Olivier Sheik Amamuddy

List of Publications by Year
in descending order

14	490	840776	1058476
papers	citations	11	14
		h-index	g-index

17	17	17	618
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Slipknot or Crystallographic Error: A Computational Analysis of the Plasmodium falciparum DHFR Structural Folds. International Journal of Molecular Sciences, 2022, 23, 1514.	4.1	3
2	Deciphering Isoniazid Drug Resistance Mechanisms on Dimeric Mycobacterium tuberculosis KatG via Post-molecular Dynamics Analyses Including Combined Dynamic Residue Network Metrics. ACS Omega, 2022, 7, 13313-13332.	3.5	9
3	MDM-TASK-web: MD-TASK and MODE-TASK web server for analyzing protein dynamics. Computational and Structural Biotechnology Journal, 2021, 19, 5059-5071.	4.1	18
4	Polyphenols Epigallocatechin Gallate and Resveratrol, and Polyphenol-Functionalized Nanoparticles Prevent Enterovirus Infection through Clustering and Stabilization of the Viruses. Pharmaceutics, 2021, 13, 1182.	4.5	15
5	Allosteric pockets and dynamic residue network hubs of falcipain 2 in mutations including those linked to artemisinin resistance. Computational and Structural Biotechnology Journal, 2021, 19, 5647-5666.	4.1	13
6	Novel dynamic residue network analysis approaches to study allosteric modulation: SARS-CoV-2 Mpro and its evolutionary mutations as a case study. Computational and Structural Biotechnology Journal, 2021, 19, 6431-6455.	4.1	14
7	Impact of Early Pandemic Stage Mutations on Molecular Dynamics of SARS-CoV-2 M^{pro}. Journal of Chemical Information and Modeling, 2020, 60, 5080-5102.	5.4	62
8	Determining the unbinding events and conserved motions associated with the pyrazinamide release due to resistance mutations of Mycobacterium tuberculosis pyrazinamidase. Computational and Structural Biotechnology Journal, 2020, 18, 1103-1120.	4.1	13
9	Integrated Computational Approaches and Tools for Allosteric Drug Discovery. International Journal of Molecular Sciences, 2020, 21, 847.	4.1	73
10	Characterizing early drug resistance-related events using geometric ensembles from HIV protease dynamics. Scientific Reports, 2018, 8, 17938.	3.3	24
11	MODE-TASK: large-scale protein motion tools. Bioinformatics, 2018, 34, 3759-3763.	4.1	45
12	Improving fold resistance prediction of HIV-1 against protease and reverse transcriptase inhibitors using artificial neural networks. BMC Bioinformatics, 2017, 18, 369.	2.6	24
13	Structure-Based Analysis of Single Nucleotide Variants in the Renin-Angiotensinogen Complex. Global Heart, 2017, 12, 121.	2.3	31
14	MD-TASK: a software suite for analyzing molecular dynamics trajectories. Bioinformatics, 2017, 33, 2768-2771.	4.1	142