

Paulo VilaÃ§a

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

804
citations

1307594

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h-index

839539

18
g-index

22
all docs

22
docs citations

22
times ranked

1253
citing authors

#	ARTICLE	IF	CITATIONS
1	OptFlux: an open-source software platform for in silico metabolic engineering. BMC Systems Biology, 2010, 4, 45.	3.0	321
2	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
3	Reconstruction of a genome-scale metabolic model for Actinobacillus succinogenes 130Z. BMC Systems Biology, 2018, 12, 61.	3.0	22
4	A computational tool for the simulation and optimization of microbial strains accounting integrated metabolic/regulatory information. BioSystems, 2011, 103, 435-441.	2.0	17
5	Sequence based heuristics for two-dimensional bin packing problems. Engineering Optimization, 2009, 41, 773-791.	2.6	15
6	Genome-Wide Semi-Automated Annotation of Transporter Systems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 443-456.	3.0	14
7	Discovery and implementation of a novel pathway for n-butanol production via 2-oxoglutarate. Biotechnology for Biofuels, 2019, 12, 230.	6.2	12
8	CBFA: phenotype prediction integrating metabolic models with constraints derived from experimental data. BMC Systems Biology, 2014, 8, 123.	3.0	7
9	Development and application of efficient pathway enumeration algorithms for metabolic engineering applications. Computer Methods and Programs in Biomedicine, 2015, 118, 134-146.	4.7	7
10	An integrated network visualization framework towards metabolic engineering applications. BMC Bioinformatics, 2014, 15, 420.	2.6	6
11	Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models. Lecture Notes in Computer Science, 2010, , 205-216.	1.3	6
12	An integrated computational environment for elementary modes analysis of biochemical networks. International Journal of Data Mining and Bioinformatics, 2012, 6, 382.	0.1	4
13	Analyzing and Designing Cell Factories with OptFlux. Methods in Molecular Biology, 2018, 1716, 37-76.	0.9	4
14	A Critical Evaluation of Automatic Atom Mapping Algorithms and Tools. Advances in Intelligent Systems and Computing, 2017, , 257-264.	0.6	2
15	An Algorithm to Assemble Gene-Protein-Reaction Associations for Genome-Scale Metabolic Model Reconstruction. Lecture Notes in Computer Science, 2012, , 118-128.	1.3	2
16	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. ACS Synthetic Biology, 2019, 8, 976-988.	3.8	1
17	Network Visualization Tools to Enhance Metabolic Engineering Platforms. Advances in Intelligent Systems and Computing, 2013, , 137-144.	0.6	1
18	Reg4OptFlux: an OptFlux plug-in that comprises meta-heuristics approaches for Metabolic engineering using integrated models. , 2014, , .		0

#	ARTICLE	IF	CITATIONS
19	In Silico Predictions for Fucoxanthin Production by the Diatom Phaeodactylum Tricornutum. Advances in Intelligent Systems and Computing, 2019, , 139-148.	0.6	0
20	A Study on the Robustness of Strain Optimization Algorithms. Advances in Intelligent and Soft Computing, 2011, , 329-336.	0.2	0