

Maciek R Antoniewicz

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84
papers

6,031
citations

45
h-index

77
g-index

86
ext. papers

7,114
ext. citations

8.7
avg, IF

6.7
L-index

#	Paper	IF	Citations
84	Elementary metabolite units (EMU): a novel framework for modeling isotopic distributions. <i>Metabolic Engineering</i> , 2007 , 9, 68-86	9.7	426
83	A roadmap for interpreting (13)C metabolite labeling patterns from cells. <i>Current Opinion in Biotechnology</i> , 2015 , 34, 189-201	11.4	368
82	Determination of confidence intervals of metabolic fluxes estimated from stable isotope measurements. <i>Metabolic Engineering</i> , 2006 , 8, 324-37	9.7	349
81	Quantifying reductive carboxylation flux of glutamine to lipid in a brown adipocyte cell line. <i>Journal of Biological Chemistry</i> , 2008 , 283, 20621-7	5.4	230
80	Accurate assessment of amino acid mass isotopomer distributions for metabolic flux analysis. <i>Analytical Chemistry</i> , 2007 , 79, 7554-9	7.8	208
79	An elementary metabolite unit (EMU) based method of isotopically nonstationary flux analysis. <i>Biotechnology and Bioengineering</i> , 2008 , 99, 686-99	4.9	203
78	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, 277-92	9.7	197
77	Hexokinase-2 depletion inhibits glycolysis and induces oxidative phosphorylation in hepatocellular carcinoma and sensitizes to metformin. <i>Nature Communications</i> , 2018 , 9, 446	17.4	193
76	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	9.7	190
75	Methods and advances in metabolic flux analysis: a mini-review. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2015 , 42, 317-25	4.2	139
74	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, 6477-82	11.5	134
73	Parallel labeling experiments with [1,2-(13)C]glucose and [U-(13)C]glutamine provide new insights into CHO cell metabolism. <i>Metabolic Engineering</i> , 2013 , 15, 34-47	9.7	114
72	Engineering the biological conversion of methanol to specialty chemicals in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2017 , 39, 49-59	9.7	106
71	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	3.7	106
70	Central metabolic responses to the overproduction of fatty acids in <i>Escherichia coli</i> based on 13C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2014 , 111, 575-85	4.9	99
69	A guide to C metabolic flux analysis for the cancer biologist. <i>Experimental and Molecular Medicine</i> , 2018 , 50, 1-13	12.8	96
68	Towards dynamic metabolic flux analysis in CHO cell cultures. <i>Biotechnology Journal</i> , 2012 , 7, 61-74	5.6	95

67	Measuring deuterium enrichment of glucose hydrogen atoms by gas chromatography/mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 3211-6	7.8	89
66	COMPLETE-MFA: complementary parallel labeling experiments technique for metabolic flux analysis. <i>Metabolic Engineering</i> , 2013 , 20, 49-55	9.7	87
65	CO fixation by anaerobic non-photosynthetic mixotrophy for improved carbon conversion. <i>Nature Communications</i> , 2016 , 7, 12800	17.4	86
64	Dynamic metabolic flux analysis (DMFA): a framework for determining fluxes at metabolic non-steady state. <i>Metabolic Engineering</i> , 2011 , 13, 745-55	9.7	85
63	¹³ C metabolic flux analysis: optimal design of isotopic labeling experiments. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 1116-21	11.4	84
62	Rational design of ¹³ C-labeling experiments for metabolic flux analysis in mammalian cells. <i>BMC Systems Biology</i> , 2012 , 6, 43	3.5	79
61	Tandem mass spectrometry: a novel approach for metabolic flux analysis. <i>Metabolic Engineering</i> , 2011 , 13, 225-33	9.7	77
60	Integrated ¹³ C-metabolic flux analysis of 14 parallel labeling experiments in Escherichia coli. <i>Metabolic Engineering</i> , 2015 , 28, 151-158	9.7	76
59	Parallel labeling experiments with [U- ¹³ C]glucose validate E. coli metabolic network model for ¹³ C metabolic flux analysis. <i>Metabolic Engineering</i> , 2012 , 14, 533-41	9.7	75
58	Dynamic metabolic flux analysis--tools for probing transient states of metabolic networks. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 973-8	11.4	74
57	High-resolution C metabolic flux analysis. <i>Nature Protocols</i> , 2019 , 14, 2856-2877	18.8	73
56	Comprehensive analysis of glucose and xylose metabolism in Escherichia coli under aerobic and anaerobic conditions by C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017 , 39, 9-18	9.7	73
55	Resolving the TCA cycle and pentose-phosphate pathway of Clostridium acetobutylicum ATCC 824: Isotopomer analysis, in vitro activities and expression analysis. <i>Biotechnology Journal</i> , 2011 , 6, 300-5	5.6	73
54	Publishing ¹³ C metabolic flux analysis studies: a review and future perspectives. <i>Metabolic Engineering</i> , 2013 , 20, 42-8	9.7	71
53	Selection of tracers for ¹³ C-metabolic flux analysis using elementary metabolite units (EMU) basis vector methodology. <i>Metabolic Engineering</i> , 2012 , 14, 150-61	9.7	67
52	Measuring complete isotopomer distribution of aspartate using gas chromatography/tandem mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 4628-32	7.8	67
51	Parallel labeling experiments and metabolic flux analysis: Past, present and future methodologies. <i>Metabolic Engineering</i> , 2013 , 16, 21-32	9.7	64
50	Genome-Scale Metabolic Model for the Green Alga Chlorella vulgaris UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. <i>Plant Physiology</i> , 2016 , 172, 589-602	6.6	62

