

Mario Alberto Martínez-Núñez

List of Publications by Year in descending order

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Version: 2024-02-01

24
papers

370
citations

1039406

9
h-index

839053

18
g-index

25
all docs

25
docs citations

25
times ranked

535
citing authors

#	ARTICLE	IF	CITATIONS
1	Nonribosomal peptides synthetases and their applications in industry. Sustainable Chemical Processes, 2016, 4, .	2.3	75
2	Abundance, diversity and domain architecture variability in prokaryotic DNA-binding transcription factors. PLoS ONE, 2018, 13, e0195332.	1.1	62
3	Genome-Wide Association Study Reveals Candidate Genes for Litter Size Traits in Pelibuey Sheep. Animals, 2020, 10, 434.	1.0	33
4	New insights into the regulatory networks of paralogous genes in bacteria. Microbiology (United Kingdom), 2017, 163, 1167-1178.	0.7	31
5	Lessons from the modular organization of the transcriptional regulatory network of <i>Bacillus subtilis</i> . BMC Systems Biology, 2013, 7, 127.	3.0	26
6	Increments and Duplication Events of Enzymes and Transcription Factors Influence Metabolic and Regulatory Diversity in Prokaryotes. PLoS ONE, 2013, 8, e69707.	1.1	18
7	RNA-seq Transcriptome Analysis in Ovarian Tissue of Pelibuey Breed to Explore the Regulation of Prolificacy. Genes, 2019, 10, 358.	1.0	17
8	Evaluation of the Abundance of DNA-Binding Transcription Factors in Prokaryotes. Genes, 2020, 11, 52.	1.0	14
9	Dissecting the protein architecture of DNA-binding transcription factors in bacteria and archaea. Microbiology (United Kingdom), 2017, 163, 1167-1178.	0.7	13
10	Analysis of some phenotypic traits of feces-borne temperate lambdoid bacteriophages from different immunity groups: a high incidence of cor+, FhuA-dependent phages. Archives of Virology, 2008, 153, 1271-1280.	0.9	10
11	The Repertoire of DNA-Binding Transcription Factors in Prokaryotes: Functional and Evolutionary Lessons. Science Progress, 2012, 95, 315-329.	1.0	9
12	The lifestyle of prokaryotic organisms influences the repertoire of promiscuous enzymes. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1625-1631.	1.5	9
13	Mining the Yucatan Coastal Microbiome for the Identification of Non-Ribosomal Peptides Synthetase (NRPS) Genes. Toxins, 2020, 12, 349.	1.5	9
14	<i>Pseudocrossidium replicatum</i> (Taylor) R.H. Zander is a fully desiccation-tolerant moss that expresses an inducible molecular mechanism in response to severe abiotic stress. Plant Molecular Biology, 2021, 107, 387-404.	2.0	7
15	Functional Prediction of Hypothetical Transcription Factors of <i>Escherichia coli</i> K-12 Based on Expression Data. Computational and Structural Biotechnology Journal, 2018, 16, 157-166.	1.9	6
16	Identification of Novel Conotoxin Precursors from the Cone Snail <i>Conus spurius</i> by High-Throughput RNA Sequencing. Marine Drugs, 2021, 19, 547.	2.2	6
17	Dissecting the Repertoire of DNA-Binding Transcription Factors of the Archaeon <i>Pyrococcus furiosus</i> DSM 3638. Life, 2018, 8, 40.	1.1	5
18	Do lifestyles influence the presence of promiscuous enzymes in bacteria and Archaea metabolism?. Sustainable Chemical Processes, 2016, 4, .	2.3	4

#	ARTICLE	IF	CITATIONS
19	Complete Genome Sequence of Houston Virus, a Newly Discovered Mosquito-Specific Virus Isolated from <i>Culex quinquefasciatus</i> in Mexico. <i>Microbiology Resource Announcements</i> , 2018, 7, .	0.3	4
20	Comparing Sediment Microbiomes in Contaminated and Pristine Wetlands along the Coast of Yucatan. <i>Microorganisms</i> , 2021, 9, 877.	1.6	4
21	Tracing the Repertoire of Promiscuous Enzymes along the Metabolic Pathways in Archaeal Organisms. <i>Life</i> , 2017, 7, 30.	1.1	3
22	Voices of biotech research. <i>Nature Biotechnology</i> , 2021, 39, 281-286.	9.4	3
23	Epigenetics knocks on synthetic biology's door. <i>FEMS Microbiology Letters</i> , 2016, 363, fnw191.	0.7	1
24	Comparative genomics of DNA-binding transcription factors in archaeal and bacterial organisms. <i>PLoS ONE</i> , 2021, 16, e0254025.	1.1	0