

Jose Arturo Molina-Mora

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

295
citations

1307366

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h-index

996849

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25
all docs

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docs citations

25
times ranked

295
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the mutation T1117I in the spike and the lineage B.1.1.389 of SARS-CoV-2 circulating in Costa Rica. <i>Gene Reports</i> , 2022, 27, 101554.	0.4	13
2	Alterations in common marmoset gut microbiome associated with duodenal strictures. <i>Scientific Reports</i> , 2022, 12, 5277.	1.6	8
3	Metagenomic pipeline for identifying co-infections among distinct SARS-CoV-2 variants of concern: study cases from Alpha to Omicron. <i>Scientific Reports</i> , 2022, 12, .	1.6	15
4	Clinical Profiles at the Time of Diagnosis of SARS-CoV-2 Infection in Costa Rica During the Pre-vaccination Period Using a Machine Learning Approach. <i>Phenomics</i> , 2022, 2, 312-322.	0.9	12
5	Set-theory based benchmarking of three different variant callers for targeted sequencing. <i>BMC Bioinformatics</i> , 2021, 22, 20.	1.2	0
6	Genomic context of the two integrons of ST-111 <i>Pseudomonas aeruginosa</i> AG1: A VIM-2-carrying old-acquaintance and a novel IMP-18-carrying integron. <i>Infection, Genetics and Evolution</i> , 2021, 89, 104740.	1.0	7
7	Molecular Determinants of Antibiotic Resistance in the Costa Rican <i>Pseudomonas aeruginosa</i> AG1 by a Multi-omics Approach: A Review of 10 Years of Study. <i>Phenomics</i> , 2021, 1, 129-142.	0.9	9
8	A first perturbome of <i>Pseudomonas aeruginosa</i> : Identification of core genes related to multiple perturbations by a machine learning approach. <i>BioSystems</i> , 2021, 205, 104411.	0.9	6
9	SARS-CoV-2 genomic surveillance in Costa Rica: Evidence of a divergent population and an increased detection of a spike T1117I mutation. <i>Infection, Genetics and Evolution</i> , 2021, 92, 104872.	1.0	25
10	High Efficacy of Therapeutic Equine Hyperimmune Antibodies Against SARS-CoV-2 Variants of Concern. <i>Frontiers in Medicine</i> , 2021, 8, 735853.	1.2	7
11	Avances de la bioinformática en Costa Rica: vista retrospectiva y perspectivas. <i>Revista De Biología Tropical</i> , 2021, 69, 1204-1223.	0.1	0
12	Transcriptomic determinants of the response of ST-111 <i>Pseudomonas aeruginosa</i> AG1 to ciprofloxacin identified by a top-down systems biology approach. <i>Scientific Reports</i> , 2020, 10, 13717.	1.6	13
13	Two-dimensional gel electrophoresis (2D-GE) image analysis based on CellProfiler. <i>Medicine (United Tj ETQq1 1 0.784314 rgBT /Over</i>	0.4	5
14	Proteogenomic analysis of the <i>Clostridium difficile</i> exoproteome reveals a correlation between phylogenetic distribution and virulence potential. <i>Anaerobe</i> , 2020, 62, 102151.	1.0	5
15	High quality 3C de novo assembly and annotation of a multidrug resistant ST-111 <i>Pseudomonas aeruginosa</i> genome: Benchmark of hybrid and non-hybrid assemblers. <i>Scientific Reports</i> , 2020, 10, 1392.	1.6	32
16	A hybrid mathematical modeling approach of the metabolic fate of a fluorescent sphingolipid analogue to predict cancer chemosensitivity. <i>Computers in Biology and Medicine</i> , 2018, 97, 8-20.	3.9	7
17	Effect of Heart Rate Variability Biofeedback on Sport Performance, a Systematic Review. <i>Applied Psychophysiology Biofeedback</i> , 2017, 42, 235-245.	1.0	109
18	Phenotypic and Genotypic Characterization of Multidrug-Resistant <i>Bacteroides</i> , <i>Parabacteroides</i> spp., and <i>Pseudoflavonifractor</i> from a Costa Rican Hospital. <i>Microbial Drug Resistance</i> , 2014, 20, 478-484.	0.9	15