# Mark P Styczynski

List of Publications by Year
in descending order



| 51 | 1,416 | 430754 | 345118 |
|---|---|---|---|
| papers | citations | 18 h-index | 36 g-index |

| 59 | 59 | 59 | 2270 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Diverse classes of constraints enable broader applicability of a linear programming-based dynamic metabolic modeling framework. Scientific Reports, 2022, 12, 762. | 1.6 | 0 |
| 2 | Metabolomics Analysis of Cell-Free Systems Using. Methods in Molecular Biology, 2022, 2433, 217-226. | 0.4 | 0 |
| 3 | Systems biology-based analysis of cell-free systems. Current Opinion in Biotechnology, 2022, 75, 102703. | 3.3 | 4 |
| 4 | Untargeted plasma metabolomic analysis of wild bottlenose dolphins (Tursiops truncatus) indicate protein degradation when in poorer health. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2022, 42, 100991. | 0.4 | 1 |
| 5 | Nucleic Acid Partitioning in PEG-Ficoll Protocells. Journal of Chemical & Engineering Data, 2022, 67, 1964-1971. | 1.0 | 1 |
| 6 | Low-cost, point-of-care biomarker quantification. Current Opinion in Biotechnology, 2022, 76, 102738. | 3.3 | 9 |
| 7 | SCOUR: a stepwise machine learning framework for predicting metabolite-dependent regulatory interactions. BMC Bioinformatics, 2021, 22, 365. | 1.2 | 2 |
| 8 | Effective Use of Linear DNA in Cell-Free Expression Systems. Frontiers in Bioengineering and Biotechnology, 2021, 9, 715328. | 2.0 | 15 |
| 9 | Dramatic transcriptomic differences in Macaca mulatta and Macaca fascicularis with Plasmodium knowlesi infections. Scientific Reports, 2021, 11, 19519. | 1.6 | 5 |
| 10 | Metabolic Dynamics in Escherichia coli-Based Cell-Free Systems. ACS Synthetic Biology, 2021, 10, 2252-2265. | 1.9 | 11 |
| 11 | Protocell arrays for simultaneous detection of diverse analytes. Nature Communications, 2021, 12, 5724. | 5.8 | 18 |
| 12 | Point-of-Care Analyte Quantification and Digital Readout via Lysate-Based Cell-Free Biosensors Interfaced with Personal Glucose Monitors. ACS Synthetic Biology, 2021, 10, 2862-2869. | 1.9 | 6 |
| 13 | LK-DFBA: a linear programming-based modeling strategy for capturing dynamics and metabolite-dependent regulation in metabolism. BMC Bioinformatics, 2020, 21, 93. | 1.2 | 7 |
| 14 | The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View. Trends in Cancer, 2020, 6, 192-204. | 3.8 | 162 |
| 15 | Active Analyte Import Improves the Dynamic Range and Sensitivity of a Vitamin B<sub>12</sub> Biosensor. ACS Synthetic Biology, 2020, 9, 402-411. | 1.9 | 22 |
| 16 | ElectroPen: An ultra-lowâ€“cost, electricity-free, portable electroporator. PLoS Biology, 2020, 18, e3000589. | 2.6 | 16 |
| 17 | Humoral immunity prevents clinical malaria during Plasmodium relapses without eliminating gametocytes. PLoS Pathogens, 2019, 15, e1007974. | 2.1 | 17 |
| 18 | Metabolic Profiling of Escherichia coli-Based Cell-Free Expression Systems for Process Optimization. Industrial & Engineering Chemistry Research, 2019, 58, 22472-22482. | 1.8 | 30 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Point-of-care biomarker quantification enabled by sample-specific calibration. Science Advances, 2019, 5, eaax4473. | 4.7 | 73 |
| 20 | The Metabolomics Societyâ€"Current State of the Membership and Future Directions. Metabolites, 2019, 9, 89. | 1.3 | 2 |
| 21 | Gas Chromatographyâ€"Mass Spectrometry Microbial Metabolomics for Applications in Strain Optimization. Methods in Molecular Biology, 2019, 1927, 179-189. | 0.4 | 1 |
| 22 | Dynamic and tunable metabolite control for robust minimal-equipment assessment of serum zinc. Nature Communications, 2019, 10, 5514. | 5.8 | 26 |
| 23 | Small molecule signaling, regulation, and potential applications in cellular therapeutics. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2018, 10, e1405. | 6.6 | 14 |
| 24 | Metabolic modeling helps interpret transcriptomic changes during malaria. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 2329-2340. | 1.8 | 18 |
| 25 | NS-kNN: a modified k-nearest neighbors approach for imputing metabolomics data. Metabolomics, 2018, 14, 153. | 1.4 | 44 |
| 26 | Systems Biology-Based Investigation of Hostâ€"Plasmodium Interactions. Trends in Parasitology, 2018, 34, 617-632. | 1.5 | 19 |
| 27 | Metabolomics Analysis of the Toxic Effects of the Production of Lycopene and Its Precursors. Frontiers in Microbiology, 2018, 9, 760. | 1.5 | 19 |
| 28 | Development of a Pigment-Based Whole-Cell Zinc Biosensor for Human Serum. ACS Synthetic Biology, 2018, 7, 267-275. | 1.9 | 59 |
| 29 | Precise control of lycopene production to enable a fast-responding, minimal-equipment biosensor. Metabolic Engineering, 2017, 43, 46-53. | 3.6 | 23 |
| 30 | Integrative analysis associates monocytes with insufficient erythropoiesis during acute Plasmodium cynomolgi malaria in rhesus macaques. Malaria Journal, 2017, 16, 384. | 0.8 | 20 |
| 31 | Live demonstration: A 1024-pixel CMOS multi-modality sensing array for cell-based assays. , 2016, , . | | 1 |
| 32 | Editorial overview: Systems biology-the intersection of experiments and computation, underpinning biotechnology. Current Opinion in Biotechnology, 2016, 39, iv-vi. | 3.3 | 0 |
| 33 | OVCAR-3 Spheroid-Derived Cells Display Distinct Metabolic Profiles. PLoS ONE, 2015, 10, e0118262. | 1.1 | 29 |
| 34 | A tree-like Bayesian structure learning algorithm for small-sample datasets from complex biological model systems. BMC Systems Biology, 2015, 9, 49. | 3.0 | 6 |
| 35 | A Multi-Modality CMOS Sensor Array for Cell-Based Assay and Drug Screening. IEEE Transactions on Biomedical Circuits and Systems, 2015, 9, 801-814. | 2.7 | 65 |
| 36 | Differential metabolite levels in response to spawning-induced inappetence in Atlantic salmon Salmo salar. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2015, 13, 52-59. | 0.4 | 13 |

