Nature Communications</i> , 2019, 10, 1351.	5.8	56
261	IsoCor: isotope correction for high-resolution MS labeling experiments. <i>Bioinformatics</i> , 2019, 35, 4484-4487.	1.8	107
262	Network Modeling of Liver Metabolism to Predict Plasma Metabolite Changes During Short-Term Fasting in the Laboratory Rat. <i>Frontiers in Physiology</i> , 2019, 10, 161.	1.3	6
263	<sup>13</sup> C metabolic flux analysis-guided metabolic engineering of <i>Escherichia coli</i> for improved acetol production from glycerol. <i>Biotechnology for Biofuels</i> , 2019, 12, 29.	6.2	19
264	From <i>Escherichia coli</i> mutant <sup>13</sup> C labeling data to a core kinetic model: A kinetic model parameterization pipeline. <i>PLoS Computational Biology</i> , 2019, 15, e1007319.	1.5	28
265	Sugar phosphate analysis with baseline separation and soft ionization by gas chromatography-negative chemical ionization-mass spectrometry improves flux estimation of bidirectional reactions in cancer cells. <i>Metabolic Engineering</i> , 2019, 51, 43-49.	3.6	16
266	Genome-Scale Fluxome of <i>Synechococcus elongatus</i> UTEX 2973 Using Transient <sup>13</sup> C-Labeling Data. <i>Plant Physiology</i> , 2019, 179, 761-769.	2.3	57
267	Microbial Metabolomics. <i>Methods in Molecular Biology</i> , 2019, , .	0.4	8
268	Dynamic <sup>13</sup> C Labeling of Fast Turnover Metabolites for Analysis of Metabolic Fluxes and Metabolite Channeling. <i>Methods in Molecular Biology</i> , 2019, 1859, 301-316.	0.4	4
269	The challenge and potential of photosynthesis: unique considerations for metabolic flux measurements in photosynthetic microorganisms. <i>Biotechnology Letters</i> , 2019, 41, 35-45.	1.1	12
270	Glycerol metabolism of <i>Pichia pastoris</i> ( <i>Komagataella</i> spp.) characterised by <sup>13</sup> C-based metabolic flux analysis. <i>New Biotechnology</i> , 2019, 50, 52-59.	2.4	25
271	Glutamate-oxaloacetate transaminase activity promotes palmitate lipotoxicity in rat hepatocytes by enhancing anaplerosis and citric acid cycle flux. <i>Journal of Biological Chemistry</i> , 2019, 294, 3081-3090.	1.6	25
272	Tracing metabolic fluxes using mass spectrometry: Stable isotope-resolved metabolomics in health and disease. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 120, 115371.	5.8	12
273	Mapping <i>Salmonella typhimurium</i> pathways using <sup>13</sup> C metabolic flux analysis. <i>Metabolic Engineering</i> , 2019, 52, 303-314.	3.6	3
274	Deletion of four genes in <i>Escherichia coli</i> enables preferential consumption of xylose and secretion of glucose. <i>Metabolic Engineering</i> , 2019, 52, 168-177.	3.6	24
275	Glycerol not lactate is the major net carbon source for gluconeogenesis in mice during both short and prolonged fasting. <i>Molecular Metabolism</i> , 2020, 31, 36-44.	3.0	34



#	ARTICLE	IF	CITATIONS
276	Analysing central metabolism in ultra-high resolution: At the crossroads of carbon and nitrogen. <i>Molecular Metabolism</i> , 2020, 33, 38-47.	3.0	12
277	Genome-Scale Model-Based Identification of Metabolite Indicators for Early Detection of Kidney Toxicity. <i>Toxicological Sciences</i> , 2020, 173, 293-312.	1.4	5
278	<sup>13</sup> C-Metabolic Flux Analysis in Developing Flax ( <i>Linum usitatissimum</i> L.) Embryos to Understand Storage Lipid Biosynthesis. <i>Metabolites</i> , 2020, 10, 14.	1.3	6
279	Disruption of redox homeostasis for combinatorial drug efficacy in K-Ras tumors as revealed by metabolic connectivity profiling. <i>Cancer &amp; Metabolism</i> , 2020, 8, 22.	2.4	10
280	Kinetic Trans-omic Analysis Reveals Key Regulatory Mechanisms for Insulin-Regulated Glucose Metabolism in Adipocytes. <i>IScience</i> , 2020, 23, 101479.	1.9	17
281	Metabolic Flux Analysis—Linking Isotope Labeling and Metabolic Fluxes. <i>Metabolites</i> , 2020, 10, 447.	1.3	26
