Mary J Dunlop

List of Publications by Year
in descending order

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

#	Article	IF	Citations
1	Engineering microbial biofuel tolerance and export using efflux pumps. Molecular Systems Biology, 2011, 7, 487.	7.2	440
2	Engineering microbes for tolerance to next-generation biofuels. Biotechnology for Biofuels, 2011, 4, 32.	6.2	246
3	Regulatory activity revealed by dynamic correlations in gene expression noise. Nature Genetics, 2008, 40, 1493-1498.	21.4	210
4	Heterogeneity in efflux pump expression predisposes antibiotic-resistant cells to mutation. Science, 2018, 362, 686-690.	12.6	178
5	DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. PLoS Computational Biology, 2020, 16, e1007673.	3.2	137
6	A model for improving microbial biofuel production using a synthetic feedback loop. Systems and Synthetic Biology, 2010, 4, 95-104.	1.0	127
7	Stochastic expression of a multiple antibiotic resistance activator confers transient resistance in single cells. Scientific Reports, 2016, 6, 19538.	3.3	85
8	Multiple Functions of a Feed-Forward-Loop Gene Circuit. Journal of Molecular Biology, 2005, 349, 501-514.	4.2	75
9	A synthetic three-color scaffold for monitoring genetic regulation and noise. Journal of Biological Engineering, 2010, 4, 10.	4.7	67
10	Trade-Offs in Improving Biofuel Tolerance Using Combinations of Efflux Pumps. ACS Synthetic Biology, 2015, 4, 1056-1063.	3.8	61
11	Microsecond fingerprint stimulated Raman spectroscopic imaging by ultrafast tuning and spatial-spectral learning. Nature Communications, 2021, 12, 3052.	12.8	58
12	Bacterial persistence induced by salicylate via reactive oxygen species. Scientific Reports, 2017, 7, 43839.	3.3	51
13	Design and Selection of a Synthetic Feedback Loop for Optimizing Biofuel Tolerance. ACS Synthetic Biology, 2018, 7, 16-23.	3.8	47
14	Synthetic Feedback Loop Model for Increasing Microbial Biofuel Production Using a Biosensor. Frontiers in Microbiology, 2012, 3, 360.	3.5	43
15	DeLTA 2.0: A deep learning pipeline for quantifying single-cell spatial and temporal dynamics. PLoS Computational Biology, 2022, 18, e1009797.	3.2	43
16	Mathematical Modeling of RNA-Based Architectures for Closed Loop Control of Gene Expression. ACS Synthetic Biology, 2018, 7, 1219-1228.	3.8	42
17	Light-Inducible Recombinases for Bacterial Optogenetics. ACS Synthetic Biology, 2020, 9, 227-235.	3.8	42
18	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

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19	Distinct timescales of RNA regulators enable the construction of a genetic pulse generator. Biotechnology and Bioengineering, 2019, 116, 1139-1151.	3.3	40
20	Core Competencies for Undergraduates in Bioengineering and Biomedical Engineering: Findings, Consequences, and Recommendations. Annals of Biomedical Engineering, 2020, 48, 905-912.	2.5	37
21	Dynamic gene expression and growth underlie cell-to-cell heterogeneity in Escherichia coli stress response. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2115032119.	7.1	33
22	Development of a Native Escherichia coli Induction System for Ionic Liquid Tolerance. PLoS ONE, 2014, 9, e101115.	2.5	31
23	Cell-machine interfaces for characterizing gene regulatory network dynamics. Current Opinion in Systems Biology, 2019, 14, 1-8.	2.6	31
24	Programmable gene regulation for metabolic engineering using decoy transcription factor binding sites. Nucleic Acids Research, 2021, 49, 1163-1172.	14.5	29
25	Stress Introduction Rate Alters the Benefit of AcrAB-TolC Efflux Pumps. Journal of Bacteriology, 2018, 200, .	2.2	27
26	Controlling and exploiting cell-to-cell variation in metabolic engineering. Current Opinion in Biotechnology, 2019, 57, 10-16.	6.6	27
27	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
28	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
29	Antibiotic export by efflux pumps affects growth of neighboring bacteria. Scientific Reports, 2018, 8, 15120.	3.3	18
30	Customized Regulation of Diverse Stress Response Genes by the Multiple Antibiotic Resistance Activator MarA. PLoS Computational Biology, 2017, 13, e1005310.	3.2	17
31	Noise and Low-Level Dynamics Can Coordinate Multicomponent Bet Hedging Mechanisms. Biophysical Journal, 2015, 108, 184-193.	0.5	15
32	Forecasting cell fate during antibiotic exposure using stochastic gene expression. Communications Biology, 2019, 2, 259.	4.4	15
33	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
34	Expression of Heterologous Sigma Factor Expands the Searchable Space for Biofuel Tolerance Mechanisms. ACS Synthetic Biology, 2017, 6, 1343-1350.	3.8	10
35	Active degradation of MarA controls coordination of its downstream targets. PLoS Computational Biology, 2018, 14, e1006634.	3.2	10
36	Salicylate Increases Fitness Cost Associated withÂMarA-Mediated Antibiotic Resistance. Biophysical Journal, 2019, 117, 563-571.	0.5	10

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37	Phenotypic Diversity Using Bimodal and Unimodal Expression of Stress Response Proteins. Biophysical Journal, 2016, 110, 2278-2287.	0.5	6
38	Making Waves with Synthetic Oscillators. Cell Systems, 2018, 6, 406-407.	6.2	6
39	Transcriptional Tuning of Mevalonate Pathway Enzymes to Identify the Impact on Limonene Production in Escherichia coli. ACS Omega, 2022, 7, 18331-18338.	3.5	6
40	Anticipating antibiotic resistance. Science, 2022, 375, 818-819.	12.6	3
41	Quantitative Single-Cell Gene Expression Measurements in Bacteria Using Time-Lapse Microscopy. Microscopy and Microanalysis, 2014, 20, 1174-1175.	0.4	2
42	Performing selections under dynamic conditions for synthetic biology applications. Integrative Biology (United Kingdom), 2016, 8, 556-563.	1.3	1
43	DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.		0
44	DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.		0
45	DeLTA: Automated cell segmentation, tracking, and lineage reconstruction using deep learning. , 2020, 16, e1007673.		0