

Maciek R Antoniewicz

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 | 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 | 9.7 | 0 |
| 83 | Coordinated reprogramming of metabolism and cell function in adipocytes from proliferation to differentiation.. <i>Metabolic Engineering</i> , 2021 , 69, 221-230 | 9.7 | 1 |
| 82 | A guide to metabolic flux analysis in metabolic engineering: Methods, tools and applications. <i>Metabolic Engineering</i> , 2021 , 63, 2-12 | 9.7 | 15 |
| 81 | 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 | 4.9 | 3 |
| 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 | 5.7 | 7 |
| 79 | 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 |
| 78 | Engineering <i>Escherichia coli</i> for methanol-dependent growth on glucose for metabolite production. <i>Metabolic Engineering</i> , 2020 , 60, 45-55 | 9.7 | 19 |
| 77 | Triggering the stringent response enhances synthetic methanol utilization in <i>Escherichia coli</i> . <i>Metabolic Engineering</i> , 2020 , 61, 1-10 | 9.7 | 7 |
| 76 | 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 |
| 75 | 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 |
| 74 | High-resolution C metabolic flux analysis. <i>Nature Protocols</i> , 2019 , 14, 2856-2877 | 18.8 | 73 |
| 73 | Synthetic methylotrophy: Strategies to assimilate methanol for growth and chemicals production. <i>Current Opinion in Biotechnology</i> , 2019 , 59, 165-174 | 11.4 | 25 |
| 72 | 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 |
| 71 | 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 | 9.7 | 26 |
| 70 | 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 |
| 69 | 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 | 5 | 21 |
| 68 | 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 | 9.7 | 14 |

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| 67 | A guide to C metabolic flux analysis for the cancer biologist. <i>Experimental and Molecular Medicine</i> , 2018 , 50, 1-13 | 12.8 | 96 |
| 66 | 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 |
| 65 | 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 |
| 64 | Predicting Dynamic Metabolic Demands in the Photosynthetic Eukaryote. <i>Plant Physiology</i> , 2018 , 176, 450-462 | 6.6 | 34 |
| 63 | Methanol assimilation in Escherichia coli 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 |
| 62 | Expression of heterologous non-oxidative pentose phosphate pathway from Bacillus methanolicus and phosphoglucose isomerase deletion improves methanol assimilation and metabolite production by a synthetic Escherichia coli methylotroph. <i>Metabolic Engineering</i> , 2018 , 45, 75-85 | 9.7 | 53 |
| 61 | 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 |
| 60 | 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 |
| 59 | Enzyme I facilitates reverse flux from pyruvate to phosphoenolpyruvate in Escherichia coli. <i>Nature Communications</i> , 2017 , 8, 14316 | 17.4 | 27 |
| 58 | Fast growth phenotype of E. coli K-12 from adaptive laboratory evolution does not require intracellular flux rewiring. <i>Metabolic Engineering</i> , 2017 , 44, 100-107 | 9.7 | 45 |
| 57 | Metabolism of the fast-growing bacterium Vibrio natriegens elucidated by C metabolic flux analysis. <i>Metabolic Engineering</i> , 2017 , 44, 191-197 | 9.7 | 45 |
| 56 | 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 |
| 55 | Engineering the biological conversion of methanol to specialty chemicals in Escherichia coli. <i>Metabolic Engineering</i> , 2017 , 39, 49-59 | 9.7 | 106 |
| 54 | 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 |
| 53 | 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 |
| 52 | (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 |
| 51 | CO fixation by anaerobic non-photosynthetic mixotrophy for improved carbon conversion. <i>Nature Communications</i> , 2016 , 7, 12800 | 17.4 | 86 |
| 50 | 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 |

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| 49 | 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 |
| 48 | 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 |
| 47 | A key role for transketolase-like 1 in tumor metabolic reprogramming. <i>Oncotarget</i> , 2016 , 7, 51875-51893 | 7.3 | 30 |
| 46 | Evolution of E. coli on [U-13C]Glucose Reveals a Negligible Isotopic Influence on Metabolism and Physiology. <i>PLoS ONE</i> , 2016 , 11, e0151130 | 3.7 | 38 |
| 45 | 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 |
| 44 | 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 |
| 43 | Comprehensive metabolic modeling of multiple 13C-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 |
| 42 | Characterization of physiological responses to 22 gene knockouts in Escherichia coli central carbon metabolism. <i>Metabolic Engineering</i> , 2016 , 37, 102-113 | 9.7 | 39 |
| 41 | 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 |
| 40 | 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 |
| 39 | Integrated 13C-metabolic flux analysis of 14 parallel labeling experiments in Escherichia coli. <i>Metabolic Engineering</i> , 2015 , 28, 151-158 | 9.7 | 76 |
| 38 | A roadmap for interpreting (13)C metabolite labeling patterns from cells. <i>Current Opinion in Biotechnology</i> , 2015 , 34, 189-201 | 11.4 | 368 |
| 37 | (13)C-metabolic flux analysis of co-cultures: A novel approach. <i>Metabolic Engineering</i> , 2015 , 31, 132-9 | 9.7 | 60 |
| 36 | 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 |
| 35 | 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 |
| 34 | 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 |
| 33 | 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 |
| 32 | Parallel labeling experiments validate Clostridium acetobutylicum metabolic network model for (13)C metabolic flux analysis. <i>Metabolic Engineering</i> , 2014 , 26, 23-33 | 9.7 | 48 |