282	In Vivo Estimates of Liver Metabolic Flux Assessed by <sup>13</sup> C-Propionate and <sup>13</sup> C-Lactate Are Impacted by Tracer Recycling and Equilibrium Assumptions. <i>Cell Reports</i> , 2020, 32, 107986.	2.9	29
283	Cellular sensing of extracellular purine nucleosides triggers an innate IFN- $\gamma$ response. <i>Science Advances</i> , 2020, 6, eaba3688.	4.7	24
284	Branched chain amino acids and carbohydrate restriction exacerbate ketogenesis and hepatic mitochondrial oxidative dysfunction during NAFLD. <i>FASEB Journal</i> , 2020, 34, 14832-14849.	0.2	19
285	Mechanism-based identification of plasma metabolites associated with liver toxicity. <i>Toxicology</i> , 2020, 441, 152493.	2.0	10
286	K-FIT: An accelerated kinetic parameterization algorithm using steady-state fluxomic data. <i>Metabolic Engineering</i> , 2020, 61, 197-205.	3.6	35
287	Metabolic Rearrangements Causing Elevated Proline and Polyhydroxybutyrate Accumulation During the Osmotic Adaptation Response of <i>Bacillus megaterium</i> . <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 47.	2.0	16
288	Cancer Cell Metabolites: Updates on Current Tracing Methods. <i>ChemBioChem</i> , 2020, 21, 3476-3488.	1.3	5
289	Metabolic flux analysis reaching genome wide coverage: lessons learned and future perspectives. <i>Current Opinion in Chemical Engineering</i> , 2020, 30, 17-25.	3.8	7
290	Vitamin E does not prevent Western diet-induced NASH progression and increases metabolic flux dysregulation in mice. <i>Journal of Lipid Research</i> , 2020, 61, 707-721.	2.0	12
291	Investigating <i>E. coli</i> Coculture for Resveratrol Production with <sup>13</sup> C Metabolic Flux Analysis. <i>Journal of Agricultural and Food Chemistry</i> , 2020, 68, 3466-3473.	2.4	16
292	Computational data mining method for isotopomer analysis in the quantitative assessment of metabolic reprogramming. <i>Scientific Reports</i> , 2020, 10, 286.	1.6	7
293	Systematic identification and elimination of flux bottlenecks in the aldehyde production pathway of <i>Synechococcus elongatus</i> PCC 7942. <i>Metabolic Engineering</i> , 2020, 60, 56-65.	3.6	36

#	ARTICLE	IF	CITATIONS
294	Sink/Source Balance of Leaves Influences Amino Acid Pools and Their Associated Metabolic Fluxes in Winter Oilseed Rape ( <i>Brassica napus</i> L.). <i>Metabolites</i> , 2020, 10, 150.	1.3	14
295	<sup>13</sup> C Metabolic Flux Analysis of <i>Escherichia coli</i> Engineered for Gamma-aminobutyrate Production. <i>Biotechnology Journal</i> , 2020, 15, e1900346.	1.8	14
296	ScalaFlux: A scalable approach to quantify fluxes in metabolic subnetworks. <i>PLoS Computational Biology</i> , 2020, 16, e1007799.	1.5	12
297	Utilizing tandem mass spectrometry for metabolic flux analysis. <i>Laboratory Investigation</i> , 2021, 101, 423-429.	1.7	6
298	Induced pluripotent stem cells can utilize lactate as a metabolic substrate to support proliferation. <i>Biotechnology Progress</i> , 2021, 37, e3090.	1.3	9
299	Estimation of linear and cyclic electron flows in photosynthesis based on <sup>13</sup> C-metabolic flux analysis. <i>Journal of Bioscience and Bioengineering</i> , 2021, 131, 277-282.	1.1	6
300	Recent advances in constraint and machine learning-based metabolic modeling by leveraging stoichiometric balances, thermodynamic feasibility and kinetic law formalisms. <i>Metabolic Engineering</i> , 2021, 63, 13-33.	3.6	26
301	Tumor Reliance on Cytosolic versus Mitochondrial One-Carbon Flux Depends on Folate Availability. <i>Cell Metabolism</i> , 2021, 33, 190-198.e6.	7.2	31
302	A guide to metabolic flux analysis in metabolic engineering: Methods, tools and applications. <i>Metabolic Engineering</i> , 2021, 63, 2-12.	3.6	67
