

# 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  | 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         |
| 2  | A genomic catalog of Earth's microbiomes. <i>Nature Biotechnology</i> , 2021, 39, 499-509.  | 17.5 | 457       |
| 3  | 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       |
| 4  | 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         |
| 5  | 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         |
| 6  | MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.  | 17.5 | 314       |
| 7  | 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        |
| 8  | 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         |
| 9  | 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         |
| 10 | A pathway for every product? Tools to discover and design plant metabolism. <i>Plant Science</i> , 2018, 273, 61-70.  | 3.6  | 18        |
| 11 | Reconstruction and Analysis of Central Metabolism in Microbes. <i>Methods in Molecular Biology</i> , 2018, 1716, 111-129.   | 0.9  | 1         |
| 12 | Methods for automated genome-scale metabolic model reconstruction. <i>Biochemical Society Transactions</i> , 2018, 46, 931-936.   | 3.4  | 51        |
| 13 | KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.   | 17.5 | 955       |
| 14 | 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        |
| 15 | Computing and Applying Atomic Regulons to Understand Gene Expression and Regulation. <i>Frontiers in Microbiology</i> , 2016, 7, 1819.  | 3.5  | 7         |
| 16 | Constructing and Analyzing Metabolic Flux Models of Microbial Communities. <i>Springer Protocols</i> , 2016, , 247-273.   | 0.3  | 8         |
| 17 | Enabling comparative modeling of closely related genomes: example genus <i>Brucella</i> . <i>3 Biotech</i> , 2015, 5, 101-105.  | 2.2  | 5         |
| 18 | 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        |

| #  | 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 | 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         |