

# Mary J Dunlop

## List of Publications by Year in descending order

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Version: 2024-02-01

45  
papers

2,437  
citations

304368

22  
h-index

264894

42  
g-index

59  
all docs

59  
docs citations

59  
times ranked

2842  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | DeLTA 2.0: A deep learning pipeline for quantifying single-cell spatial and temporal dynamics. PLoS Computational Biology, 2022, 18, e1009797.  | 1.5 | 43        |
| 2  | Anticipating antibiotic resistance. Science, 2022, 375, 818-819.  | 6.0 | 3         |
| 3  | Dynamic gene expression and growth underlie cell-to-cell heterogeneity in <i>Escherichia coli</i> stress response. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115032119. | 3.3 | 33        |
| 4  | Transcriptional Tuning of Mevalonate Pathway Enzymes to Identify the Impact on Limonene Production in <i>Escherichia coli</i> . ACS Omega, 2022, 7, 18331-18338.  | 1.6 | 6         |
| 5  | Microsecond fingerprint stimulated Raman spectroscopic imaging by ultrafast tuning and spatial-spectral learning. Nature Communications, 2021, 12, 3052.  | 5.8 | 58        |
| 6  | Programmable gene regulation for metabolic engineering using decoy transcription factor binding sites. Nucleic Acids Research, 2021, 49, 1163-1172.   | 6.5 | 29        |
| 7  | Functional roles of microbial cell-to-cell heterogeneity and emerging technologies for analysis and control. Current Opinion in Microbiology, 2020, 57, 87-94.  | 2.3 | 19        |
| 8  | Core Competencies for Undergraduates in Bioengineering and Biomedical Engineering: Findings, Consequences, and Recommendations. Annals of Biomedical Engineering, 2020, 48, 905-912.  | 1.3 | 37        |
| 9  | Light-Inducible Recombinases for Bacterial Optogenetics. ACS Synthetic Biology, 2020, 9, 227-235.   | 1.9 | 42        |
| 10 | DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. PLoS Computational Biology, 2020, 16, e1007673.   | 1.5 | 137       |
| 11 | Mapping the Role of AcrAB-TolC Efflux Pumps in the Evolution of Antibiotic Resistance Reveals Near-MIC Treatments Facilitate Resistance Acquisition. MSphere, 2020, 5, .  | 1.3 | 14        |
| 12 | DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.   |     | 0         |
| 13 | DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.   |     | 0         |
| 14 | DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.   |     | 0         |
| 15 | Forecasting cell fate during antibiotic exposure using stochastic gene expression. Communications Biology, 2019, 2, 259.  | 2.0 | 15        |
| 16 | Salicylate Increases Fitness Cost Associated with MarA-Mediated Antibiotic Resistance. Biophysical Journal, 2019, 117, 563-571.   | 0.2 | 10        |
| 17 | Cell-machine interfaces for characterizing gene regulatory network dynamics. Current Opinion in Systems Biology, 2019, 14, 1-8.   | 1.3 | 31        |
| 18 | Distinct timescales of RNA regulators enable the construction of a genetic pulse generator. Biotechnology and Bioengineering, 2019, 116, 1139-1151.   | 1.7 | 40        |

