Mary J Dunlop

List of Publications by Year in descending order

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304743 265206 2,437 45 22 42 h-index citations g-index papers 59 59 59 2842 docs citations times ranked citing authors all docs

#	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.	3.2	43
2	Anticipating antibiotic resistance. Science, 2022, 375, 818-819.	12.6	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.	7.1	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.	3.5	6
5	Microsecond fingerprint stimulated Raman spectroscopic imaging by ultrafast tuning and spatial-spectral learning. Nature Communications, 2021, 12, 3052.	12.8	58
6	Programmable gene regulation for metabolic engineering using decoy transcription factor binding sites. Nucleic Acids Research, 2021, 49, 1163-1172.	14.5	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.	5.1	19
8	Core Competencies for Undergraduates in Bioengineering and Biomedical Engineering: Findings, Consequences, and Recommendations. Annals of Biomedical Engineering, 2020, 48, 905-912.	2.5	37
9	Light-Inducible Recombinases for Bacterial Optogenetics. ACS Synthetic Biology, 2020, 9, 227-235.	3.8	42
10	DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. PLoS Computational Biology, 2020, 16, e1007673.	3.2	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, .	2.9	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.	4.4	15
16	Salicylate Increases Fitness Cost Associated withÂMarA-Mediated Antibiotic Resistance. Biophysical Journal, 2019, 117, 563-571.	0.5	10
17	Cell-machine interfaces for characterizing gene regulatory network dynamics. Current Opinion in Systems Biology, 2019, 14, 1-8.	2.6	31
18	Distinct timescales of RNA regulators enable the construction of a genetic pulse generator. Biotechnology and Bioengineering, 2019, 116, 1139-1151.	3.3	40

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19	Controlling and exploiting cell-to-cell variation in metabolic engineering. Current Opinion in Biotechnology, 2019, 57, 10-16.	6.6	27
20	Making Waves with Synthetic Oscillators. Cell Systems, 2018, 6, 406-407.	6.2	6
21	Mathematical Modeling of RNA-Based Architectures for Closed Loop Control of Gene Expression. ACS Synthetic Biology, 2018, 7, 1219-1228.	3.8	42
22	Design and Selection of a Synthetic Feedback Loop for Optimizing Biofuel Tolerance. ACS Synthetic Biology, 2018, 7, 16-23.	3.8	47
23	Stress Introduction Rate Alters the Benefit of AcrAB-TolC Efflux Pumps. Journal of Bacteriology, 2018, 200, .	2.2	27
24	Heterogeneity in efflux pump expression predisposes antibiotic-resistant cells to mutation. Science, 2018, 362, 686-690.	12.6	178
25	Active degradation of MarA controls coordination of its downstream targets. PLoS Computational Biology, 2018, 14, e1006634.	3.2	10
26	Antibiotic export by efflux pumps affects growth of neighboring bacteria. Scientific Reports, 2018, 8, 15120.	3.3	18
27	Bacterial persistence induced by salicylate via reactive oxygen species. Scientific Reports, 2017, 7, 43839.	3.3	51
28	Expression of Heterologous Sigma Factor Expands the Searchable Space for Biofuel Tolerance Mechanisms. ACS Synthetic Biology, 2017, 6, 1343-1350.	3.8	10
29	Customized Regulation of Diverse Stress Response Genes by the Multiple Antibiotic Resistance Activator MarA. PLoS Computational Biology, 2017, 13, e1005310.	3.2	17
30	Phenotypic Diversity Using Bimodal and Unimodal Expression of Stress Response Proteins. Biophysical Journal, 2016, 110, 2278-2287.	0.5	6
31	Stochastic expression of a multiple antibiotic resistance activator confers transient resistance in single cells. Scientific Reports, 2016, 6, 19538.	3.3	85
32	Performing selections under dynamic conditions for synthetic biology applications. Integrative Biology (United Kingdom), 2016, 8, 556-563.	1.3	1
33	Engineering improved bio-jet fuel tolerance in Escherichia coli using a transgenic library from the hydrocarbon-degrader Marinobacter aquaeolei. Biotechnology for Biofuels, 2015, 8, 165.	6.2	22
34	Noise and Low-Level Dynamics Can Coordinate Multicomponent Bet Hedging Mechanisms. Biophysical Journal, 2015, 108, 184-193.	0.5	15
35	Trade-Offs in Improving Biofuel Tolerance Using Combinations of Efflux Pumps. ACS Synthetic Biology, 2015, 4, 1056-1063.	3.8	61
36	Development of a Native Escherichia coli Induction System for Ionic Liquid Tolerance. PLoS ONE, 2014, 9, e101115.	2.5	31

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37	Quantitative Single-Cell Gene Expression Measurements in Bacteria Using Time-Lapse Microscopy. Microscopy and Microanalysis, 2014, 20, 1174-1175.	0.4	2
38	Tunable Stochastic Pulsing in the Escherichia coli Multiple Antibiotic Resistance Network from Interlinked Positive and Negative Feedback Loops. PLoS Computational Biology, 2013, 9, e1003229.	3.2	41
39	Synthetic Feedback Loop Model for Increasing Microbial Biofuel Production Using a Biosensor. Frontiers in Microbiology, 2012, 3, 360.	3.5	43
40	Engineering microbial biofuel tolerance and export using efflux pumps. Molecular Systems Biology, 2011, 7, 487.	7.2	440
41	Engineering microbes for tolerance to next-generation biofuels. Biotechnology for Biofuels, 2011, 4, 32.	6.2	246
42	A model for improving microbial biofuel production using a synthetic feedback loop. Systems and Synthetic Biology, 2010, 4, 95-104.	1.0	127
43	A synthetic three-color scaffold for monitoring genetic regulation and noise. Journal of Biological Engineering, 2010, 4, 10.	4.7	67
44	Regulatory activity revealed by dynamic correlations in gene expression noise. Nature Genetics, 2008, 40, 1493-1498.	21.4	210
45	Multiple Functions of a Feed-Forward-Loop Gene Circuit. Journal of Molecular Biology, 2005, 349, 501-514.	4.2	75