

Rodrigo Jardim

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

300
citations

1306789

7
h-index

940134

16
g-index

20
all docs

20
docs citations

20
times ranked

754
citing authors

#	ARTICLE	IF	CITATIONS
1	GAP: Enhancing Semantic Interoperability of Genomic Datasets and Provenance Through Nanopublications. <i>Communications in Computer and Information Science</i> , 2022, , 336-348.	0.4	0
2	Core of the saliva microbiome: an analysis of the MG-RAST data. <i>BMC Oral Health</i> , 2021, 21, 351.	0.8	11
3	Events linked to Geosmin and 2-methylisoborneol (2-MIB) in a Water Supply in the State of Rio de Janeiro, Brazil: a case study. <i>International Journal of Hydrology</i> , 2021, 5, 214-220.	0.2	4
4	2020 taxonomic update for phylum Negarnaviricota (Riboviria: Orthornavirae), including the large orders Bunyavirales and Mononegavirales. <i>Archives of Virology</i> , 2020, 165, 3023-3072.	0.9	184
5	Água de reÁso: uma alternativa sustentÁvel para o Brasil. <i>Engenharia Sanitaria E Ambiental</i> , 2020, 25, 791-808.	0.1	9
6	Evaluating FAIRness of Genomic Databases. <i>Lecture Notes in Computer Science</i> , 2020, , 128-137.	1.0	2
7	AporÁ virus, a novel mammarenavirus (Bunyvirales: Arenaviridae) related to highly pathogenic virus from South America. <i>Memorias Do Instituto Oswaldo Cruz</i> , 2019, 114, e180586.	0.8	7
8	Multilocus Analysis Resolves the European Finch Epidemic Strain of <i>Trichomonas gallinae</i> and Suggests Introgression from Divergent Trichomonads. <i>Genome Biology and Evolution</i> , 2019, 11, 2391-2402.	1.1	17
9	Systematic Identification and Classification of β -Lactamases Based on Sequence Similarity Criteria: β -Lactamase Annotation. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431879735.	0.6	15
10	Mining of potential drug targets through the identification of essential and analogous enzymes in the genomes of pathogens of <i>Glycine max</i> , <i>Zea mays</i> and <i>Solanum lycopersicum</i> . <i>PLoS ONE</i> , 2018, 13, e0197511.	1.1	3
11	Homology Inference Based on a Reconciliation Approach for the Comparative Genomics of Protozoa. <i>Evolutionary Bioinformatics</i> , 2018, 14, 117693431878513.	0.6	1
12	Managing workflows on top of a cloud computing orchestrator for using heterogeneous environments on e-Science. <i>International Journal of Web and Grid Services</i> , 2017, 13, 375.	0.4	2
13	ProtozoaDB 2.0: A <i>Trypanosoma Brucei</i> Case Study. <i>Pathogens</i> , 2017, 6, 32.	1.2	1
14	Improved orthologous databases to ease protozoan targets inference. <i>Parasites and Vectors</i> , 2015, 8, 494.	1.0	2
15	An Orthology-Based Analysis of Pathogenic Protozoa Impacting Global Health: An Improved Comparative Genomics Approach with Prokaryotes and Model Eukaryote Orthologs. <i>OMICS A Journal of Integrative Biology</i> , 2014, 18, 524-538.	1.0	8
16	STINGRAY: system for integrated genomic resources and analysis. <i>BMC Research Notes</i> , 2014, 7, 132.	0.6	5
17	The Comparative Genomics and Phylogenomics of <i>Leishmania Amazonensis</i> Parasite. <i>Evolutionary Bioinformatics</i> , 2014, 10, EBO.S13759.	0.6	23