

Sibei Xu

List of Publications by Year in descending order

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14
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684
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687363

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581
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#	ARTICLE	IF	CITATIONS
1	Machine Learning of Bacterial Transcriptomes Reveals Responses Underlying Differential Antibiotic Susceptibility. <i>MSphere</i> , 2021, 6, e0044321.	2.9	12
2	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
3	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
4	Adaptive laboratory evolution of <i>Escherichia coli</i> under acid stress. <i>Microbiology (United Kingdom)</i> , 2020, 166, 141-148.	1.8	28
5	Pseudogene repair driven by selection pressure applied in experimental evolution. <i>Nature Microbiology</i> , 2019, 4, 386-389.	13.3	21
6	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
7	The <i>Escherichia coli</i> transcriptome mostly consists of independently regulated modules. <i>Nature Communications</i> , 2019, 10, 5536.	12.8	161
8	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
9	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
10	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
11	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
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	Modeling Method for Increased Precision and Scope of Directly Measurable Fluxes at a Genome-Scale. <i>Analytical Chemistry</i> , 2016, 88, 3844-3852.	6.5	34
14	MID Max: LC-MS/MS Method for Measuring the Precursor and Product Mass Isotopomer Distributions of Metabolic Intermediates and Cofactors for Metabolic Flux Analysis Applications. <i>Analytical Chemistry</i> , 2016, 88, 1362-1370.	6.5	48