303	Autotrophic and mixotrophic metabolism of an anammox bacterium revealed by in vivo <sup>13</sup> C and <sup>2</sup> H metabolic network mapping. <i>ISME Journal</i> , 2021, 15, 673-687.	4.4	64
304	<sup>13</sup> C-metabolic flux analysis in glycerol-assimilating strains of <i>Saccharomyces cerevisiae</i> . <i>Journal of General and Applied Microbiology</i> , 2021, 67, 142-149.	0.4	5
305	The metabolic origins of non-photorespiratory CO <sub>2</sub> release during photosynthesis: a metabolic flux analysis. <i>Plant Physiology</i> , 2021, 186, 297-314.	2.3	65
306	Exploring the metabolic fate of propanol in industrial erythromycin-producing strain via <sup>13</sup> C labeling experiments and enhancement of erythromycin production by rational metabolic engineering of <i>Saccharopolyspora erythraea</i> . <i>Biochemical and Biophysical Research Communications</i> , 2021, 542, 73-79.	1.0	12
307	Determination of the composition of heterogeneous binder solutions by surface plasmon resonance biosensing. <i>Scientific Reports</i> , 2021, 11, 3685.	1.6	6
308	Modelling Cell Metabolism: A Review on Constraint-Based Steady-State and Kinetic Approaches. <i>Processes</i> , 2021, 9, 322.	1.3	37
310	Comparative <sup>13</sup> C-metabolic flux analysis indicates elevation of ATP regeneration, carbon dioxide, and heat production in industrial <i>Saccharomyces cerevisiae</i> strains. <i>Biotechnology Journal</i> , 2022, 17, e2000438.	1.8	2
312	Robustifying Experimental Tracer Design for <sup>13</sup> C-Metabolic Flux Analysis. <i>Frontiers in Bioengineering and Biotechnology</i> , 2021, 9, 685323.	2.0	6
313	Analysis of steady-state carbon tracer experiments using akaike information criteria. <i>Metabolomics</i> , 2021, 17, 61.	1.4	3

#	ARTICLE	IF	CITATIONS
314	NAD <sup>+</sup> flux is maintained in aged mice despite lower tissue concentrations. <i>Cell Systems</i> , 2021, 12, 1160-1172.e4.	2.9	51
315	Compartment-specific metabolome labeling enables the identification of subcellular fluxes that may serve as promising metabolic engineering targets in CHO cells. <i>Bioprocess and Biosystems Engineering</i> , 2021, 44, 2567-2578.	1.7	3
316	mfapy: An open-source Python package for <sup>13</sup> C-based metabolic flux analysis. <i>Metabolic Engineering Communications</i> , 2021, 13, e00177.	1.9	11
317	<i>Metabolic Systems Biology</i> , 2009, , 5535-5552.		6
318	Steady-State <sup>13</sup> C Fluxomics Using OpenFLUX. <i>Methods in Molecular Biology</i> , 2014, 1191, 209-224.	0.4	9
319	Isotopically Nonstationary MFA (INST-MFA) of Autotrophic Metabolism. <i>Methods in Molecular Biology</i> , 2014, 1090, 181-210.	0.4	29
320	Optimization of Steady-State <sup>13</sup> C-Labeling Experiments for Metabolic Flux Analysis. <i>Methods in Molecular Biology</i> , 2014, 1090, 53-72.	0.4	4
321	<i>Fluxomics</i> , 2014, , 237-250.		3
322	Metabolic Flux Analysis: A Powerful Tool in Animal Cell Culture. <i>Cell Engineering</i> , 2015, , 521-539.	0.4	2
327	The airway epithelium undergoes metabolic reprogramming in individuals at high risk for lung cancer. <i>JCI Insight</i> , 2016, 1, e88814.	2.3	29
328	OpenFLUX2: <sup>13</sup> C-MFA modeling software package adjusted for the comprehensive analysis of single and parallel labeling experiments. <i>Microbial Cell Factories</i> , 2014, 13, 152.	1.9	13
329	A Method to Constrain Genome-Scale Models with <sup>13</sup> C Labeling Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004363.	1.5	53
330	A Kinetic Platform to Determine the Fate of Hydrogen Peroxide in <i>Escherichia coli</i> . <i>PLoS Computational Biology</i> , 2015, 11, e1004562.	1.5	37
331	Ensemble Modeling for Aromatic Production in <i>Escherichia coli</i> . <i>PLoS ONE</i> , 2009, 4, e6903.	1.1	52
332	Efficient Modeling of MS/MS Data for Metabolic Flux Analysis. <i>PLoS ONE</i> , 2015, 10, e0130213.	1.1	14