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 19 | Controlling and exploiting cell-to-cell variation in metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2019, 57, 10-16.  | 3.3 | 27        |
| 20 | Making Waves with Synthetic Oscillators. <i>Cell Systems</i> , 2018, 6, 406-407.  | 2.9 | 6         |
| 21 | Mathematical Modeling of RNA-Based Architectures for Closed Loop Control of Gene Expression. <i>ACS Synthetic Biology</i> , 2018, 7, 1219-1228.   | 1.9 | 42        |
| 22 | Design and Selection of a Synthetic Feedback Loop for Optimizing Biofuel Tolerance. <i>ACS Synthetic Biology</i> , 2018, 7, 16-23.  | 1.9 | 47        |
| 23 | Stress Introduction Rate Alters the Benefit of AcrAB-TolC Efflux Pumps. <i>Journal of Bacteriology</i> , 2018, 200, .   | 1.0 | 27        |
| 24 | Heterogeneity in efflux pump expression predisposes antibiotic-resistant cells to mutation. <i>Science</i> , 2018, 362, 686-690.  | 6.0 | 178       |
| 25 | Active degradation of MarA controls coordination of its downstream targets. <i>PLoS Computational Biology</i> , 2018, 14, e1006634.   | 1.5 | 10        |
| 26 | Antibiotic export by efflux pumps affects growth of neighboring bacteria. <i>Scientific Reports</i> , 2018, 8, 15120.   | 1.6 | 18        |
| 27 | Bacterial persistence induced by salicylate via reactive oxygen species. <i>Scientific Reports</i> , 2017, 7, 43839.  | 1.6 | 51        |
| 28 | Expression of Heterologous Sigma Factor Expands the Searchable Space for Biofuel Tolerance Mechanisms. <i>ACS Synthetic Biology</i> , 2017, 6, 1343-1350.   | 1.9 | 10        |
| 29 | Customized Regulation of Diverse Stress Response Genes by the Multiple Antibiotic Resistance Activator MarA. <i>PLoS Computational Biology</i> , 2017, 13, e1005310.  | 1.5 | 17        |
| 30 | Phenotypic Diversity Using Bimodal and Unimodal Expression of Stress Response Proteins. <i>Biophysical Journal</i> , 2016, 110, 2278-2287.  | 0.2 | 6         |
| 31 | Stochastic expression of a multiple antibiotic resistance activator confers transient resistance in single cells. <i>Scientific Reports</i> , 2016, 6, 19538.   | 1.6 | 85        |
| 32 | Performing selections under dynamic conditions for synthetic biology applications. <i>Integrative Biology (United Kingdom)</i> , 2016, 8, 556-563.  | 0.6 | 1         |
| 33 | Engineering improved bio-jet fuel tolerance in <i>Escherichia coli</i> using a transgenic library from the hydrocarbon-degrader <i>Marinobacter aquaeolei</i> . <i>Biotechnology for Biofuels</i> , 2015, 8, 165. | 6.2 | 22        |
| 34 | Noise and Low-Level Dynamics Can Coordinate Multicomponent Bet Hedging Mechanisms. <i>Biophysical Journal</i> , 2015, 108, 184-193.   | 0.2 | 15        |
| 35 | Trade-Offs in Improving Biofuel Tolerance Using Combinations of Efflux Pumps. <i>ACS Synthetic Biology</i> , 2015, 4, 1056-1063.  | 1.9 | 61        |
| 36 | Development of a Native <i>Escherichia coli</i> Induction System for Ionic Liquid Tolerance. <i>PLoS ONE</i> , 2014, 9, e101115.  | 1.1 | 31        |

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|----|---|-----|-----------|
| 37 | Quantitative Single-Cell Gene Expression Measurements in Bacteria Using Time-Lapse Microscopy. <i>Microscopy and Microanalysis</i> , 2014, 20, 1174-1175.   | 0.2 | 2         |
| 38 | Tunable Stochastic Pulsing in the Escherichia coli Multiple Antibiotic Resistance Network from Interlinked Positive and Negative Feedback Loops. <i>PLoS Computational Biology</i> , 2013, 9, e1003229. | 1.5 | 41        |
| 39 | Synthetic Feedback Loop Model for Increasing Microbial Biofuel Production Using a Biosensor. <i>Frontiers in Microbiology</i> , 2012, 3, 360.   | 1.5 | 43        |
| 40 | Engineering microbial biofuel tolerance and export using efflux pumps. <i>Molecular Systems Biology</i> , 2011, 7, 487.   | 3.2 | 440       |
| 41 | Engineering microbes for tolerance to next-generation biofuels. <i>Biotechnology for Biofuels</i> , 2011, 4, 32.  | 6.2 | 246       |
| 42 | A model for improving microbial biofuel production using a synthetic feedback loop. <i>Systems and Synthetic Biology</i> , 2010, 4, 95-104.   | 1.0 | 127       |
| 43 | A synthetic three-color scaffold for monitoring genetic regulation and noise. <i>Journal of Biological Engineering</i> , 2010, 4, 10.   | 2.0 | 67        |
| 44 | Regulatory activity revealed by dynamic correlations in gene expression noise. <i>Nature Genetics</i> , 2008, 40, 1493-1498.  | 9.4 | 210       |
| 45 | Multiple Functions of a Feed-Forward-Loop Gene Circuit. <i>Journal of Molecular Biology</i> , 2005, 349, 501-514.   | 2.0 | 75        |