

Taniya Bhardwaj

List of Publications by Year in descending order

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Version: 2024-02-01

13
papers

263
citations

1464605

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1255698

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all docs

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docs citations

20
times ranked

403
citing authors

#	ARTICLE	IF	CITATIONS
1	Reprofiling of approved drugs against SARS-CoV-2 main protease: an in-silico study. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3170-3184.	2.0	20
2	One microsecond MD simulations of the SARS-CoV-2 main protease and hydroxychloroquine complex reveal the intricate nature of binding. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 10763-10770.	2.0	2
3	Microsecond simulations and CD spectroscopy reveals the intrinsically disordered nature of SARS-CoV-2 spike-C-terminal cytoplasmic tail (residues 1242-1273) in isolation. <i>Virology</i> , 2022, 566, 42-55.	1.1	14
4	Mitoxantrone dihydrochloride, an FDA approved drug, binds with SARS-CoV-2 NSP1 C-terminal. <i>RSC Advances</i> , 2022, 12, 5648-5655.	1.7	11
5	Role of structural disorder in the multi-functionality of flavivirus proteins. <i>Expert Review of Proteomics</i> , 2022, 19, 183-196.	1.3	1
6	Understanding COVID-19 via comparative analysis of dark proteomes of SARS-CoV-2, human SARS and bat SARS-like coronaviruses. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 1655-1688.	2.4	92
7	A novel inhibitor L755507 efficiently blocks c-Myc-MAX heterodimerization and induces apoptosis in cancer cells. <i>Journal of Biological Chemistry</i> , 2021, 297, 100903.	1.6	13
8	Salvianolic acid B noncovalently interacts with disordered c-Myc: a computational and spectroscopic-based study. <i>Future Medicinal Chemistry</i> , 2021, 13, 1341-1352.	1.1	4
9	Conformational dynamics of 13 amino acids long NSP11 of SARS-CoV-2 under membrane mimetics and different solvent conditions. <i>Microbial Pathogenesis</i> , 2021, 158, 105041.	1.3	26
10	The signal peptide of the amyloid precursor protein forms amyloid-like aggregates and enhances A β 242 aggregation. <i>Cell Reports Physical Science</i> , 2021, 2, 100599.	2.8	5
11	Zika virus NS4A N-Terminal region (1-48) acts as a cofactor for inducing NTPase activity of NS3 helicase but not NS3 protease. <i>Archives of Biochemistry and Biophysics</i> , 2020, 695, 108631.	1.4	8
12	Exploring the SARS-CoV-2 structural proteins for multi-epitope vaccine development: an in-silico approach. <i>Expert Review of Vaccines</i> , 2020, 19, 887-898.	2.0	19
13	Japanese encephalitis virus – exploring the dark proteome and disorder-function paradigm. <i>FEBS Journal</i> , 2020, 287, 3751-3776.	2.2	18