333	Liver AMP-Activated Protein Kinase Is Unnecessary for Gluconeogenesis but Protects Energy State during Nutrient Deprivation. <i>PLoS ONE</i> , 2017, 12, e0170382.	1.1	20
334	A Comprehensive View on Metabolic Pathway Analysis Methodologies. <i>Current Bioinformatics</i> , 2014, 9, 295-305.	0.7	5
335	FluxPy: a Python-based free and open-source software for <sup>13</sup> C-metabolic flux analyses. <i>PeerJ</i> , 2018, 6, e4716.	0.9	9

#	ARTICLE	IF	CITATIONS
336	Metabolic Systems Biology. , 2017, , 1-23.		0
339	In Vivo and In Vitro Quantification of Glucose Kinetics: From Bedside to Bench. Endocrinology and Metabolism, 2020, 35, 733-749.	1.3	3
342	Stable Isotopes for Tracing Cardiac Metabolism in Diseases. Frontiers in Cardiovascular Medicine, 2021, 8, 734364.	1.1	5
343	Compartment-specific <sup>13</sup> C metabolic flux analysis reveals boosted NADPH availability coinciding with increased cell-specific productivity for IgG1 producing CHO cells after MTA treatment. Engineering in Life Sciences, 2021, 21, 832-847.	2.0	2
345	Assessing the impact of substrate-level enzyme regulations limiting ethanol titer in Clostridium thermocellum using a core kinetic model. Metabolic Engineering, 2022, 69, 286-301.	3.6	7
346	Coordinated reprogramming of metabolism and cell function in adipocytes from proliferation to differentiation. Metabolic Engineering, 2022, 69, 221-230.	3.6	11
347	Pool size measurements improve precision of flux estimates but increase sensitivity to unmodeled reactions outside the core network in isotopically nonstationary metabolic flux analysis (INST-MFA). Biotechnology Journal, 2022, 17, e2000427.	1.8	3
348	Metabolic Networks, Microbial Consortia, and Analogies to Smart Grids. Proceedings of the IEEE, 2022, 110, 541-556.	16.4	5
349	An efficient LC-MS method for isomer separation and detection of sugars, phosphorylated sugars, and organic acids. Journal of Experimental Botany, 2022, 73, 2938-2952.	2.4	12
351	Developmental changes in lignin composition are driven by both monolignol supply and laccase specificity. Science Advances, 2022, 8, eabm8145.	4.7	26
353	<sup>13</sup> C-metabolic flux analysis of Clostridium ljungdahlii illuminates its core metabolism under mixotrophic culture conditions. Metabolic Engineering, 2022, 72, 161-170.	3.6	6
354	Optogenetic reprogramming of carbon metabolism using light-powering microbial proton pump systems. Metabolic Engineering, 2022, 72, 227-236.	3.6	10
355	Carbon flux through photosynthesis and central carbon metabolism show distinct patterns between algae, C3 and C4 plants. Nature Plants, 2022, 8, 78-91.	4.7	49
356	Analogous Metabolic Decoupling in Pseudomonas putida and Comamonas testosteroni Implies Energetic Bypass to Facilitate Gluconeogenic Growth. MBio, 2021, 12, e0325921.	1.8	7
357	Mutants lacking global regulators, fis and arcA, in Escherichia coli enhanced growth fitness under acetate metabolism by pathway reprogramming. Applied Microbiology and Biotechnology, 2022, 106, 3231-3243.	1.7	3
358	Validation-based model selection for <sup>13</sup> C metabolic flux analysis with uncertain measurement errors. PLoS Computational Biology, 2022, 18, e1009999.	1.5	7
380	GC/MS-based <sup>13</sup> C metabolic flux analysis resolves the parallel and cyclic photomixotrophic metabolism of Synechocystis sp. PCC 6803 and selected deletion mutants including the Entner-Doudoroff and phosphoketolase pathways. Microbial Cell Factories, 2022, 21, 69.	1.9	11
381	Statin therapy inhibits fatty acid synthase via dynamic protein modifications. Nature Communications, 2022, 13, 2542.	5.8	7

#	ARTICLE	IF	CITATIONS
382	CDK12 promotes tumorigenesis but induces vulnerability to therapies inhibiting folate one-carbon metabolism in breast cancer. <i>Nature Communications</i> , 2022, 13, 2642.	5.8	15
