

Richard Szubin

List of Publications by Year in descending order

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45
papers

1,987
citations

331670

21
h-index

302126

39
g-index

46
all docs

46
docs citations

46
times ranked

2250
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	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
5	Environmental conditions dictate differential evolution of vancomycin resistance in <i>Staphylococcus aureus</i> . <i>Communications Biology</i> , 2021, 4, 793.	4.4	18
6	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
7	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321.	2.9	12
8	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
9	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
10	<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
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	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
13	High-Quality Genome-Scale Models From Error-Prone, Long-Read Assemblies. <i>Frontiers in Microbiology</i> , 2020, 11, 596626.	3.5	3
14	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
15	Synthetic cross-phyla gene replacement and evolutionary assimilation of major enzymes. <i>Nature Ecology and Evolution</i> , 2020, 4, 1402-1409.	7.8	13
16	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
17	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
18	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

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19	Genetic Determinants Enabling Medium-Dependent Adaptation to Nafcillin in Methicillin-Resistant <i>Staphylococcus aureus</i> . <i>MSystems</i> , 2020, 5, .	3.8	8
20	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	1.8	28
21	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
22	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
23	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	13.3	21
24	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
25	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43.	5.3	14
26	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
27	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322.	5.3	8
28	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
29	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
30	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
31	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
32	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
33	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
34	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
35	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
36	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

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37	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. PLoS ONE, 2018, 13, e0197272.	2.5	20
38	Adaptive laboratory evolution resolves energy depletion to maintain high aromatic metabolite phenotypes in Escherichia coli strains lacking the Phosphotransferase System. Metabolic Engineering, 2018, 48, 233-242.	7.0	43
39	Revealing genome-scale transcriptional regulatory landscape of OmpR highlights its expanded regulatory roles under osmotic stress in Escherichia coli K-12 MG1655. Scientific Reports, 2017, 7, 2181.	3.3	35
40	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	12.8	141
41	A streamlined ribosome profiling protocol for the characterization of microorganisms. BioTechniques, 2015, 58, 329-32.	1.8	33
42	Genome-wide Reconstruction of OxyR and SoxRS Transcriptional Regulatory Networks under Oxidative Stress in Escherichia coli K-12 MG1655. Cell Reports, 2015, 12, 1289-1299.	6.4	174
43	Decoding genome-wide GadEWX-transcriptional regulatory networks reveals multifaceted cellular responses to acid stress in Escherichia coli. Nature Communications, 2015, 6, 7970.	12.8	87
44	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of Escherichia coli K-12 MG1655 on Glucose Minimal Medium. Applied and Environmental Microbiology, 2015, 81, 17-30.	3.1	235
45	Deciphering Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in Escherichia coli. Nature Communications, 2014, 5, 4910.	12.8	241