

# Paulo VilaÃ§a

## List of Publications by Year in descending order

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Version: 2024-02-01

20  
papers

804  
citations

1307594

7  
h-index

839539

18  
g-index

22  
all docs

22  
docs citations

22  
times ranked

1253  
citing authors

#	ARTICLE	IF	CITATIONS
1	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
2	In Silico Predictions for Fucoxanthin Production by the Diatom <i>Phaeodactylum Tricornutum</i> . <i>Advances in Intelligent Systems and Computing</i> , 2019, , 139-148.	0.6	0
3	Discovery and implementation of a novel pathway for n-butanol production via 2-oxoglutarate. <i>Biotechnology for Biofuels</i> , 2019, 12, 230.	6.2	12
4	Turnover Dependent Phenotypic Simulation: A Quantitative Constraint-Based Simulation Method That Accommodates All Main Strain Design Strategies. <i>ACS Synthetic Biology</i> , 2019, 8, 976-988.	3.8	1
5	Analyzing and Designing Cell Factories with OptFlux. <i>Methods in Molecular Biology</i> , 2018, 1716, 37-76.	0.9	4
6	Reconstruction of a genome-scale metabolic model for <i>Actinobacillus succinogenes</i> 130Z. <i>BMC Systems Biology</i> , 2018, 12, 61.	3.0	22
7	Genome-Wide Semi-Automated Annotation of Transporter Systems. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 443-456.	3.0	14
8	A Critical Evaluation of Automatic Atom Mapping Algorithms and Tools. <i>Advances in Intelligent Systems and Computing</i> , 2017, , 257-264.	0.6	2
9	Development and application of efficient pathway enumeration algorithms for metabolic engineering applications. <i>Computer Methods and Programs in Biomedicine</i> , 2015, 118, 134-146.	4.7	7
10	CBFA: phenotype prediction integrating metabolic models with constraints derived from experimental data. <i>BMC Systems Biology</i> , 2014, 8, 123.	3.0	7
11	An integrated network visualization framework towards metabolic engineering applications. <i>BMC Bioinformatics</i> , 2014, 15, 420.	2.6	6
12	Reg4OptFlux: an OptFlux plug-in that comprises meta-heuristics approaches for Metabolic engineering using integrated models. , 2014, , .		0
13	Network Visualization Tools to Enhance Metabolic Engineering Platforms. <i>Advances in Intelligent Systems and Computing</i> , 2013, , 137-144.	0.6	1
14	An integrated computational environment for elementary modes analysis of biochemical networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 382.	0.1	4
15	An Algorithm to Assemble Gene-Protein-Reaction Associations for Genome-Scale Metabolic Model Reconstruction. <i>Lecture Notes in Computer Science</i> , 2012, , 118-128.	1.3	2
16	A computational tool for the simulation and optimization of microbial strains accounting integrated metabolic/regulatory information. <i>BioSystems</i> , 2011, 103, 435-441.	2.0	17
17	A Study on the Robustness of Strain Optimization Algorithms. <i>Advances in Intelligent and Soft Computing</i> , 2011, , 329-336.	0.2	0
18	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010, 4, 45.	3.0	321

#	ARTICLE	IF	CITATIONS
19	Metaheuristics for Strain Optimization Using Transcriptional Information Enriched Metabolic Models. Lecture Notes in Computer Science, 2010, , 205-216.	1.3	6
20	Sequence based heuristics for two-dimensional bin packing problems. Engineering Optimization, 2009, 41, 773-791.	2.6	15