

Maciek R Antoniewicz

List of Publications by Year in descending order

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84
papers

7,811
citations

44042

48
h-index

53190

85
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86
all docs

86
docs citations

86
times ranked

6589
citing authors

#	ARTICLE	IF	CITATIONS
1	Elementary metabolite units (EMU): A novel framework for modeling isotopic distributions. <i>Metabolic Engineering</i> , 2007, 9, 68-86.	3.6	514
2	A roadmap for interpreting ¹³ C metabolite labeling patterns from cells. <i>Current Opinion in Biotechnology</i> , 2015, 34, 189-201.	3.3	513
3	Determination of confidence intervals of metabolic fluxes estimated from stable isotope measurements. <i>Metabolic Engineering</i> , 2006, 8, 324-337.	3.6	423
4	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
5	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
6	Accurate Assessment of Amino Acid Mass Isotopomer Distributions for Metabolic Flux Analysis. <i>Analytical Chemistry</i> , 2007, 79, 7554-7559.	3.2	247
7	An elementary metabolite unit (EMU) based method of isotopically nonstationary flux analysis. <i>Biotechnology and Bioengineering</i> , 2008, 99, 686-699.	1.7	241
8	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
9	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
10	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
11	A guide to ¹³ C metabolic flux analysis for the cancer biologist. <i>Experimental and Molecular Medicine</i> , 2018, 50, 1-13.	3.2	165
12	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
13	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
14	Engineering the biological conversion of methanol to specialty chemicals in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2017, 39, 49-59.	3.6	137
15	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.	3.6	132
16	High-resolution ¹³ C metabolic flux analysis. <i>Nature Protocols</i> , 2019, 14, 2856-2877.	5.5	132
17	CO ₂ fixation by anaerobic non-photosynthetic mixotrophy for improved carbon conversion. <i>Nature Communications</i> , 2016, 7, 12800.	5.8	128
18	COMPLETE-MFA: Complementary parallel labeling experiments technique for metabolic flux analysis. <i>Metabolic Engineering</i> , 2013, 20, 49-55.	3.6	121

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19	Central metabolic responses to the overproduction of fatty acids in <i>Escherichia coli</i> based on ¹³ C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2014, 111, 575-585.	1.7	112
20	Measuring Deuterium Enrichment of Glucose Hydrogen Atoms by Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2011, 83, 3211-3216.	3.2	111
21	Towards dynamic metabolic flux analysis in CHO cell cultures. <i>Biotechnology Journal</i> , 2012, 7, 61-74.	1.8	107
22	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
23	¹³ C metabolic flux analysis: optimal design of isotopic labeling experiments. <i>Current Opinion in Biotechnology</i> , 2013, 24, 1116-1121.	3.3	100
24	Comprehensive analysis of glucose and xylose metabolism in <i>Escherichia coli</i> under aerobic and anaerobic conditions by ¹³ C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017, 39, 9-18.	3.6	99
25	Integrated ¹³ 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
26	Rational design of ¹³ C-labeling experiments for metabolic flux analysis in mammalian cells. <i>BMC Systems Biology</i> , 2012, 6, 43.	3.0	93
27	Publishing ¹³ C metabolic flux analysis studies: A review and future perspectives. <i>Metabolic Engineering</i> , 2013, 20, 42-48.	3.6	91
28	Tandem mass spectrometry: A novel approach for metabolic flux analysis. <i>Metabolic Engineering</i> , 2011, 13, 225-233.	3.6	90
29	Dynamic metabolic flux analysis—tools for probing transient states of metabolic networks. <i>Current Opinion in Biotechnology</i> , 2013, 24, 973-978.	3.3	89
30	Parallel labeling experiments with [U- ¹³ C]glucose validate <i>E. coli</i> metabolic network model for ¹³ C metabolic flux analysis. <i>Metabolic Engineering</i> , 2012, 14, 533-541.	3.6	86
31	Genome-Scale Metabolic Model for the Green Alga <i>Chlorella vulgaris</i> UTEX 395 Accurately Predicts Phenotypes under Autotrophic, Heterotrophic, and Mixotrophic Growth Conditions. <i>Plant Physiology</i> , 2016, 172, 589-602.	2.3	86
32	Resolving the TCA cycle and pentose-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
33	¹³ C-metabolic flux analysis of co-cultures: A novel approach. <i>Metabolic Engineering</i> , 2015, 31, 132-139.	3.6	79
34	Measuring Complete Isotopomer Distribution of Aspartate Using Gas Chromatography/Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 4628-4632.	3.2	78
35	Selection of tracers for ¹³ C-Metabolic Flux Analysis using Elementary Metabolite Units (EMU) basis vector methodology. <i>Metabolic Engineering</i> , 2012, 14, 150-161.	3.6	78
36	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

