Keesha E Erickson

List of Publications by Year
in descending order

19 papers	363 citations	840776 11 h-index	839539 18 g-index
20 all docs	20 docs citations	20 times ranked	571 citing authors

#	Article	IF	Citations
1	Spaceflight Modifies Escherichia coli Gene Expression in Response to Antibiotic Exposure and Reveals Role of Oxidative Stress Response. Frontiers in Microbiology, 2018, 9, 310.	3.5	77
2	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. Cell Systems, 2018, 7, 161-179.e14.	6.2	53
3	Transcriptome-Level Signatures in Gene Expression and Gene Expression Variability during Bacterial Adaptive Evolution. MSphere, 2017, 2, .	2.9	31
4	CRISPR Perturbation of Gene Expression Alters Bacterial Fitness under Stress and Reveals Underlying Epistatic Constraints. ACS Synthetic Biology, 2017, 6, 94-107.	3.8	29
5	Gene Expression Variability Underlies Adaptive Resistance in Phenotypically Heterogeneous Bacterial Populations. ACS Infectious Diseases, 2015, 1, 555-567.	3.8	21
6	Transcriptome-based design of antisense inhibitors potentiates carbapenem efficacy in CRE *Escherichia coli*. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 30699-30709.	7.1	20
7	The Resistome: A Comprehensive Database of Escherichia coli Resistance Phenotypes. ACS Synthetic Biology, 2016, 5, 1566-1577.	3.8	17
8	Facile accelerated specific therapeutic (FAST) platform develops antisense therapies to counter multidrug-resistant bacteria. Communications Biology, 2021, 4, 331.	4.4	17
9	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. Seminars in Cancer Biology, 2019, 54, 162-173.	9.6	16
10	Generalizing Gillespie's Direct Method to Enable Network-Free Simulations. Bulletin of Mathematical Biology, 2019, 81, 2822-2848.	1.9	15
11	ROS mediated selection for increased NADPH availability in Escherichia coli. Biotechnology and Bioengineering, 2017, 114, 2685-2689.	3.3	12
12	The Tolerome: A Database of Transcriptome-Level Contributions to Diverse *Escherichia coli* Resistance and Tolerance Phenotypes. ACS Synthetic Biology, 2017, 6, 2302-2315.	3.8	11
13	Complex systems in metabolic engineering. Current Opinion in Biotechnology, 2015, 36, 107-114.	6.6	10
14	CONSTRICTOR: Constraint Modification Provides Insight into Design of Biochemical Networks. PLoS ONE, 2014, 9, e113820.	2.5	9
15	Potentiating antibiotic efficacy via perturbation of non-essential gene expression. Communications Biology, 2021, 4, 1267.	4.4	9
16	Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. PLoS Computational Biology, 2019, 15, e1006706.	3.2	8
17	Draft Genome Sequence for a Clinical Isolate of Vancomycin-Resistant Enterococcus faecalis. Genome Announcements, 2016, 4, .	0.8	3
18	Draft Genome Sequences of Clinical Isolates of Multidrug-Resistant Acinetobacter baumannii. Genome Announcements, 2017, 5, .	0.8	2

#	Article	IF	Citations
19	A Step-by-Step Guide to Using BioNetFit. Methods in Molecular Biology, 2019, 1945, 391-419.	0.9	2