MdRimon parves

List of Publications by Year
in descending order

11 papers	460 citations	1163117 8 h-index	1281871 11 g-index
11 all docs	11 docs citations	11 times ranked	872 citing authors

#	Article	IF	Citations
1	Cysteine focused covalent inhibitors against the main protease of SARS-CoV-2. Journal of Biomolecular Structure and Dynamics, 2022, 40, 1639-1658.	3.5	20
2	Designing potent inhibitors against the multidrug resistance P-glycoprotein. Journal of Biomolecular Structure and Dynamics, 2022, 40, 9403-9415.	3.5	3
3	Investigating the binding affinity, interaction, and structure-activity-relationship of 76 prescription antiviral drugs targeting RdRp and Mpro of SARS-CoV-2. Journal of Biomolecular Structure and Dynamics, 2021, 39, 6290-6305.	3.5	29
4	A molecular modeling approach to identify effective antiviral phytochemicals against the main protease of SARS-CoV-2. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1-12.	3.5	218
5	Repurposing fusion inhibitor peptide against <scp>SARSâ€CoV</scp>â€2. Journal of Computational Chemistry, 2021, 42, 2283-2293.	3.3	14
6	Inhibition of TNF-Alpha Using Plant-Derived Small Molecules for Treatment of Inflammation-Mediated Diseases. Proceedings (mdpi), 2021, 83, 13.	0.2	1
7	Exploring the potent inhibitors and binding modes of phospholipase A2 through in silico investigation. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4221-4231.	3.5	27
8	Antiviral Peptides as Promising Therapeutics against SARS-CoV-2. Journal of Physical Chemistry B, 2020, 124, 9785-9792.	2.6	66
9	Prediction of Deleterious Non-synonymous SNPs of Human STK11 Gene by Combining Algorithms, Molecular Docking, and Molecular Dynamics Simulation. Scientific Reports, 2019, 9, 16426.	3.3	46
10	Assessment of structurally and functionally high-risk nsSNPs impacts on human bone morphogenetic protein receptor type IA (BMPR1A) by computational approach. Computational Biology and Chemistry, 2019, 80, 31-45.	2.3	28
11	Quantum chemical calculation and binding modes of H1R; a combined study of molecular docking and DFT for suggesting therapeutically potent H1R antagonist. In Silico Pharmacology, 2019, 7, 1.	3.3	8