49	(13)C-metabolic flux analysis of co-cultures: A novel approach. <i>Metabolic Engineering</i> , 2015 , 31, 132-9	9.7	60
48	Quantifying biomass composition by gas chromatography/mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 9423-7	7.8	60
47	Optimal tracers for parallel labeling experiments and C metabolic flux analysis: A new precision and synergy scoring system. <i>Metabolic Engineering</i> , 2016 , 38, 10-18	9.7	54
46	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 222-227	11.5	53
45	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	9.7	53
44	Tandem mass spectrometry for measuring stable-isotope labeling. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 48-53	11.4	52
43	Parallel labeling experiments validate <i>Clostridium acetobutylicum</i> metabolic network model for (13)C metabolic flux analysis. <i>Metabolic Engineering</i> , 2014 , 26, 23-33	9.7	48
42	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	9.7	45
41	Metabolism of the fast-growing bacterium <i>Vibrio natriegens</i> elucidated by C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017 , 44, 191-197	9.7	45
40	Parallel labeling experiments for pathway elucidation and (13)C metabolic flux analysis. <i>Current Opinion in Biotechnology</i> , 2015 , 36, 91-7	11.4	45
39	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, 127-33	11.4	45
38	Methanol assimilation in <i>Escherichia coli</i> is improved by co-utilization of threonine and deletion of leucine-responsive regulatory protein. <i>Metabolic Engineering</i> , 2018 , 45, 67-74	9.7	43
37	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	9.7	39
36	Characterization of physiological responses to 22 gene knockouts in <i>Escherichia coli</i> central carbon metabolism. <i>Metabolic Engineering</i> , 2016 , 37, 102-113	9.7	39
35	Evolution of <i>E. coli</i> on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. <i>PLoS ONE</i> , 2016 , 11, e0151130	3.7	38
34	Metabolic network reconstruction, growth characterization and 13C-metabolic flux analysis of the extremophile <i>Thermus thermophilus</i> HB8. <i>Metabolic Engineering</i> , 2014 , 24, 173-80	9.7	35
33	Evaluation of regression models in metabolic physiology: predicting fluxes from isotopic data without knowledge of the pathway. <i>Metabolomics</i> , 2006 , 2, 41-52	4.7	35
32	Measuring the Composition and Stable-Isotope Labeling of Algal Biomass Carbohydrates via Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2016 , 88, 4624-8	7.8	35

