

# Keesha E Erickson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1188500/publications.pdf>

Version: 2024-02-01

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	Facile accelerated specific therapeutic (FAST) platform develops antisense therapies to counter multidrug-resistant bacteria. <i>Communications Biology</i> , 2021, 4, 331.	4.4	17
2	Potentiating antibiotic efficacy via perturbation of non-essential gene expression. <i>Communications Biology</i> , 2021, 4, 1267.	4.4	9
3	Transcriptome-based design of antisense inhibitors potentiates carbapenem efficacy in CRE <i>Escherichia coli</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 30699-30709.	7.1	20
4	Modeling cell line-specific recruitment of signaling proteins to the insulin-like growth factor 1 receptor. <i>PLoS Computational Biology</i> , 2019, 15, e1006706.	3.2	8
5	A Step-by-Step Guide to Using BioNetFit. <i>Methods in Molecular Biology</i> , 2019, 1945, 391-419.	0.9	2
6	New insights into RAS biology reinvigorate interest in mathematical modeling of RAS signaling. <i>Seminars in Cancer Biology</i> , 2019, 54, 162-173.	9.6	16
7	Generalizing Gillespie's Direct Method to Enable Network-Free Simulations. <i>Bulletin of Mathematical Biology</i> , 2019, 81, 2822-2848.	1.9	15
8	Spaceflight Modifies <i>Escherichia coli</i> Gene Expression in Response to Antibiotic Exposure and Reveals Role of Oxidative Stress Response. <i>Frontiers in Microbiology</i> , 2018, 9, 310.	3.5	77
9	Dissecting RAF Inhibitor Resistance by Structure-based Modeling Reveals Ways to Overcome Oncogenic RAS Signaling. <i>Cell Systems</i> , 2018, 7, 161-179.e14.	6.2	53
10	Transcriptome-Level Signatures in Gene Expression and Gene Expression Variability during Bacterial Adaptive Evolution. <i>MSphere</i> , 2017, 2, .	2.9	31
11	Draft Genome Sequences of Clinical Isolates of Multidrug-Resistant <i>Acinetobacter baumannii</i> . <i>Genome Announcements</i> , 2017, 5, .	0.8	2
12	The Tolerome: A Database of Transcriptome-Level Contributions to Diverse <i>Escherichia coli</i> Resistance and Tolerance Phenotypes. <i>ACS Synthetic Biology</i> , 2017, 6, 2302-2315.	3.8	11
13	ROS mediated selection for increased NADPH availability in <i>Escherichia coli</i> . <i>Biotechnology and Bioengineering</i> , 2017, 114, 2685-2689.	3.3	12
14	CRISPR Perturbation of Gene Expression Alters Bacterial Fitness under Stress and Reveals Underlying Epistatic Constraints. <i>ACS Synthetic Biology</i> , 2017, 6, 94-107.	3.8	29
15	The Resistome: A Comprehensive Database of <i>Escherichia coli</i> Resistance Phenotypes. <i>ACS Synthetic Biology</i> , 2016, 5, 1566-1577.	3.8	17
16	Draft Genome Sequence for a Clinical Isolate of Vancomycin-Resistant <i>Enterococcus faecalis</i> . <i>Genome Announcements</i> , 2016, 4, .	0.8	3
17	Gene Expression Variability Underlies Adaptive Resistance in Phenotypically Heterogeneous Bacterial Populations. <i>ACS Infectious Diseases</i> , 2015, 1, 555-567.	3.8	21
18	Complex systems in metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2015, 36, 107-114.	6.6	10

#	ARTICLE	IF	CITATIONS
19	CONSTRUCTOR: Constraint Modification Provides Insight into Design of Biochemical Networks. PLoS ONE, 2014, 9, e113820.	2.5	9