Yara Seif

List of Publications by Year in descending order

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	Machine learning and structural analysis of Mycobacterium tuberculosis pan-genome identifies genetic signatures of antibiotic resistance. Nature Communications, 2018, 9, 4306.	12.8	126
2	Genome-scale metabolic reconstructions of multiple Salmonella strains reveal serovar-specific metabolic traits. Nature Communications, 2018, 9, 3771.	12.8	109
3	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
4	Updated and standardized genome-scale reconstruction of Mycobacterium tuberculosis H37Rv, iEK1011, simulates flux states indicative of physiological conditions. BMC Systems Biology, 2018, 12, 25.	3.0	63
5	A workflow for generating multi-strain genome-scale metabolic models of prokaryotes. Nature Protocols, 2020, 15, 1-14.	12.0	62
6	Revealing 29 sets of independently modulated genes in <i>Staphylococcus aureus</i> , their regulators, and role in key physiological response. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 17228-17239.	7.1	60
7	Adaptive evolution reveals a tradeoff between growth rate and oxidative stress during naphthoquinone-based aerobic respiration. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25287-25292.	7.1	56
8	OxyR Is a Convergent Target for Mutations Acquired during Adaptation to Oxidative Stress-Prone Metabolic States. Molecular Biology and Evolution, 2020, 37, 660-667.	8.9	52
9	A computational knowledge-base elucidates the response of Staphylococcus aureus to different media types. PLoS Computational Biology, 2019, 15, e1006644.	3.2	41
10	iCN718, an Updated and Improved Genome-Scale Metabolic Network Reconstruction of Acinetobacter baumannii AYE. Frontiers in Genetics, 2018, 9, 121.	2.3	40
11	Escherichia coli B2 strains prevalent in inflammatory bowel disease patients have distinct metabolic capabilities that enable colonization of intestinal mucosa. BMC Systems Biology, 2018, 12, 66.	3.0	39
12	Metabolic and genetic basis for auxotrophies in Gram-negative species. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 6264-6273.	7.1	39
13	Systems Biology and Pangenome of <i>Salmonella</i> O-Antigens. MBio, 2019, 10, .	4.1	26
14	Elucidation of Regulatory Modes for Five Two-Component Systems in Escherichia coli Reveals Novel Relationships. MSystems, 2020, 5, .	3.8	25
15	Pangenome Analytics Reveal Two-Component Systems as Conserved Targets in ESKAPEE Pathogens. MSystems, 2021, 6, .	3.8	24
16	Strain-Specific Metabolic Requirements Revealed by a Defined Minimal Medium for Systems Analyses of <i>Staphylococcus aureus</i>. Applied and Environmental Microbiology, 2019, 85, .	3.1	21
17	Environmental conditions dictate differential evolution of vancomycin resistance in Staphylococcus aureus. Communications Biology, 2021, 4, 793.	4.4	18
18	Path to improving the life cycle and quality of genome-scale models of metabolism. Cell Systems, 2021, 12, 842-859.	6.2	16

#	Article	IF	Citations
19	Characterization of CA-MRSA TCH1516 exposed to nafcillin in bacteriological and physiological media. Scientific Data, 2019, 6, 43.	5.3	14
20	Profiling the effect of nafcillin on HA-MRSA D712 using bacteriological and physiological media. Scientific Data, 2019, 6, 322.	5.3	8
21	Identifying the effect of vancomycin on health care–associated methicillin-resistant <i>Staphylococcus aureus</i> strains using bacteriological and physiological media. GigaScience, 2021, 10, .	6.4	5