31	(13)C metabolic flux analysis of the extremely thermophilic, fast growing, xylose-utilizing Geobacillus strain LC300. <i>Metabolic Engineering</i> , 2016 , 33, 148-157	9.7	34
30	Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote. <i>Plant Physiology</i> , 2018 , 176, 450-462	6.6	34
29	Evidence for transketolase-like TKTL1 flux in CHO cells based on parallel labeling experiments and (13)C-metabolic flux analysis. <i>Metabolic Engineering</i> , 2016 , 37, 72-78	9.7	30
28	A key role for transketolase-like 1 in tumor metabolic reprogramming. <i>Oncotarget</i> , 2016 , 7, 51875-51897	5.3	30
27	Complete genome sequence, metabolic model construction and phenotypic characterization of Geobacillus LC300, an extremely thermophilic, fast growing, xylose-utilizing bacterium. <i>Metabolic Engineering</i> , 2015 , 32, 74-81	9.7	28
26	Enzyme I facilitates reverse flux from pyruvate to phosphoenolpyruvate in Escherichia coli. <i>Nature Communications</i> , 2017 , 8, 14316	17.4	27
25	Metabolism in dense microbial colonies: C metabolic flux analysis of E. coli grown on agar identifies two distinct cell populations with acetate cross-feeding. <i>Metabolic Engineering</i> , 2018 , 49, 242-247	9.7	27
24	Metabolic flux responses to deletion of 20 core enzymes reveal flexibility and limits of E. coli metabolism. <i>Metabolic Engineering</i> , 2019 , 55, 249-257	9.7	26
23	Synthetic methylotrophy: Strategies to assimilate methanol for growth and chemicals production. <i>Current Opinion in Biotechnology</i> , 2019 , 59, 165-174	11.4	25
22	Heterotrophic bacteria from an extremely phosphate-poor lake have conditionally reduced phosphorus demand and utilize diverse sources of phosphorus. <i>Environmental Microbiology</i> , 2016 , 18, 656-67	5.2	24
21	Tracing metabolism from lignocellulosic biomass and gaseous substrates to products with stable-isotopes. <i>Current Opinion in Biotechnology</i> , 2017 , 43, 86-95	11.4	22
20	How adaptive evolution reshapes metabolism to improve fitness: recent advances and future outlook. <i>Current Opinion in Chemical Engineering</i> , 2018 , 22, 209-215	5.4	22
19	C metabolic flux analysis of three divergent extremely thermophilic bacteria: Geobacillus sp. LC300, Thermus thermophilus HB8, and Rhodothermus marinus DSM 4252. <i>Metabolic Engineering</i> , 2017 , 44, 182-190	9.7	21
18	A guide to deciphering microbial interactions and metabolic fluxes in microbiome communities. <i>Current Opinion in Biotechnology</i> , 2020 , 64, 230-237	11.4	21
17	Co-utilization of glucose and xylose by evolved Thermus thermophilus LC113 strain elucidated by (13)C metabolic flux analysis and whole genome sequencing. <i>Metabolic Engineering</i> , 2016 , 37, 63-71	9.7	21
16	From Escherichia coli mutant 13C labeling data to a core kinetic model: A kinetic model parameterization pipeline. <i>PLoS Computational Biology</i> , 2019 , 15, e1007319	5	21
15	Engineering Escherichia coli for methanol-dependent growth on glucose for metabolite production. <i>Metabolic Engineering</i> , 2020 , 60, 45-55	9.7	19
14	An unconventional uptake rate objective function approach enhances applicability of genome-scale models for mammalian cells. <i>Npj Systems Biology and Applications</i> , 2019 , 5, 25	5	16

13	Comprehensive metabolic modeling of multiple ¹³ 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	5.2	16
12	Improving synthetic methylotrophy via dynamic formaldehyde regulation of pentose phosphate pathway genes and redox perturbation. <i>Metabolic Engineering</i> , 2020 , 57, 247-255	9.7	15
11	A guide to metabolic flux analysis in metabolic engineering: Methods, tools and applications. <i>Metabolic Engineering</i> , 2021 , 63, 2-12	9.7	15
10	Tandem Mass Spectrometry for C Metabolic Flux Analysis: Methods and Algorithms Based on EMU Framework. <i>Frontiers in Microbiology</i> , 2019 , 10, 31	5.7	14
9	Using multiple tracers for ¹³ C metabolic flux analysis. <i>Methods in Molecular Biology</i> , 2013 , 985, 353-65	1.4	14
8	Deletion of four genes in Escherichia coli enables preferential consumption of xylose and secretion of glucose. <i>Metabolic Engineering</i> , 2019 , 52, 168-177	9.7	14
7	Triggering the stringent response enhances synthetic methanol utilization in Escherichia coli. <i>Metabolic Engineering</i> , 2020 , 61, 1-10	9.7	7
6	Adaptive laboratory evolution of methylotrophic Escherichia coli enables synthesis of all amino acids from methanol-derived carbon. <i>Applied Microbiology and Biotechnology</i> , 2021 , 105, 869-876	5.7	7
5	Improving the Methanol Tolerance of an Methylotroph via Adaptive Laboratory Evolution Enhances Synthetic Methanol Utilization. <i>Frontiers in Microbiology</i> , 2021 , 12, 638426	5.7	7
4	Regulatory interventions improve the biosynthesis of limiting amino acids from methanol carbon to improve synthetic methylotrophy in Escherichia coli. <i>Biotechnology and Bioengineering</i> , 2021 , 118, 43-57	4.9	3
3	Coordinated reprogramming of metabolism and cell function in adipocytes from proliferation to differentiation.. <i>Metabolic Engineering</i> , 2021 , 69, 221-230	9.7	1
2	Laboratory evolution of multiple E. coli strains reveals unifying principles of adaptation but diversity in driving genotypes		1
1	C-metabolic flux analysis of Clostridium ljungdahlii illuminates its core metabolism under mixotrophic culture conditions.. <i>Metabolic Engineering</i> , 2022 , 72, 161-170	9.7	0