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| 31 | Central metabolic responses to the overproduction of fatty acids in Escherichia coli based on 13C-metabolic flux analysis. <i>Biotechnology and Bioengineering</i> , 2014 , 111, 575-85 | 4.9 | 99 |
| 30 | Quantifying biomass composition by gas chromatography/mass spectrometry. <i>Analytical Chemistry</i> , 2014 , 86, 9423-7 | 7.8 | 60 |
| 29 | Metabolic flux analysis of Escherichia coli knockouts: lessons from the Keio collection and future outlook. <i>Current Opinion in Biotechnology</i> , 2014 , 28, 127-33 | 11.4 | 45 |
| 28 | Metabolic network reconstruction, growth characterization and 13C-metabolic flux analysis of the extremophile Thermus thermophilus HB8. <i>Metabolic Engineering</i> , 2014 , 24, 173-80 | 9.7 | 35 |
| 27 | 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 |
| 26 | 13C metabolic flux analysis: optimal design of isotopic labeling experiments. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 1116-21 | 11.4 | 84 |
| 25 | Publishing 13C metabolic flux analysis studies: a review and future perspectives. <i>Metabolic Engineering</i> , 2013 , 20, 42-8 | 9.7 | 71 |
| 24 | COMPLETE-MFA: complementary parallel labeling experiments technique for metabolic flux analysis. <i>Metabolic Engineering</i> , 2013 , 20, 49-55 | 9.7 | 87 |
| 23 | Tandem mass spectrometry for measuring stable-isotope labeling. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 48-53 | 11.4 | 52 |
| 22 | 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 |
| 21 | Using multiple tracers for 13C metabolic flux analysis. <i>Methods in Molecular Biology</i> , 2013 , 985, 353-65 | 1.4 | 14 |
| 20 | Parallel labeling experiments and metabolic flux analysis: Past, present and future methodologies. <i>Metabolic Engineering</i> , 2013 , 16, 21-32 | 9.7 | 64 |
| 19 | Selection of tracers for 13C-metabolic flux analysis using elementary metabolite units (EMU) basis vector methodology. <i>Metabolic Engineering</i> , 2012 , 14, 150-61 | 9.7 | 67 |
| 18 | Towards dynamic metabolic flux analysis in CHO cell cultures. <i>Biotechnology Journal</i> , 2012 , 7, 61-74 | 5.6 | 95 |
| 17 | Parallel labeling experiments with [U-13C]glucose validate E. coli metabolic network model for 13C metabolic flux analysis. <i>Metabolic Engineering</i> , 2012 , 14, 533-41 | 9.7 | 75 |
| 16 | Measuring complete isotopomer distribution of aspartate using gas chromatography/tandem mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 4628-32 | 7.8 | 67 |
| 15 | Rational design of 13C-labeling experiments for metabolic flux analysis in mammalian cells. <i>BMC Systems Biology</i> , 2012 , 6, 43 | 3.5 | 79 |
| 14 | 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 |

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| 13 | 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 |
| 12 | Resolving the TCA cycle and pentose-phosphate pathway of <i>Clostridium acetobutylicum</i> ATCC 824: Isotopomer analysis, in vitro activities and expression analysis. <i>Biotechnology Journal</i> , 2011 , 6, 300-5 | 5.6 | 73 |
| 11 | Measuring deuterium enrichment of glucose hydrogen atoms by gas chromatography/mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 3211-6 | 7.8 | 89 |
| 10 | Tandem mass spectrometry: a novel approach for metabolic flux analysis. <i>Metabolic Engineering</i> , 2011 , 13, 225-33 | 9.7 | 77 |
| 9 | 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 |
| 8 | 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 |
| 7 | An elementary metabolite unit (EMU) based method of isotopically nonstationary flux analysis. <i>Biotechnology and Bioengineering</i> , 2008 , 99, 686-99 | 4.9 | 203 |
| 6 | Accurate assessment of amino acid mass isotopomer distributions for metabolic flux analysis. <i>Analytical Chemistry</i> , 2007 , 79, 7554-9 | 7.8 | 208 |
| 5 | Elementary metabolite units (EMU): a novel framework for modeling isotopic distributions. <i>Metabolic Engineering</i> , 2007 , 9, 68-86 | 9.7 | 426 |
| 4 | 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 |
| 3 | Determination of confidence intervals of metabolic fluxes estimated from stable isotope measurements. <i>Metabolic Engineering</i> , 2006 , 8, 324-37 | 9.7 | 349 |
| 2 | 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 |
| 1 | Laboratory evolution of multiple <i>E. coli</i> strains reveals unifying principles of adaptation but diversity in driving genotypes | | 1 |