

# Jose P Faria

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2061170/publications.pdf>

Version: 2024-02-01

20  
papers

2,100  
citations

933447

10  
h-index

839539

18  
g-index

26  
all docs

26  
docs citations

26  
times ranked

2879  
citing authors

#	ARTICLE	IF	CITATIONS
1	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	17.5	955
2	A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.	17.5	457
3	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
4	The ModelSEED Biochemistry Database for the integration of metabolic annotations and the reconstruction, comparison and analysis of metabolic models for plants, fungi and microbes. <i>Nucleic Acids Research</i> , 2021, 49, D575-D588.	14.5	119
5	Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , 2018, 46, 931-936.	3.4	51
6	Genome-scale bacterial transcriptional regulatory networks: reconstruction and integrated analysis with metabolic models. <i>Briefings in Bioinformatics</i> , 2014, 15, 592-611.	6.5	30
7	A pathway for every product? Tools to discover and design plant metabolism. <i>Plant Science</i> , 2018, 273, 61-70.	3.6	18
8	Reconstruction of the Regulatory Network for <i>Bacillus subtilis</i> and Reconciliation with Gene Expression Data. <i>Frontiers in Microbiology</i> , 2016, 7, 275.	3.5	14
9	A review of methods for the reconstruction and analysis of integrated genome-scale models of metabolism and regulation. <i>Biochemical Society Transactions</i> , 2020, 48, 1889-1903.	3.4	14
10	Constructing and Analyzing Metabolic Flux Models of Microbial Communities. <i>Springer Protocols</i> , 2016, , 247-273.	0.3	8
11	Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 1819.	3.5	7
12	Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015, 5, 101-105.	2.2	5
13	Draft Genome Sequence of <i>Rhodococcus</i> sp. Strain ATCC 49988, a Quinoline-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	4
14	Application of the Metabolic Modeling Pipeline in KBase to Categorize Reactions, Predict Essential Genes, and Predict Pathways in an Isolate Genome. <i>Methods in Molecular Biology</i> , 2022, 2349, 291-320.	0.9	4
15	Reconstruction and Analysis of Central Metabolism in Microbes. <i>Methods in Molecular Biology</i> , 2018, 1716, 111-129.	0.9	1
16	Draft Genome Sequence of <i>Pseudarthrobacter</i> sp. Strain ATCC 49442 (Formerly <i>Micrococcus luteus</i> ), a Pyridine-Degrading Bacterium. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	1
17	Analysis of the Effect of Reversibility Constraints on the Predictions of Genome-Scale Metabolic Models. <i>Advances in Intelligent and Soft Computing</i> , 2010, , 209-215.	0.2	1
18	Towards the Reconstruction of Integrated Genome-Scale Models of Metabolism and Gene Expression. <i>Advances in Intelligent Systems and Computing</i> , 2020, , 173-181.	0.6	0

#	ARTICLE	IF	CITATIONS
19	Tapping the Wealth of Microbial Data in High-Throughput Metabolic Model Reconstruction. <i>Methods in Molecular Biology</i> , 2014, 1191, 19-45.	0.9	0
20	Draft Genome Sequence of 2-Methylpyridine-, 2-Ethylpyridine-, and 2-Hydroxypyridine-Degrading <i>Arthrobacter</i> sp. Strain ATCC 49987. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	0