

# Ali Ebrahim

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4315296/publications.pdf>

Version: 2024-02-01

23  
papers

3,832  
citations

331259

21  
h-index

642321

23  
g-index

28  
all docs

28  
docs citations

28  
times ranked

4359  
citing authors

#	ARTICLE	IF	CITATIONS
1	Computation of condition-dependent proteome allocation reveals variability in the macro and micro nutrient requirements for growth. PLoS Computational Biology, 2021, 17, e1007817.	1.5	3
2	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
3	DynamicME: dynamic simulation and refinement of integrated models of metabolism and protein expression. BMC Systems Biology, 2019, 13, 2.	3.0	45
4	Predicting proteome allocation, overflow metabolism, and metal requirements in a model acetogen. PLoS Computational Biology, 2019, 15, e1006848.	1.5	46
5	COBRAME: A computational framework for genome-scale models of metabolism and gene expression. PLoS Computational Biology, 2018, 14, e1006302.	1.5	123
6	ChIP-exo interrogation of Crp, DNA, and RNAP holoenzyme interactions. PLoS ONE, 2018, 13, e0197272.	1.1	20
7	solveME: fast and reliable solution of nonlinear ME models. BMC Bioinformatics, 2016, 17, 391.	1.2	39
8	Principles of proteome allocation are revealed using proteomic data and genome-scale models. Scientific Reports, 2016, 6, 36734.	1.6	31
9	Multi-omic data integration enables discovery of hidden biological regularities. Nature Communications, 2016, 7, 13091.	5.8	141
10	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	6.5	746
11	Do genome-scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	3.2	68
12	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	1.5	344
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.	3.3	82
14	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.	3.3	42
15	Use of Adaptive Laboratory Evolution To Discover Key Mutations Enabling Rapid Growth of <i>Escherichia coli</i> K-12 MG1655 on Glucose Minimal Medium. Applied and Environmental Microbiology, 2015, 81, 17-30.	1.4	235
16	Determining the Control Circuitry of Redox Metabolism at the Genome-Scale. PLoS Genetics, 2014, 10, e1004264.	1.5	67
17	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. Molecular Systems Biology, 2014, 10, 737.	3.2	41
18	Evolution of <i>Escherichia coli</i> to 42 °C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	3.5	145

#	ARTICLE	IF	CITATIONS
19	GIM3E: condition-specific models of cellular metabolism developed from metabolomics and expression data. <i>Bioinformatics</i> , 2013, 29, 2900-2908.	1.8	122
20	COBRAPy: COstraints-Based Reconstruction and Analysis for Python. <i>BMC Systems Biology</i> , 2013, 7, 74.	3.0	973
21	Characterizing acetogenic metabolism using a genome-scale metabolic reconstruction of <i>Clostridium ljungdahlii</i> . <i>Microbial Cell Factories</i> , 2013, 12, 118.	1.9	145
22	Sulfide-Driven Microbial Electrosynthesis. <i>Environmental Science &amp; Technology</i> , 2013, 47, 568-573.	4.6	101
23	Electrical Detection of TATA Binding Protein at DNA-Modified Microelectrodes. <i>Journal of the American Chemical Society</i> , 2008, 130, 2924-2925.	6.6	85