383	Analysis and modeling tools of metabolic flux. , 2022, , 45-68.		0
385	CeCaFLUX: the first web server for standardized and visual instationary <sup>13</sup> C metabolic flux analysis. <i>Bioinformatics</i> , 2022, 38, 3481-3483.	1.8	0
386	Constitutive expression of the global regulator AbrB restores the growth defect of a genome-reduced <i>Bacillus subtilis</i> strain and improves its metabolite production. <i>DNA Research</i> , 2022, 29, .	1.5	1
387	Recent Progress in Analysis of Intermediary Metabolism by <i>ex vivo</i> <sup>13</sup> C NMR. <i>NMR in Biomedicine</i> , 0, , .	1.6	2
388	Metabolic flux analysis: a comprehensive review on sample preparation, analytical techniques, data analysis, computational modelling, and main application areas. <i>RSC Advances</i> , 2022, 12, 25528-25548.	1.7	10
389	<sup>13</sup> C metabolic flux analysis: Classification and characterization from the perspective of mathematical modeling and application in physiological research of neural cell. <i>Frontiers in Molecular Neuroscience</i> , 0, 15, .	1.4	0
390	Tracing metabolic flux in vivo: basic model structures of tracer methodology. <i>Experimental and Molecular Medicine</i> , 2022, 54, 1311-1322.	3.2	7
391	A synthetic C2 auxotroph of <i>Pseudomonas putida</i> for evolutionary engineering of alternative sugar catabolic routes. <i>Metabolic Engineering</i> , 2022, 74, 83-97.	3.6	13
392	Experimental Evolution Reveals Unifying Systems-Level Adaptations but Diversity in Driving Genotypes. <i>MSystems</i> , 2022, 7, .	1.7	7
394	Metabolic synergy in <i>Camelina</i> reproductive tissues for seed development. <i>Science Advances</i> , 2022, 8, .	4.7	11
395	Glucagon changes substrate preference in gluconeogenesis. <i>Journal of Biological Chemistry</i> , 2022, 298, 102708.	1.6	4
396	Isotope-Assisted Metabolic Flux Analysis: A Powerful Technique to Gain New Insights into the Human Metabolome in Health and Disease. <i>Metabolites</i> , 2022, 12, 1066.	1.3	5
397	Advances of stable isotope technology in food safety analysis and nutrient metabolism research. <i>Food Chemistry</i> , 2023, 408, 135191.	4.2	5
398	Integrated flux and pool size analysis in plant central metabolism reveals unique roles of glycine and serine during photorespiration. <i>Nature Plants</i> , 2023, 9, 169-178.	4.7	27
399	Online Monitoring of Penicillin Manufacture Based on Production Variables and Metabolic Fluxes. <i>Industrial &amp; Engineering Chemistry Research</i> , 2023, 62, 1480-1491.	1.8	0
400	Isotopically non-stationary metabolic flux analysis of heterotrophic <i>Arabidopsis thaliana</i> cell cultures. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
401	Validation of carbon isotopologue distribution measurements by GC-MS and application to <sup>13</sup> C-metabolic flux analysis of the tricarboxylic acid cycle in <i>Brassica napus</i> leaves. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	3

#	ARTICLE	IF	CITATIONS
402	Comparative study of two <i>Saccharomyces cerevisiae</i> strains with kinetic models at genome-scale. <i>Metabolic Engineering</i> , 2023, 76, 1-17.	3.6	7
405	Effect of light fluctuations on photosynthesis and metabolic flux in <i>Synechocystis</i> sp. PCC 6803. <i>Biotechnology Progress</i> , 2023, 39, .	1.3	1
406	<sup>13</sup> C-Metabolic flux analysis of 3T3-L1 adipocytes illuminates its core metabolism under hypoxia. <i>Metabolic Engineering</i> , 2023, 76, 158-166.	3.6	4
407	Interpreting metabolic complexity via isotope-assisted metabolic flux analysis. <i>Trends in Biochemical Sciences</i> , 2023, 48, 553-567.	3.7	2
408	Global determination of reaction rates and lipid turnover kinetics in <i>Mus musculus</i> . <i>Cell Metabolism</i> , 2023, 35, 711-721.e4.	7.2	4