Pedro Henrique Monteiro Torres

List of Publications by Year
in descending order

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25 papers	586 citations	686830 13 h-index	642321 23 g-index
26 all docs	26 docs citations	26 times ranked	983 citing authors

#	Article	IF	Citations
1	Key Topics in Molecular Docking for Drug Design. International Journal of Molecular Sciences, 2019, 20, 4574.	1.8	245
2	Genomic and structural features of the yellow fever virus from the 2016â€“2017 Brazilian outbreak. Journal of General Virology, 2018, 99, 536-548.	1.3	50
3	The Aâ€“Z of Zika drug discovery. Drug Discovery Today, 2018, 23, 1833-1847.	3.2	48
4	SARS-CoV-2 3D database: understanding the coronavirus proteome and evaluating possible drug targets. Briefings in Bioinformatics, 2021, 22, 769-780.	3.2	31
5	Predicted structural mimicry of spike receptor-binding motifs from highly pathogenic human coronaviruses. Computational and Structural Biotechnology Journal, 2021, 19, 3938-3953.	1.9	25
6	Compound profiling and 3D-QSAR studies of hydrazone derivatives with activity against intracellular Trypanosoma cruzi. Bioorganic and Medicinal Chemistry, 2016, 24, 1608-1618.	1.4	23
7	The Molecular Organization of Human cGMP Specific Phosphodiesterase 6 (PDE6): Structural Implications of Somatic Mutations in Cancer and Retinitis Pigmentosa. Computational and Structural Biotechnology Journal, 2019, 17, 378-389.	1.9	20
8	Investigation of the binding mode of a novel cruzain inhibitor by docking, molecular dynamics, ab initio and MM/PBSA calculations. Journal of Computer-Aided Molecular Design, 2018, 32, 591-605.	1.3	18
9	ProCarbDB: a database of carbohydrate-binding proteins. Nucleic Acids Research, 2020, 48, D368-D375.	6.5	17
10	Unraveling HIV protease flaps dynamics by Constant pH Molecular Dynamics simulations. Journal of Structural Biology, 2016, 195, 216-226.	1.3	15
11	Insights into cytochrome bc1 complex binding mode of antimalarial 2-hydroxy-1,4-naphthoquinones through molecular modelling. Memorias Do Instituto Oswaldo Cruz, 2017, 112, 299-308.	0.8	15
12	Improving Blind Docking in DOCK6 through an Automated Preliminary Fragment Probing Strategy. Molecules, 2021, 26, 1224.	1.7	14
13	Structural analysis of the Nâ€terminal fragment of the antiangiogenic protein endostatin: A molecular dynamics study. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2684-2692.	1.5	13
14	Mabellini: a genome-wide database for understanding the structural proteome and evaluating prospective antimicrobial targets of the emerging pathogen Mycobacterium abscessus. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	12
15	COSMIC Cancer Gene Census 3D database: understanding the impacts of mutations on cancer targets. Briefings in Bioinformatics, 2021, 22, .	3.2	8
16	Inhibiting Mycobacterium tuberculosis CoaBC by targeting an allosteric site. Nature Communications, 2021, 12, 143.	5.8	8
17	Computational drug discovery for the Zika virus. Brazilian Journal of Pharmaceutical Sciences, 2018, 54, .	1.2	6
18	Dataset showing the impact of the protonation states on molecular dynamics of HIV protease. Data in Brief, 2016, 8, 1144-1150.	0.5	3

#	Article	IF	Citations
19	ProtCHOIR: a tool for proteome-scale generation of homo-oligomers. Briefings in Bioinformatics, 2021, 22, .	3.2	3
20	G Protein-Coupled Receptors. Revista Virtual De Quimica, 2013, 5, .	0.1	3
21	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.4	3
22	Structure-Guided Computational Approaches to Unravel Druggable Proteomic Landscape of Mycobacterium leprae. Frontiers in Molecular Biosciences, 2021, 8, 663301.	1.6	2
23	New Treatments for Chagas Disease and the Relationship between Chagasic Patients and Cancers. Cancer Research Journal, 2014, 2, 11.	0.0	2
24	A novel receptor for plateletâ€activating factor and lysophosphatidylcholine in Trypanosoma cruzi. Molecular Microbiology, 2021, 116, 890-908.	1.2	1
25	Alternative Model for RND-Type Efflux Pump. Journal of the Brazilian Chemical Society, 2016, , .	0.6	0