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|---|---|---|---|
| 37 | From genome-scale data to models of infectious disease: A Bayesian network-based strategy to drive model development. Mathematical Biosciences, 2015, 270, 156-168. | 0.9 | 8 |
| 38 | Precise metabolic engineering of carotenoid biosynthesis in Escherichia coli towards a low-cost biosensor. Metabolic Engineering, 2015, 31, 171-180. | 3.6 | 28 |
| 39 | Precision metabolic engineering: The design of responsive, selective, and controllable metabolic systems. Metabolic Engineering, 2015, 31, 123-131. | 3.6 | 56 |
| 40 | Manipulation of metabolism in complex eukaryotic systems to control cellular state. Current Opinion in Chemical Engineering, 2015, 10, 63-69. | 3.8 | 4 |
| 41 | Improved metabolite profile smoothing for flux estimation. Molecular BioSystems, 2015, 11, 2394-2405. | 2.9 | 6 |
| 42 | Metabolomics identifies the intersection of phosphoethanolamine with menaquinone-triggered apoptosis in an in vitro model of leukemia. Molecular BioSystems, 2015, 11, 2406-2416. | 2.9 | 25 |
| 43 | Comparative transcriptomics and metabolomics in a rhesus macaque drug administration study. Frontiers in Cell and Developmental Biology, 2014, 2, 54. | 1.8 | 15 |
| 44 | Distinct metabolic responses of an ovarian cancer stem cell line. BMC Systems Biology, 2014, 8, 134. | 3.0 | 23 |
| 45 | Applications of metabolomics in cancer research. Journal of Carcinogenesis, 2013, 12, 9. | 2.5 | 83 |
| 46 | Systematic Applications of Metabolomics in Metabolic Engineering. Metabolites, 2012, 2, 1090-1122. | 1.3 | 20 |
| 47 | BLOSUM62 miscalculations improve search performance. Nature Biotechnology, 2008, 26, 274-275. | 9.4 | 79 |
| 48 | Systematic Identification of Conserved Metabolites in GC/MS Data for Metabolomics and Biomarker Discovery. Analytical Chemistry, 2007, 79, 966-973. | 3.2 | 223 |
| 49 | Overview of computational methods for the inference of gene regulatory networks. Computers and Chemical Engineering, 2005, 29, 519-534. | 2.0 | 48 |
| 50 | Reliable computation of equilibrium states and bifurcations in food chain models. Computers and Chemical Engineering, 2004, 28, 1981-1996. | 2.0 | 9 |
| 51 | An extension and novel solution to the (l,d)-motif challenge problem. Genome Informatics, 2004, 15, 63-71. | 0.4 | 11 |