Colton J Lloyd

List of Publications by Year
in descending order

24 papers	1,701 citations	516710 16 h-index	752698 20 g-index
31 all docs	31 docs citations	31 times ranked	1749 citing authors

#	ARTICLE	IF	CITATIONS
1	Pangenome analysis of Enterobacteria reveals richness of secondary metabolite gene clusters and their associated gene sets. Synthetic and Systems Biotechnology, 2022, 7, 900-910.	3.7	9
2	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth. PLoS Computational Biology, 2021, 17, e1007817.	3.2	3
3	Genome‐scale metabolic modeling reveals key features of a minimal gene set. Molecular Systems Biology, 2021, 17, e10099.	7.2	15
4	Kinetic profiling of metabolic specialists demonstrates stability and consistency of in vivo enzyme turnover numbers. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23182-23190.	7.1	65
5	Reconstructing organisms in silico: genome-scale models and their emerging applications. Nature Reviews Microbiology, 2020, 18, 731-743.	28.6	158
6	Cellular responses to reactive oxygen species are predicted from molecular mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14368-14373.	7.1	79
7	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
8	BOFdat: Generating biomass objective functions for genome-scale metabolic models from experimental data. PLoS Computational Biology, 2019, 15, e1006971.	3.2	83
9	The genetic basis for adaptation of model-designed syntrophic co-cultures. PLoS Computational Biology, 2019, 15, e1006213.	3.2	17
10	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. PLoS Computational Biology, 2019, 15, e1006848.	3.2	46
11	Genome-scale model of metabolism and gene expression provides a multi-scale description of acid stress responses in Escherichia coli. PLoS Computational Biology, 2019, 15, e1007525.	3.2	37
12	Title is missing!. , 2019, 15, e1007525.		0
13	Title is missing!. , 2019, 15, e1007525.		0
14	Title is missing!. , 2019, 15, e1007525.		0
15	Title is missing!. , 2019, 15, e1007525.		0
16	Machine learning applied to enzyme turnover numbers reveals protein structural correlates and improves metabolic models. Nature Communications, 2018, 9, 5252.	12.8	151
17	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
18	Laboratory Evolution to Alternating Substrate Environments Yields Distinct Phenotypic and Genetic Adaptive Strategies. Applied and Environmental Microbiology, 2017, 83, .	3.1	76

#	Article	IF	Citations
19	iML1515, a knowledgebase that computes Escherichia coli traits. Nature Biotechnology, 2017, 35, 904-908.	17.5	425
20	Global transcriptional regulatory network for *Escherichia coli* robustly connects gene expression to transcription factor activities. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10286-10291.	7.1	89
21	solveME: fast and reliable solution of nonlinear ME models. BMC Bioinformatics, 2016, 17, 391.	2.6	39
22	Principles of proteome allocation are revealed using proteomic data and genome-scale models. Scientific Reports, 2016, 6, 36734.	3.3	31
23	Next-generation genome-scale models for metabolic engineering. Current Opinion in Biotechnology, 2015, 35, 23-29.	6.6	144
24	Systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 10810-10815.	7.1	42