

Julio Augusto Freyre-González

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

405
citations

1040056

9
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940533

16
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28
all docs

28
docs citations

28
times ranked

421
citing authors

#	ARTICLE	IF	CITATIONS
1	Curation, inference, and assessment of a globally reconstructed gene regulatory network for <i>Streptomyces coelicolor</i> . <i>Scientific Reports</i> , 2022, 12, 2840.	3.3	5
2	System Principles Governing the Organization, Architecture, Dynamics, and Evolution of Gene Regulatory Networks. <i>Frontiers in Bioengineering and Biotechnology</i> , 2022, 10, .	4.1	5
3	Partition Quantitative Assessment (PQA): A Quantitative Methodology to Assess the Embedded Noise in Clustered Omics and Systems Biology Data. <i>Applied Sciences (Switzerland)</i> , 2021, 11, 5999.	2.5	0
4	<i>Corynebacterium glutamicum</i> Regulation beyond Transcription: Organizing Principles and Reconstruction of an Extended Regulatory Network Incorporating Regulations Mediated by Small RNA and Protein-Protein Interactions. <i>Microorganisms</i> , 2021, 9, 1395.	3.6	5
5	Abasy Atlas v2.2: The most comprehensive and up-to-date inventory of meta-curated, historical, bacterial regulatory networks, their completeness and system-level characterization. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 1228-1237.	4.1	19
6	Evolutionary constraints on the complexity of genetic regulatory networks allow predictions of the total number of genetic interactions. <i>Scientific Reports</i> , 2019, 9, 3618.	3.3	11
7	Functional architecture and global properties of the <i>Corynebacterium glutamicum</i> regulatory network: Novel insights from a dataset with a high genomic coverage. <i>Journal of Biotechnology</i> , 2017, 257, 199-210.	3.8	16
8	Abasy Atlas: a comprehensive inventory of systems, global network properties and systems-level elements across bacteria. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw089.	3.0	19
9	Calcitriol increases Dicer expression and modifies the microRNAs signature in SiHa cervical cancer cells. <i>Biochemistry and Cell Biology</i> , 2015, 93, 376-384.	2.0	24
10	Mathematical modeling of the apo and holo transcriptional regulation in <i>Escherichia coli</i> . <i>Molecular BioSystems</i> , 2015, 11, 994-1003.	2.9	2
11	Lessons from the modular organization of the transcriptional regulatory network of <i>Bacillus subtilis</i> . <i>BMC Systems Biology</i> , 2013, 7, 127.	3.0	26
12	Anti-Sigma Factors in <i>E. coli</i> : Common Regulatory Mechanisms Controlling Sigma Factors Availability. <i>Current Genomics</i> , 2013, 14, 378-387.	1.6	25
13	Prokaryotic regulatory systems biology: Common principles governing the functional architectures of <i>Bacillus subtilis</i> and <i>Escherichia coli</i> unveiled by the natural decomposition approach. <i>Journal of Biotechnology</i> , 2012, 161, 278-286.	3.8	19
14	Molecular characterization of chloranilic acid degradation in <i>Pseudomonas putida</i> TQ07. <i>Journal of Microbiology</i> , 2011, 49, 974-980.	2.8	2
15	Identification of network topological units coordinating the global expression response to glucose in <i>Bacillus subtilis</i> and its comparison to <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2009, 9, 176.	3.3	5
16	Functional architecture of <i>Escherichia coli</i> : new insights provided by a natural decomposition approach. <i>Genome Biology</i> , 2008, 9, R154.	9.6	56
17	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2007, 7, 53.	3.3	59
18	Modular analysis of the transcriptional regulatory network of <i>E. coli</i> . <i>Trends in Genetics</i> , 2005, 21, 16-20.	6.7	99