Diego C B Mariano

List of Publications by Year in descending order

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1040056 794594 43 510 9 19 citations g-index h-index papers 46 46 46 667 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Propedia: a database for protein–peptide identification based on a hybrid clustering algorithm. BMC Bioinformatics, 2021, 22, 1.	2.6	261
2	Genome Sequence of Lactococcus lactis subsp. lactis NCDO 2118, a GABA-Producing Strain. Genome Announcements, 2014, 2, .	0.8	31
3	The genome anatomy of Corynebacterium pseudotuberculosis VD57 a highly virulent strain causing Caseous lymphadenitis. Standards in Genomic Sciences, 2016, 11, 29.	1.5	20
4	Characterization of glucose-tolerant \hat{l}^2 -glucosidases used in biofuel production under the bioinformatics perspective: a systematic review. Genetics and Molecular Research, 2017, 16, .	0.2	19
5	Whole-genome optical mapping reveals a mis-assembly between two rRNA operons of Corynebacterium pseudotuberculosis strain 1002. BMC Genomics, 2016, 17, 315.	2.8	17
6	Molecular Dynamics Gives New Insights into the Glucose Tolerance and Inhibition Mechanisms on \hat{l}^2 -Glucosidases. Molecules, 2019, 24, 3215.	3.8	17
7	Introducing Programming Skills for Life Science Students. Biochemistry and Molecular Biology Education, 2019, 47, 288-295.	1.2	16
8	MapRepeat: an approach for effective assembly of repetitive regions in prokaryotic genomes. Bioinformation, $2015,11,276-279.$	0.5	12
9	A Computational Method to Propose Mutations in Enzymes Based on Structural Signature Variation (SSV). International Journal of Molecular Sciences, 2019, 20, 333.	4.1	11
10	Proteingo: Motivation, user experience, and learning of molecular interactions in biological complexes. Entertainment Computing, 2019, 29, 31-42.	2.9	10
11	Conformational flexibility correlates with glucose tolerance for point mutations in β-glucosidases – a computational study. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1621-1634.	3.5	10
12	Glutantl̂ ase: a database for improving the rational design of glucose-tolerant \hat{l}^2 -glucosidases. BMC Molecular and Cell Biology, 2020, 21, 50.	2.0	9
13	SIMBA: a web tool for managing bacterial genome assembly generated by Ion PGM sequencing technology. BMC Bioinformatics, 2016, 17, 456.	2.6	8
14	Complete genome sequence of Streptococcus agalactiae strain GBS85147 serotype of type Ia isolated from human oropharynx. Standards in Genomic Sciences, 2016, 11, 39.	1.5	6
15	Proteus: An algorithm for proposing stabilizing mutation pairs based on interactions observed in known protein 3D structures. BMC Bioinformatics, 2020, 21, 275.	2.6	6
16	Molecular and genetic characterization of a large Brazilian cohort presenting hearing loss. Human Genetics, 2022, 141, 519-538.	3.8	6
17	Genome Sequence of Corynebacterium ulcerans Strain FRC11. Genome Announcements, 2015, 3, .	0.8	5
18	CMRegNet–An interspecies reference database for corynebacterial and mycobacterial regulatory networks. BMC Genomics, 2015, 16, 452.	2.8	5

#	Article	IF	Citations
19	Complete Genome Sequence of the Attenuated Corynebacterium pseudotuberculosis Strain T1. Genome Announcements, 2016, 4, .	0.8	5
20	Transcriptome analysis of Corynebacterium pseudotuberculosis biovar Equi in two conditions of the environmental stress. Gene, 2018, 677, 349-360.	2.2	5
21	Genome Sequence of Corynebacterium ulcerans Strain 210932. Genome Announcements, 2014, 2, .	0.8	4
22	VTR: A Web Tool for Identifying Analogous Contacts on Protein Structures and Their Complexes. Frontiers in Bioinformatics, 2021, 1 , .	2.1	4
23	Complete Genome Sequence of Corynebacterium pseudotuberculosis Strain 12C. Genome Announcements, 2015, 3, .	0.8	3
24	Draft Genome Sequence of Toxigenic Corynebacterium ulcerans Strain 04-7514, Isolated from a Dog in France. Genome Announcements, 2016, 4, .	0.8	3
25	Draft Genome Sequence of a Virulent Strain of Pasteurella Multocida Isolated From Alpaca. Journal of Genomics, 2017, 5, 68-70.	0.9	3
26	Métricas de avaliação em machine learning: acurácia, sensibilidade, precisão, especificidade e F-score. , 0, , .		3
27	E-Volve: understanding the impact of mutations in SARS-CoV-2 variants spike protein on antibodies and ACE2 affinity through patterns of chemical interactions at protein interfaces. PeerJ, 2022, 10, e13099.	2.0	3
28	Draft Genome Sequence of Corynebacterium ulcerans Strain 04-3911, Isolated from Humans. Genome Announcements, 2016, 4, .	0.8	2
29	Draft Genome Sequence of Toxigenic <i>Corynebacterium ulcerans</i> Strain 03-8664 Isolated from a Human Throat. Genome Announcements, 2016, 4, .	0.8	2
30	Uma estratégia para engajamento de participantes de eventos online. , 0, , .		1
31	ToxAnalyzer: A user-friendly web tool for interactive data analysis and visualization of chemical compounds from the Comparative Toxicogenomics Database (CTD)â,, Computational Toxicology, 2021, 19, 100170.	3.3	1
32	Milk-Way algorithm for ligand-based virtual screening: CDK2 case study. Trends in Developmental Biology, 0, 13, 1.	1.0	1
33	WordPress sem fronteiras: do básico à construção de sites completos. , 2020, , .		1
34	Whole-Genome Sequence of Corynebacterium auriscanis Strain CIP 106629 Isolated from a Dog with Bilateral Otitis from the United Kingdom. Genome Announcements, 2016, 4, .	0.8	0
35	Biopython: uma breve introdu $ ilde{A}$ § $ ilde{A}$ £o $ ilde{A}$ manipula $ ilde{A}$ § $ ilde{A}$ £o de dados biol $ ilde{A}$ 3gicos em Python usando Colab. , 0, , .		0
36	Alinhamentos estruturais: métodos de sobreposição de proteÃnas e outras moléculas. , 0, , .		0

#	Article	IF	CITATIONS
37	Editorial – BIOINFO #01., 0, , .		O
38	Tipos de cobertura em sequenciamento genômico., 0, , .		0
39	Din $ ilde{A}^{\varphi}$ mica molecular: como mostrar um filme completo em uma folha de papel?. , 0, , .		0
40	From In-Person to the Online World: Insights Into Organizing Events in Bioinformatics. Frontiers in Bioinformatics, 2021, 1 , .	2.1	0
41	A Brief History of Bioinformatics Told by Data Visualization. Lecture Notes in Computer Science, 2020, , 235-246.	1.3	0
42	Bootstrap 5 – Guia Rápido para Iniciantes. , 2022, , .		0
43	Using Computers to Improve Biofuel Production. Frontiers for Young Minds, 0, 10, .	0.8	0