

Richard Szubin

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

1,987
citations

331670

21
h-index

302126

39
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46
all docs

46
docs citations

46
times ranked

2250
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2014, 5, 4910.	12.8	241
2	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of <i>Escherichia coli</i> K-12 MG1655 on Glucose Minimal Medium. <i>Applied and Environmental Microbiology</i> , 2015, 81, 17-30.	3.1	235
3	Genome-wide Reconstruction of OxyR and SoxRS Transcriptional Regulatory Networks under Oxidative Stress in <i>Escherichia coli</i> K-12 MG1655. <i>Cell Reports</i> , 2015, 12, 1289-1299.	6.4	174
4	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
5	Multi-omic data integration enables discovery of hidden biological regularities. <i>Nature Communications</i> , 2016, 7, 13091.	12.8	141
6	Decoding genome-wide GadEWX-transcriptional regulatory networks reveals multifaceted cellular responses to acid stress in <i>Escherichia coli</i> . <i>Nature Communications</i> , 2015, 6, 7970.	12.8	87
7	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14368-14373.	7.1	79
8	Revealing 29 sets of independently modulated genes in <i>Staphylococcus aureus</i> , their regulators, and role in key physiological response. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 17228-17239.	7.1	60
9	Evolution of gene knockout strains of <i>E. coli</i> reveal regulatory architectures governed by metabolism. <i>Nature Communications</i> , 2018, 9, 3796.	12.8	59
10	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 25287-25292.	7.1	56
11	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. <i>Molecular Biology and Evolution</i> , 2020, 37, 660-667.	8.9	52
12	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in <i>Escherichia coli</i> strains lacking the Phosphotransferase System. <i>Metabolic Engineering</i> , 2018, 48, 233-242.	7.0	43
13	Adaptation to the coupling of glycolysis to toxic methylglyoxal production in <i>tpiA</i> deletion strains of <i>Escherichia coli</i> requires synchronized and counterintuitive genetic changes. <i>Metabolic Engineering</i> , 2018, 48, 82-93.	7.0	38
14	Metagenomics-Based, Strain-Level Analysis of <i>Escherichia coli</i> From a Time-Series of Microbiome Samples From a Crohn's Disease Patient. <i>Frontiers in Microbiology</i> , 2018, 9, 2559.	3.5	37
15	Revealing genome-scale transcriptional regulatory landscape of OmpR highlights its expanded regulatory roles under osmotic stress in <i>Escherichia coli</i> K-12 MG1655. <i>Scientific Reports</i> , 2017, 7, 2181.	3.3	35
16	A streamlined ribosome profiling protocol for the characterization of microorganisms. <i>BioTechniques</i> , 2015, 58, 329-32.	1.8	33
17	Comparative Genome-Scale Metabolic Modeling of Metallo-Beta-Lactamase-Producing Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates. <i>Frontiers in Cellular and Infection Microbiology</i> , 2019, 9, 161.	3.9	33
18	Unraveling the functions of uncharacterized transcription factors in <i>Escherichia coli</i> using CHIP-exo. <i>Nucleic Acids Research</i> , 2021, 49, 9696-9710.	14.5	30

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19	Generation of ionic liquid tolerant <i>Pseudomonas putida</i> KT2440 strains via adaptive laboratory evolution. <i>Green Chemistry</i> , 2020, 22, 5677-5690.	9.0	29
20	Genome-scale analysis of Methicillin-resistant <i>Staphylococcus aureus</i> USA300 reveals a tradeoff between pathogenesis and drug resistance. <i>Scientific Reports</i> , 2018, 8, 2215.	3.3	28
21	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	1.8	28
22	Elucidation of Regulatory Modes for Five Two-Component Systems in <i>Escherichia coli</i> Reveals Novel Relationships. <i>MSystems</i> , 2020, 5, .	3.8	25
23	Machine learning from <i>Pseudomonas aeruginosa</i> transcriptomes identifies independently modulated sets of genes associated with known transcriptional regulators. <i>Nucleic Acids Research</i> , 2022, 50, 3658-3672.	14.5	25
24	Growth Adaptation of <i>gnd</i> and <i>sdhCB</i> <i>Escherichia coli</i> Deletion Strains Diverges From a Similar Initial Perturbation of the Transcriptome. <i>Frontiers in Microbiology</i> , 2018, 9, 1793.	3.5	23
25	Draft Genome Sequences of Four Metallo-Beta-Lactamase-Producing Multidrug-Resistant <i>Klebsiella pneumoniae</i> Clinical Isolates, Including Two Colistin-Resistant Strains, from Cairo, Egypt. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	23
26	Multiple Optimal Phenotypes Overcome Redox and Glycolytic Intermediate Metabolite Imbalances in <i>Escherichia coli</i> <i>pgi</i> Knockout Evolutions. <i>Applied and Environmental Microbiology</i> , 2018, 84, .	3.1	22
27	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	13.3	21
28	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. <i>PLoS ONE</i> , 2018, 13, e0197272.	2.5	20
29	Environmental conditions dictate differential evolution of vancomycin resistance in <i>Staphylococcus aureus</i> . <i>Communications Biology</i> , 2021, 4, 793.	4.4	18
30	RiboRid: A low cost, advanced, and ultra-efficient method to remove ribosomal RNA for bacterial transcriptomics. <i>PLoS Genetics</i> , 2021, 17, e1009821.	3.5	16
31	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43.	5.3	14
32	Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. <i>Nature Ecology and Evolution</i> , 2020, 4, 1402-1409.	7.8	13
33	Restoration of fitness lost due to dysregulation of the pyruvate dehydrogenase complex is triggered by ribosomal binding site modifications. <i>Cell Reports</i> , 2021, 35, 108961.	6.4	13
34	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321.	2.9	12
35	Reduced Production of Bacterial Membrane Vesicles Predicts Mortality in ST45/USA600 Methicillin-Resistant <i>Staphylococcus aureus</i> Bacteremia. <i>Antibiotics</i> , 2020, 9, 2.	3.7	11
36	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322.	5.3	8

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37	Distinct Subpopulations of Intravalvular Methicillin-Resistant <i>Staphylococcus aureus</i> with Variable Susceptibility to Daptomycin in Tricuspid Valve Endocarditis. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	8
38	Genetic Determinants Enabling Medium-Dependent Adaptation to Nafcillin in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020, 5, .	3.8	8
39	Identifying the effect of vancomycin on health care-associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. <i>GigaScience</i> , 2021, 10, .	6.4	5
40	Rapid resistance development to three antistaphylococcal therapies in antibiotic-tolerant <i>Staphylococcus aureus</i> bacteremia. <i>PLoS ONE</i> , 2021, 16, e0258592.	2.5	5
41	<i>Escherichia coli</i> Data-Driven Strain Design Using Aggregated Adaptive Laboratory Evolution Mutational Data. <i>ACS Synthetic Biology</i> , 2021, 10, 3379-3395.	3.8	5
42	A systems approach discovers the role and characteristics of seven LysR type transcription factors in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2022, 12, 7274.	3.3	5
43	Gapless, Unambiguous Genome Sequence for <i>Escherichia coli</i> C, a Workhorse of Industrial Biology. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.6	3
44	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 596626.	3.5	3
45	Genome Sequence Comparison of <i>Staphylococcus aureus</i> TX0117 and a Beta-Lactamase-Cured Derivative Shows Increased Cationic Peptide Resistance Accompanying Mutations in <i>relA</i> and <i>mnaA</i> . <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	2