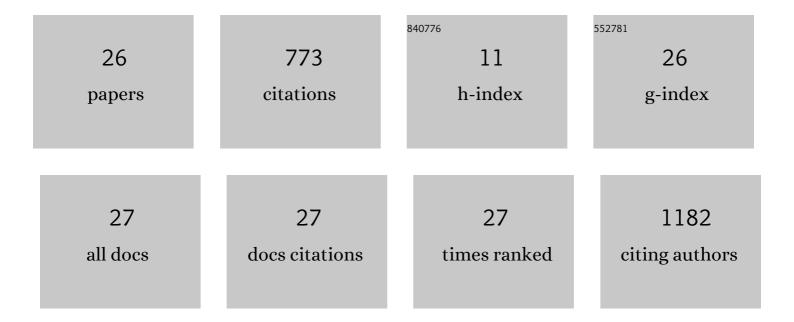
## Rosa MarÃ-a Gutiérrez-RÃ-os

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2683502/publications.pdf

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#	Article	IF	CITATIONS
1	The Alpha Variant (B.1.1.7) of SARS-CoV-2 Failed to Become Dominant in Mexico. Microbiology Spectrum, 2022, 10, e0224021.	3.0	21
2	Characterization of Enterobacter cloacae BAGM01 Producing a Thermostable and Alkaline-Tolerant Rhamnolipid Biosurfactant from the Gulf of Mexico. Marine Biotechnology, 2021, 23, 106-126.	2.4	13
3	Distribution and preservation of the components of the engulfment. What is beyond representative genomes?. PLoS ONE, 2021, 16, e0246651.	2.5	4
4	Bacteria From the Southern Gulf of Mexico: Baseline, Diversity, Hydrocarbon-Degrading Potential and Future Applications. Frontiers in Marine Science, 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. Frontiers in Microbiology, 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. Frontiers in Microbiology, 2020, 11, 1825.	3.5	16
7	Structure and Evolution of Acinetobacter baumannii Plasmids. Frontiers in Microbiology, 2020, 11, 1283.	3.5	59
8	Functional and Genomic Characterization of a Pseudomonas aeruginosa Strain Isolated From the Southwestern Gulf of Mexico Reveals an Enhanced Adaptation for Long-Chain Alkane Degradation. Frontiers in Marine Science, 2019, 6, .	2.5	31
9	Prediction of protein architectures involved in the signaling-pathway initiating sporulation in Firmicutes. BMC Research Notes, 2019, 12, 686.	1.4	4
10	Phenotypic and genomic analysis of Zymomonas mobilis ZM4 mutants with enhanced ethanol tolerance. Biotechnology Reports (Amsterdam, Netherlands), 2019, 23, e00328.	4.4	6
11	Bacterial Diversity and the Geochemical Landscape in the Southwestern Gulf of Mexico. Frontiers in Microbiology, 2018, 9, 2528.	3.5	39
12	Reactant pairs and reaction organization patterns produced by a new rule-based approach. BMC Research Notes, 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. G3: Genes, Genomes, Genetics, 2018, 8, 2167-2172.	1.8	3
14	Analysis of sequencing strategies and tools for taxonomic annotation: Defining standards for progressive metagenomics. Scientific Reports, 2018, 8, 12034.	3.3	93
15	Identification of reaction organization patterns that naturally cluster enzymatic transformations. BMC Systems Biology, 2018, 12, 63.	3.0	3
16	Analysis of SpoOM function in Bacillus subtilis. PLoS ONE, 2017, 12, e0172737.	2.5	10
17	Global transcriptomic analysis of an engineered Escherichia coli strain lacking the phosphoenolpyruvate: carbohydrate phosphotransferase system during shikimic acid production in rich culture medium. Microbial Cell Factories, 2014, 13, 28.	4.0	16
18	Lessons from the modular organization of the transcriptional regulatory network of Bacillus subtilis. BMC Systems Biology, 2013, 7, 127.	3.0	26

#	Article	IF	CITATIONS
19	Prokaryotic regulatory systems biology: Common principles governing the functional architectures of Bacillus subtilis and Escherichia coli unveiled by the natural decomposition approach. Journal of Biotechnology, 2012, 161, 278-286.	3.8	19
20	Transcriptional profiling of fetal hypothalamic TRH neurons. BMC Genomics, 2011, 12, 222.	2.8	8
21	New insights into the regulatory networks of paralogous genes in bacteria. Microbiology (United) Tj ETQq1 1 0.78	4314 rgB 1.8	T /Overlock
22	Identification of network topological units coordinating the global expression response to glucose in Bacillus subtilis and its comparison to Escherichia coli. BMC Microbiology, 2009, 9, 176.	3.3	5
23	The repABC plasmid family. Plasmid, 2008, 60, 19-37.	1.4	172
24	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in Escherichia coli. BMC Microbiology, 2007, 7, 53.	3.3	59
25	Environmental conditions and transcriptional regulation in <i>Escherichia coli</i> : a physiological integrative approach. Biotechnology and Bioengineering, 2003, 84, 743-749.	3.3	15
26	Regulatory Network of <i>Escherichia coli</i> : Consistency Between Literature Knowledge and Microarray Profiles. Genome Research, 2003, 13, 2435-2443.	5.5	104