Kiran Bharat Lokhande

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/931158/publications.pdf

Version: 2024-02-01

22 papers 411 citations

759055 12 h-index 19 g-index

25 all docs

25 docs citations

25 times ranked

418 citing authors

#	Article	IF	CITATIONS
1	Molecular docking and simulation studies on SARS-CoV-2 M ^{pro} reveals Mitoxantrone, Leucovorin, Birinapant, and Dynasore as potent drugs against COVID-19. Journal of Biomolecular Structure and Dynamics, 2021, 39, 7294-7305.	2.0	82
2	Sensing the interactions between carbohydrate-binding agents and <i>N</i> -linked glycans of SARS-CoV-2 spike glycoprotein using molecular docking and simulation studies. Journal of Biomolecular Structure and Dynamics, 2022, 40, 3880-3898.	2.0	33
3	Biflavonoids from <i>Rhus succedanea</i> as probable natural inhibitors against SARS-CoV-2: a molecular docking and molecular dynamics approach. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4376-4388.	2.0	33
4	Molecular interaction studies of Deguelin and its derivatives with Cyclin D1 and Cyclin E in cancer cell signaling pathway: The computational approach. Scientific Reports, 2019, 9, 1778.	1.6	31
5	Probing intermolecular interactions and binding stability of kaempferol, quercetin and resveratrol derivatives with PPAR-Î ³ : docking, molecular dynamics and MM/GBSA approach to reveal potent PPAR-Î ³ agonist against cancer. Journal of Biomolecular Structure and Dynamics, 2022, 40, 971-981.	2.0	24
6	Antioxidant, anti-quorum sensing, biofilm inhibitory activities and chemical composition of Patchouli essential oil: $\langle i \rangle$ in \hat{A} iro and \hat{A} in silico \hat{A} is approach. Journal of Biomolecular Structure and Dynamics, 2022, 40, 154-165.	2.0	21
7	An in silico scientific basis for <scp>LL</scp> â€37 as a therapeutic for Covidâ€19. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1029-1043.	1.5	21
8	Exploring conformational changes of PPAR-Æ" complexed with novel kaempferol, quercetin, and resveratrol derivatives to understand binding mode assessment: a small-molecule checkmate to cancer therapy. Journal of Molecular Modeling, 2020, 26, 242.	0.8	18
9	Molecular Modeling, Docking, Dynamics and Simulation of Gefitinib and its Derivatives with EGFR in Non-small Cell Lung Cancer. Current Computer-Aided Drug Design, 2018, 14, 246-252.	0.8	18
10	Novel B, C-ring truncated deguelin derivatives reveals as potential inhibitors of cyclin D1 and cyclin E using molecular docking and molecular dynamic simulation. Molecular Diversity, 2022, 26, 2295-2309.	2.1	18
11	In vivo and molecular docking studies using whole extract and phytocompounds of Aegle marmelos fruit protective effects against Isoproterenol-induced Myocardial infarction in rats. Biomedicine and Pharmacotherapy, 2017, 91, 880-889.	2.5	17
12	High throughput virtual screening and molecular dynamics simulation analysis of phytomolecules against BfmR of <i>Acinetobacter baumannii</i> : anti-virulent drug development campaign. Journal of Biomolecular Structure and Dynamics, 2023, 41, 2698-2712.	2.0	17
13	Computational data of phytoconstituents from Hibiscus rosa-sinensis on various anti-obesity targets. Data in Brief, 2019, 24, 103994.	0.5	16
14	<i>In Silico</i> Exploration of Phytoconstituents From <i>Phyllanthus emblica</i> and <i>Aegle marmelos</i> as Potential Therapeutics Against SARS-CoV-2 RdRp. Bioinformatics and Biology Insights, 2021, 15, 117793222110274.	1.0	14
15	Carbohydrate-Binding Agents: Potential of Repurposing for COVID-19 Therapy. Current Protein and Peptide Science, 2020, 21, 1085-1096.	0.7	13
16	GC-MS profiling of Bauhinia variegata major phytoconstituents with computational identification of potential lead inhibitors of SARS-CoV-2 Mpro. Computers in Biology and Medicine, 2022, 147, 105679.	3.9	12
17	Molecular profiling of multidrug-resistant river water isolates: insights into resistance mechanism and potential inhibitors. Environmental Science and Pollution Research, 2020, 27, 27279-27292.	2.7	11
18	Detection of Nail Oncometabolite SAICAR in Oral Cancer Patients and Its Molecular Interactions with PKM2 Enzyme. International Journal of Environmental Research and Public Health, 2021, 18, 11225.	1,2	4

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19	An immunoprophylactic evaluation of Ld-ODC derived HLA-A0201 restricted peptides against visceral leishmaniasis. Journal of Biomolecular Structure and Dynamics, 2021, , 1-11.	2.0	2
20	Data on docking of phytoconstituents of Actinidia deliciosa on dengue viral targets. Data in Brief, 2019, 25, 103996.	0.5	1
21	Transferrin binding protein-B from Neisseria meningitidis C as a novel carrier protein in glycoconjugate preparation: an in silico approach. Journal of Biomolecular Structure and Dynamics, 2021, , 1-11.	2.0	1
22	Novel nitrogen-containing heterocyclic compounds in GPR109A as an anti-hyperlipidemic: Homology modeling, docking, dynamic simulation studies. Journal of Research in Pharmacy, 2020, 24, 452-463.	0.1	0