

Olivier Sheik Amamuddy

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

490
citations

840776

11
h-index

1058476

14
g-index

17
all docs

17
docs citations

17
times ranked

618
citing authors

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