

Yara Seif

List of Publications by Year in descending order

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Version: 2024-02-01

21
papers

976
citations

567281

15
h-index

713466

21
g-index

28
all docs

28
docs citations

28
times ranked

1181
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. <i>MSystems</i> , 2021, 6, .	3.8	24
3	Environmental conditions dictate differential evolution of vancomycin resistance in <i>Staphylococcus aureus</i> . <i>Communications Biology</i> , 2021, 4, 793.	4.4	18
4	Path to improving the life cycle and quality of genome-scale models of metabolism. <i>Cell Systems</i> , 2021, 12, 842-859.	6.2	16
5	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
6	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. <i>Nature Protocols</i> , 2020, 15, 1-14.	12.0	62
7	Metabolic and genetic basis for auxotrophies in Gram-negative species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 6264-6273.	7.1	39
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	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
10	Systems Biology and Pangenome of <i>Salmonella</i> O-Antigens. <i>MBio</i> , 2019, 10, .	4.1	26
11	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of <i>Staphylococcus aureus</i> . <i>Applied and Environmental Microbiology</i> , 2019, 85, .	3.1	21
12	A computational knowledge-base elucidates the response of <i>Staphylococcus aureus</i> to different media types. <i>PLoS Computational Biology</i> , 2019, 15, e1006644.	3.2	41
13	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. <i>PLoS Computational Biology</i> , 2019, 15, e1006971.	3.2	83
14	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 43.	5.3	14
15	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. <i>Scientific Data</i> , 2019, 6, 322.	5.3	8
16	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
17	Updated and standardized genome-scale reconstruction of <i>Mycobacterium tuberculosis</i> H37Rv, iEK1011, simulates flux states indicative of physiological conditions. <i>BMC Systems Biology</i> , 2018, 12, 25.	3.0	63
18	Machine learning and structural analysis of <i>Mycobacterium tuberculosis</i> pan-genome identifies genetic signatures of antibiotic resistance. <i>Nature Communications</i> , 2018, 9, 4306.	12.8	126

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19	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. <i>Nature Communications</i> , 2018, 9, 3771.	12.8	109
20	<i>Escherichia coli</i> B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. <i>BMC Systems Biology</i> , 2018, 12, 66.	3.0	39
21	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of <i>Acinetobacter baumannii</i> AYE. <i>Frontiers in Genetics</i> , 2018, 9, 121.	2.3	40