

Pedro Henrique Monteiro Torres

List of Publications by Year in descending order

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25
papers

586
citations

687363

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642732

23
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26
all docs

26
docs citations

26
times ranked

983
citing authors

#	ARTICLE	IF	CITATIONS
1	SARS-CoV-2 3D database: understanding the coronavirus proteome and evaluating possible drug targets. Briefings in Bioinformatics, 2021, 22, 769-780.	6.5	31
2	Improving Blind Docking in DOCK6 through an Automated Preliminary Fragment Probing Strategy. Molecules, 2021, 26, 1224.	3.8	14
3	ProtCHOIR: a tool for proteome-scale generation of homo-oligomers. Briefings in Bioinformatics, 2021, 22, .	6.5	3
4	Structure-Guided Computational Approaches to Unravel Druggable Proteomic Landscape of Mycobacterium leprae. Frontiers in Molecular Biosciences, 2021, 8, 663301.	3.5	2
5	COSMIC Cancer Gene Census 3D database: understanding the impacts of mutations on cancer targets. Briefings in Bioinformatics, 2021, 22, .	6.5	8
6	A novel receptor for platelet-activating factor and lysophosphatidylcholine in Trypanosoma cruzi. Molecular Microbiology, 2021, 116, 890-908.	2.5	1
7	Predicted structural mimicry of spike receptor-binding motifs from highly pathogenic human coronaviruses. Computational and Structural Biotechnology Journal, 2021, 19, 3938-3953.	4.1	25
8	Inhibiting Mycobacterium tuberculosis CoaBC by targeting an allosteric site. Nature Communications, 2021, 12, 143.	12.8	8
9	ProCarbDB: a database of carbohydrate-binding proteins. Nucleic Acids Research, 2020, 48, D368-D375.	14.5	17
10	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.9	3
11	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, .	3.0	12
12	Key Topics in Molecular Docking for Drug Design. International Journal of Molecular Sciences, 2019, 20, 4574.	4.1	245
13	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.	4.1	20
14	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.	2.9	18
15	Computational drug discovery for the Zika virus. Brazilian Journal of Pharmaceutical Sciences, 2018, 54, .	1.2	6
16	The A-Z of Zika drug discovery. Drug Discovery Today, 2018, 23, 1833-1847.	6.4	48
17	Genomic and structural features of the yellow fever virus from the 2016-2017 Brazilian outbreak. Journal of General Virology, 2018, 99, 536-548.	2.9	50
18	Insights into cytochrome bc1 complex binding mode of antimalarial 2-hydroxy-1,4-naphthoquinones through molecular modelling. Memórias Do Instituto Oswaldo Cruz, 2017, 112, 299-308.	1.6	15

#	ARTICLE	IF	CITATIONS
19	Dataset showing the impact of the protonation states on molecular dynamics of HIV protease. Data in Brief, 2016, 8, 1144-1150.	1.0	3
20	Unraveling HIV protease flaps dynamics by Constant pH Molecular Dynamics simulations. Journal of Structural Biology, 2016, 195, 216-226.	2.8	15
21	Compound profiling and 3D-QSAR studies of hydrazone derivatives with activity against intracellular Trypanosoma cruzi. Bioorganic and Medicinal Chemistry, 2016, 24, 1608-1618.	3.0	23
22	Alternative Model for RND-Type Efflux Pump. Journal of the Brazilian Chemical Society, 2016, , .	0.6	0
23	New Treatments for Chagas Disease and the Relationship between Chagasic Patients and Cancers. Cancer Research Journal, 2014, 2, 11.	0.0	2
24	G Protein-Coupled Receptors. Revista Virtual De Quimica, 2013, 5, .	0.4	3
25	Structural analysis of the N-terminal fragment of the antiangiogenic protein endostatin: A molecular dynamics study. Proteins: Structure, Function and Bioinformatics, 2011, 79, 2684-2692.	2.6	13