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37	Parallel labeling experiments and metabolic flux analysis: Past, present and future methodologies. <i>Metabolic Engineering</i> , 2013, 16, 21-32.	3.6	73
38	Quantifying Biomass Composition by Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 9423-9427.	3.2	70
39	Dissecting the genetic and metabolic mechanisms of adaptation to the knockout of a major metabolic enzyme in <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 222-227.	3.3	70
40	Optimal tracers for parallel labeling experiments and ¹³ C metabolic flux analysis: A new precision and synergy scoring system. <i>Metabolic Engineering</i> , 2016, 38, 10-18.	3.6	68
41	A guide to metabolic flux analysis in metabolic engineering: Methods, tools and applications. <i>Metabolic Engineering</i> , 2021, 63, 2-12.	3.6	67
42	Metabolism of the fast-growing bacterium <i>Vibrio natriegens</i> elucidated by ¹³ C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017, 44, 191-197.	3.6	63
43	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
44	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.	3.6	59
45	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.	3.6	57
46	Parallel labeling experiments for pathway elucidation and ¹³ C metabolic flux analysis. <i>Current Opinion in Biotechnology</i> , 2015, 36, 91-97.	3.3	57
47	Tandem mass spectrometry for measuring stable-isotope labeling. <i>Current Opinion in Biotechnology</i> , 2013, 24, 48-53.	3.3	56
48	Evolution of <i>E. coli</i> on [U- ¹³ C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. <i>PLoS ONE</i> , 2016, 11, e0151130.	1.1	54
49	Synthetic methylotrophy: Strategies to assimilate methanol for growth and chemicals production. <i>Current Opinion in Biotechnology</i> , 2019, 59, 165-174.	3.3	51
50	Characterization of physiological responses to 22 gene knockouts in <i>Escherichia coli</i> central carbon metabolism. <i>Metabolic Engineering</i> , 2016, 37, 102-113.	3.6	50
51	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
52	¹³ 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
53	Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote <i>Chlorella vulgaris</i> . <i>Plant Physiology</i> , 2018, 176, 450-462.	2.3	49
54	A key role for transketolase-like 1 in tumor metabolic reprogramming. <i>Oncotarget</i> , 2016, 7, 51875-51897.	0.8	43

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55	Metabolic network reconstruction, growth characterization and ¹³ C-metabolic flux analysis of the extremophile <i>Thermus thermophilus</i> HB8. <i>Metabolic Engineering</i> , 2014, 24, 173-180.	3.6	41
56	Enzyme I facilitates reverse flux from pyruvate to phosphoenolpyruvate in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2017, 8, 14316.	5.8	41
57	Evaluation of regression models in metabolic physiology: predicting fluxes from isotopic data without knowledge of the pathway. <i>Metabolomics</i> , 2006, 2, 41-52.	1.4	40
58	¹³ 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
59	Metabolism in dense microbial colonies: ¹³ 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
60	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
61	A guide to deciphering microbial interactions and metabolic fluxes in microbiome communities. <i>Current Opinion in Biotechnology</i> , 2020, 64, 230-237.	3.3	40
62	Complete genome sequence, metabolic model construction and phenotypic characterization of <i>Geobacillus</i> LC300, an extremely thermophilic, fast growing, xylose-utilizing bacterium. <i>Metabolic Engineering</i> , 2015, 32, 74-81.	3.6	38
63	Measuring the Composition and Stable-Isotope Labeling of Algal Biomass Carbohydrates via Gas Chromatography/Mass Spectrometry. <i>Analytical Chemistry</i> , 2016, 88, 4624-4628.	3.2	38
64	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.	3.6	37
65	¹³ 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
66	Engineering <i>Escherichia coli</i> for methanol-dependent growth on glucose for metabolite production. <i>Metabolic Engineering</i> , 2020, 60, 45-55.	3.6	32
67	How adaptive evolution reshapes metabolism to improve fitness: recent advances and future outlook. <i>Current Opinion in Chemical Engineering</i> , 2018, 22, 209-215.	3.8	30
68	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.	1.4	30
69	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, 656-667.	1.8	29
70	From <i>Escherichia coli</i> mutant ¹³ C labeling data to a core kinetic model: A kinetic model parameterization pipeline. <i>PLoS Computational Biology</i> , 2019, 15, e1007319.	1.5	28
71	Co-utilization of glucose and xylose by evolved <i>Thermus thermophilus</i> LC113 strain elucidated by ¹³ C metabolic flux analysis and whole genome sequencing. <i>Metabolic Engineering</i> , 2016, 37, 63-71.	3.6	27
72	Tracing metabolism from lignocellulosic biomass and gaseous substrates to products with stable-isotopes. <i>Current Opinion in Biotechnology</i> , 2017, 43, 86-95.	3.3	26

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73	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
74	Improving synthetic methylotrophy via dynamic formaldehyde regulation of pentose phosphate pathway genes and redox perturbation. <i>Metabolic Engineering</i> , 2020, 57, 247-255.	3.6	24
75	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.	1.5	20
76	Computational Approaches in Metabolic Engineering. <i>Journal of Biomedicine and Biotechnology</i> , 2010, 2010, 1-7.	3.0	19
77	Improving the Methanol Tolerance of an <i>Escherichia coli</i> Methylotroph via Adaptive Laboratory Evolution Enhances Synthetic Methanol Utilization. <i>Frontiers in Microbiology</i> , 2021, 12, 638426.	1.5	18
78	Tandem Mass Spectrometry for ¹³ C Metabolic Flux Analysis: Methods and Algorithms Based on EMU Framework. <i>Frontiers in Microbiology</i> , 2019, 10, 31.	1.5	16
79	Using Multiple Tracers for ¹³ C Metabolic Flux Analysis. <i>Methods in Molecular Biology</i> , 2013, 985, 353-365.	0.4	15
80	Adaptive laboratory evolution of methylotrophic <i>Escherichia coli</i> enables synthesis of all amino acids from methanol-derived carbon. <i>Applied Microbiology and Biotechnology</i> , 2021, 105, 869-876.	1.7	14
81	Triggering the stringent response enhances synthetic methanol utilization in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2020, 61, 1-10.	3.6	13
82	Coordinated reprogramming of metabolism and cell function in adipocytes from proliferation to differentiation. <i>Metabolic Engineering</i> , 2022, 69, 221-230.	3.6	11
83	Regulatory interventions improve the biosynthesis of limiting amino acids from methanol carbon to improve synthetic methylotrophy in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2021, 118, 43-57.	1.7	8
84	¹³ C-metabolic flux analysis of <i>Clostridium ljungdahlii</i> illuminates its core metabolism under mixotrophic culture conditions. <i>Metabolic Engineering</i> , 2022, 72, 161-170.	3.6	6