

# Mario Alberto Martínez-Núñez

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

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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	Voices of biotech research. Nature Biotechnology, 2021, 39, 281-286.	9.4	3
2	Comparing Sediment Microbiomes in Contaminated and Pristine Wetlands along the Coast of Yucatan. Microorganisms, 2021, 9, 877.	1.6	4
3	Pseudocrossidium replicatum (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
4	Comparative genomics of DNA-binding transcription factors in archaeal and bacterial organisms. PLoS ONE, 2021, 16, e0254025.	1.1	0
5	Identification of Novel Conotoxin Precursors from the Cone Snail Conus spurius by High-Throughput RNA Sequencing. Marine Drugs, 2021, 19, 547.	2.2	6
6	Mining the Yucatan Coastal Microbiome for the Identification of Non-Ribosomal Peptides Synthetase (NRPS) Genes. Toxins, 2020, 12, 349.	1.5	9
7	Genome-Wide Association Study Reveals Candidate Genes for Litter Size Traits in Pelibuey Sheep. Animals, 2020, 10, 434.	1.0	33
8	Evaluation of the Abundance of DNA-Binding Transcription Factors in Prokaryotes. Genes, 2020, 11, 52.	1.0	14
9	RNA-seq Transcriptome Analysis in Ovarian Tissue of Pelibuey Breed to Explore the Regulation of Prolificacy. Genes, 2019, 10, 358.	1.0	17
10	Functional Prediction of Hypothetical Transcription Factors of Escherichia coli K-12 Based on Expression Data. Computational and Structural Biotechnology Journal, 2018, 16, 157-166.	1.9	6
11	Complete Genome Sequence of Houston Virus, a Newly Discovered Mosquito-Specific Virus Isolated from Culex quinquefasciatus in Mexico. Microbiology Resource Announcements, 2018, 7, .	0.3	4
12	Dissecting the Repertoire of DNA-Binding Transcription Factors of the Archaeon Pyrococcus furiosus DSM 3638. Life, 2018, 8, 40.	1.1	5
13	Abundance, diversity and domain architecture variability in prokaryotic DNA-binding transcription factors. PLoS ONE, 2018, 13, e0195332.	1.1	62
14	Tracing the Repertoire of Promiscuous Enzymes along the Metabolic Pathways in Archaeal Organisms. Life, 2017, 7, 30.	1.1	3
15	Dissecting the protein architecture of DNA-binding transcription factors in bacteria and archaea. Microbiology (United Kingdom), 2017, 163, 1167-1178.	0.7	13
16	Epigenetics knocks on synthetic biology's door. FEMS Microbiology Letters, 2016, 363, fnw191.	0.7	1
17	Nonribosomal peptides synthetases and their applications in industry. Sustainable Chemical Processes, 2016, 4, .	2.3	75
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	The lifestyle of prokaryotic organisms influences the repertoire of promiscuous enzymes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1625-1631.	1.5	9
20	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
21	Increments and Duplication Events of Enzymes and Transcription Factors Influence Metabolic and Regulatory Diversity in Prokaryotes. <i>PLoS ONE</i> , 2013, 8, e69707.	1.1	18
22	The Repertoire of DNA-Binding Transcription Factors in Prokaryotes: Functional and Evolutionary Lessons. <i>Science Progress</i> , 2012, 95, 315-329.	1.0	9
23	New insights into the regulatory networks of paralogous genes in bacteria. <i>Microbiology (United Kingdom)</i> 151: 1074-1084. doi:10.1099/mic/0/000000.0	0.7	31
24	Analysis of some phenotypic traits of feces-borne temperate lambdoid bacteriophages from different immunity groups: a high incidence of <i>cor+</i> , <i>FhuA</i> -dependent phages. <i>Archives of Virology</i> , 2008, 153, 1271-1280.	0.9	10