

Rosa María-Gutiérrez-Ramos

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

773
citations

840776

11
h-index

552781

26
g-index

27
all docs

27
docs citations

27
times ranked

1182
citing authors

#	ARTICLE	IF	CITATIONS
1	The Alpha Variant (B.1.1.7) of SARS-CoV-2 Failed to Become Dominant in Mexico. <i>Microbiology Spectrum</i> , 2022, 10, e0224021.	3.0	21
2	Characterization of <i>Enterobacter cloacae</i> BAGM01 Producing a Thermostable and Alkaline-Tolerant Rhamnolipid Biosurfactant from the Gulf of Mexico. <i>Marine Biotechnology</i> , 2021, 23, 106-126.	2.4	13
3	Distribution and preservation of the components of the engulfment. What is beyond representative genomes?. <i>PLoS ONE</i> , 2021, 16, e0246651.	2.5	4
4	Bacteria From the Southern Gulf of Mexico: Baseline, Diversity, Hydrocarbon-Degrading Potential and Future Applications. <i>Frontiers in Marine Science</i> , 2021, 8, .	2.5	11
5	Definition of the Metagenomic Profile of Ocean Water Samples From the Gulf of Mexico Based on Comparison With Reference Samples From Sites Worldwide. <i>Frontiers in Microbiology</i> , 2021, 12, 781497.	3.5	3
6	Metagenomic Profiling and Microbial Metabolic Potential of Perdido Fold Belt (NW) and Campeche Knolls (SE) in the Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2020, 11, 1825.	3.5	16
7	Structure and Evolution of <i>Acinetobacter baumannii</i> Plasmids. <i>Frontiers in Microbiology</i> , 2020, 11, 1283.	3.5	59
8	Functional and Genomic Characterization of a <i>Pseudomonas aeruginosa</i> Strain Isolated From the Southwestern Gulf of Mexico Reveals an Enhanced Adaptation for Long-Chain Alkane Degradation. <i>Frontiers in Marine Science</i> , 2019, 6, .	2.5	31
9	Prediction of protein architectures involved in the signaling-pathway initiating sporulation in Firmicutes. <i>BMC Research Notes</i> , 2019, 12, 686.	1.4	4
10	Phenotypic and genomic analysis of <i>Zymomonas mobilis</i> ZM4 mutants with enhanced ethanol tolerance. <i>Biotechnology Reports (Amsterdam, Netherlands)</i> , 2019, 23, e00328.	4.4	6
11	Bacterial Diversity and the Geochemical Landscape in the Southwestern Gulf of Mexico. <i>Frontiers in Microbiology</i> , 2018, 9, 2528.	3.5	39
12	Reactant pairs and reaction organization patterns produced by a new rule-based approach. <i>BMC Research Notes</i> , 2018, 11, 608.	1.4	1
13	BLAST-XYPlot Viewer: A Tool for Performing BLAST in Whole-Genome Sequenced Bacteria/Archaea and Visualize Whole Results Simultaneously. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 2167-2172.	1.8	3
14	Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. <i>Scientific Reports</i> , 2018, 8, 12034.	3.3	93
15	Identification of reaction organization patterns that naturally cluster enzymatic transformations. <i>BMC Systems Biology</i> , 2018, 12, 63.	3.0	3
16	Analysis of Spo0M function in <i>Bacillus subtilis</i> . <i>PLoS ONE</i> , 2017, 12, e0172737.	2.5	10
17	Global transcriptomic analysis of an engineered <i>Escherichia coli</i> strain lacking the phosphoenolpyruvate: carbohydrate phosphotransferase system during shikimic acid production in rich culture medium. <i>Microbial Cell Factories</i> , 2014, 13, 28.	4.0	16
18	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

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19	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
20	Transcriptional profiling of fetal hypothalamic TRH neurons. <i>BMC Genomics</i> , 2011, 12, 222.	2.8	8
21	New insights into the regulatory networks of paralogous genes in bacteria. <i>Microbiology (United Kingdom)</i> 151:1073-1084 (2007). Tj ETQq1 1 0.784314 rgBT /Overloc 1.8 31	1.8	31
22	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
23	The repABC plasmid family. <i>Plasmid</i> , 2008, 60, 19-37.	1.4	172
24	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
25	Environmental conditions and transcriptional regulation in <i>Escherichia coli</i> : a physiological integrative approach. <i>Biotechnology and Bioengineering</i> , 2003, 84, 743-749.	3.3	15
26	Regulatory Network of <i>Escherichia coli</i> : Consistency Between Literature Knowledge and Microarray Profiles. <i>Genome Research</i> , 2003, 13, 2435-2443.	5.5	104