

Akhil Kumar

List of Publications by Year in descending order

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Version: 2024-02-01

19
papers

397
citations

840585

11
h-index

839398

18
g-index

19
all docs

19
docs citations

19
times ranked

683
citing authors

#	ARTICLE	IF	CITATIONS
1	Molecular docking based virtual screening of natural compounds as potential BACE1 inhibitors: 3D QSAR pharmacophore mapping and molecular dynamics analysis. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 239-249.	2.0	44
2	Determination of potential inhibitors based on isatin derivatives against SARS-CoV-2 main protease (m ^{pro}): a molecular docking, molecular dynamics and structure-activity relationship studies. <i>Journal of Biomolecular Structure and Dynamics</i> , 2022, 40, 3110-3128.	2.0	41
3	Changing Paradigm from one Target one Ligand Towards Multi-target Directed Ligand Design for Key Drug Targets of Alzheimer Disease: An Important Role of In Silico Methods in Multi-target Directed Ligands Design. <i>Current Neuropharmacology</i> , 2018, 16, 726-739.	1.4	40
4	Molecular insight into amyloid oligomer destabilizing mechanism of flavonoid derivative 2-(4-hydroxyphenyl)-3-hydroxychromen-4-one. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1252-1263.	2.0	37
5	Docking, molecular dynamics, binding energy-MM-PBSA studies of naphthofuran derivatives to identify potential dual inhibitors against BACE-1 and GSK-3 β . <i>Journal of Biomolecular Structure and Dynamics</i> , 2019, 37, 275-290.	2.0	37
6	The Flavonoid Derivative 2-(4-benzyloxyphenyl)-3-hydroxychromen-4-one Protects Against A β 242-Induced Neurodegeneration in Transgenic <i>Drosophila</i> : Insights from In Silico and In Vivo Studies. <i>Neurotoxicity Research</i> , 2014, 26, 331-350.	1.3	34
7	Virtual screening, ADMET profiling, molecular docking and dynamics approaches to search for potent selective natural molecules based inhibitors against metallothionein-III to study Alzheimer's disease. <i>Methods</i> , 2015, 83, 105-110.	1.9	34
8	Gallic acid-based indanone derivative interacts synergistically with tetracycline by inhibiting efflux pump in multidrug resistant <i>E. coli</i> . <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 2311-2325.	1.7	27
9	Investigation of naphthofuran moiety as potential dual inhibitor against BACE-1 and GSK-3 β : molecular dynamics simulations, binding energy, and network analysis to identify first-in-class dual inhibitors against Alzheimer's disease. <i>Journal of Molecular Modeling</i> , 2017, 23, 239.	0.8	20
10	Molecular investigation of active binding site of isoniazid (INH) and insight into resistance mechanism of S315T-MtKatG in <i>Mycobacterium tuberculosis</i> . <i>Tuberculosis</i> , 2017, 105, 18-27.	0.8	19
11	Molecular docking and simulation studies to give insight of surfactin amyloid interaction for destabilizing Alzheimer's A β 242 protofibrils. <i>Medicinal Chemistry Research</i> , 2016, 25, 1616-1622.	1.1	18
12	The effect of Benzothiazolone on the expression of Metallothionein in modulating Alzheimer's disease. <i>Brain and Behavior</i> , 2017, 7, e00799.	1.0	11
13	Structural investigations into the binding mode of novel neolignans Cmp10 and Cmp19 microtubule stabilizers by in silico molecular docking, molecular dynamics, and binding free energy calculations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 1232-1240.	2.0	8
14	Screening of Anti-mycobacterial Phytochemical Compounds for Potential Inhibitors against <i>Mycobacterium Tuberculosis</i> Isocitrate Lyase. <i>Current Topics in Medicinal Chemistry</i> , 2019, 19, 600-608.	1.0	8
15	A physicochemical descriptor based method for effective and rapid screening of dual inhibitors against BACE-1 and GSK-3 β as targets for Alzheimer's disease. <i>Computational Biology and Chemistry</i> , 2017, 71, 1-9.	1.1	6
16	Computational Modeling of Multi-target-Directed Inhibitors Against Alzheimer's Disease. <i>Neuromethods</i> , 2018, , 533-571.	0.2	6
17	Molecular insight into multiple RpoB clinical mutants of <i>Mycobacterium tuberculosis</i> : An attempt to probe structural variations in rifampicin binding site underlying drug resistance. <i>International Journal of Biological Macromolecules</i> , 2018, 120, 2200-2214.	3.6	5
18	Current Trends in Docking Methodologies. <i>Advances in Medical Technologies and Clinical Practice Book Series</i> , 2016, , 320-338.	0.3	1

#	ARTICLE	IF	CITATIONS
19	Current Trends in Docking Methodologies., 2017, , 829-847.		1