Ali Ebrahim

List of Publications by Year
in descending order

23 papers	3,832 citations	331670 21 h-index	642732 23 g-index
28 all docs	28 docs citations	28 times ranked	4359 citing authors

#	Article	IF	Citations
1	COBRApy: COnstraints-Based Reconstruction and Analysis for Python. BMC Systems Biology, 2013, 7, 74.	3.0	973
2	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
3	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
4	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
5	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	7.2	178
6	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of Clostridium ljungdahlii. Microbial Cell Factories, 2013, 12, 118.	4.0	145
7	Evolution of Escherichia coli to 42 Â°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	8.9	145
8	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	12.8	141
9	COBRAme: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	3.2	123
10	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. Bioinformatics, 2013, 29, 2900-2908.	4.1	122
11	Sulfide-Driven Microbial Electrosynthesis. Environmental Science & Technology, 2013, 47, 568-573.	10.0	101
12	Electrical Detection of TATA Binding Protein at DNA-Modified Microelectrodes. Journal of the American Chemical Society, 2008, 130, 2924-2925.	13.7	85
13	Model-driven discovery of underground metabolic functions in <i>Escherichia coli</i>. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 929-934.	7.1	82
14	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
15	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. PLoS Genetics, 2014, 10, e1004264.	3.5	67
16	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. PLoS Computational Biology, 2019, 15, e1006848.	3.2	46
17	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
18	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

#	Article	IF	Citations
19	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. Molecular Systems Biology, 2014, 10, 737.	7.2	41
20	solveME: fast and reliable solution of nonlinear ME models. BMC Bioinformatics, 2016, 17, 391.	2.6	39
21	Principles of proteome allocation are revealed using proteomic data and genome-scale models. Scientific Reports, 2016, 6, 36734.	3.3	31
22	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. PLoS ONE, 2018, 13, e0197272.	2.5	20
23	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