Vikram Dalal

List of Publications by Year in descending order

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40	921	393982	500791
papers	citations	19 h-index	28 g-index

44	44	44	356
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational investigation of potent inhibitors against YsxC: structure-based pharmacophore modeling, molecular docking, molecular dynamics, and binding free energy. Journal of Biomolecular Structure and Dynamics, 2023, 41, 930-941.	2.0	15
2	Promising antivirals for PLpro of SARS-CoV-2 using virtual screening, molecular docking, dynamics, and MMPBSA. Journal of Biomolecular Structure and Dynamics, 2023, 41, 4650-4666.	2.0	18
3	Biochemical characterization and structure-basedin silicoscreening of potent inhibitor molecules against the 1 cys peroxiredoxin of bacterioferritin comigratory protein family fromCandidatus Liberibacter asiaticus. Journal of Biomolecular Structure and Dynamics, 2023, 41, 5776-5788.	2.0	4
4	Computational guided identification of novel potent inhibitors of N-terminal domain of nucleocapsid protein of severe acute respiratory syndrome coronavirus 2. Journal of Biomolecular Structure and Dynamics, 2022, 40, 4084-4099.	2.0	31
5	Antagonistic interaction between TTA-A2 and paclitaxel for anti-cancer effects by complex formation with T-type calcium channel. Journal of Biomolecular Structure and Dynamics, 2022, 40, 2395-2406.	2.0	19
6	In-silico screening and identification of potential inhibitors against 2Cys peroxiredoxin ofCandidatusLiberibacter asiaticus. Journal of Biomolecular Structure and Dynamics, 2022, 40, 8725-8739.	2.0	10
7	Identification of potential inhibitors for LLM ofStaphylococcus aureus: structure-based pharmacophore modeling, molecular dynamics, and binding free energy studies. Journal of Biomolecular Structure and Dynamics, 2022, 40, 9833-9847.	2.0	28
8	Molecular modeling and dynamics simulation of alcohol dehydrogenase enzyme from high efficacy cellulosic ethanol-producing yeast mutant strainPichia kudriavzeviiBGY1-Î³m. Journal of Biomolecular Structure and Dynamics, 2022, 40, 12022-12036.	2.0	4
9	Structural-based virtual screening and identification of novel potent antimicrobial compounds against YsxC of Staphylococcus aureus. Journal of Molecular Structure, 2022, 1255, 132476.	1.8	29
10	Quantum Mechanics/Molecular Mechanics Studies on the Catalytic Mechanism of a Novel Esterase (FmtA) of Staphylococcus aureus. Journal of Chemical Information and Modeling, 2022, 62, 2409-2420.	2.5	23
11	Erythrocytes model for oxidative stress analysis. , 2022, , 363-390.		0
12	In-silico functional and structural annotation of hypothetical protein from Klebsiella pneumonia: A potential drug target. Journal of Molecular Graphics and Modelling, 2022, 116, 108262.	1.3	23
13	Structure-Based Identification of Potential Drugs Against FmtA of Staphylococcus aureus: Virtual Screening, Molecular Dynamics, MM-GBSA, and QM/MM. Protein Journal, 2021, 40, 148-165.	0.7	47
14	A molecular docking and dynamic approach to screen inhibitors against ZnuA1 ofCandidatusLiberibacter asiaticus. Molecular Simulation, 2021, 47, 510-525.	0.9	18
15	Structure-based mimicking of hydroxylated biphenyl congeners (OHPCBs) for human transthyretin, an important enzyme of thyroid hormone system. Journal of Molecular Graphics and Modelling, 2021, 105, 107870.	1.3	29
16	Characterization of recombinant pumpkin 2S albumin and mutation studies to unravel potential DNA/RNA binding site. Biochemical and Biophysical Research Communications, 2021, 580, 28-34.	1.0	13
17	Multifunctional inhibitors of SARS-CoV-2 by MM/PBSA, essential dynamics, and molecular dynamic investigations. Journal of Molecular Graphics and Modelling, 2021, 107, 107969.	1.3	21
18	Structure of dye-decolorizing peroxidase from Bacillus subtilis in complex with veratryl alcohol. International Journal of Biological Macromolecules, 2021, 193, 601-608.	3.6	27

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19	Screening of Severe Acute Respiratory Syndrome Coronavirus 2 RNA-Dependent RNA Polymerase Inhibitors Using Computational Approach. Journal of Computational Biology, 2021, 28, 1228-1247.	0.8	13
20	Repurposing an ancient protein core structure: structural studies on FmtA, a novel esterase of Staphylococcus aureus. Acta Crystallographica Section A: Foundations and Advances, 2021, 77, C706-C706.	0.0	1
21	Molecular docking and simulation analysis for elucidation of toxic effects of dicyclohexyl phthalate (DCHP) in glucocorticoid receptor-mediated adipogenesis. Molecular Simulation, 2020, 46, 9-21.	0.9	24
22	Characterization of the heavy metal binding properties of periplasmic metal uptake protein CLas-ZnuA2. Metallomics, 2020, 12, 280-289.	1.0	11
23	Mutation studies and structure-based identification of potential inhibitor molecules against periplasmic amino acid binding protein of Candidatus Liberibacter asiaticus (CLasTcyA). International Journal of Biological Macromolecules, 2020, 147, 1228-1238.	3.6	23
24	Characterization of dye-decolorizing peroxidase from Bacillus subtilis. Archives of Biochemistry and Biophysics, 2020, 693, 108590.	1.4	61
25	Structural characterization and in-silico analysis of Momordica charantia 7S globulin for stability and ACE inhibition. Scientific Reports, 2020, 10, 1160.	1.6	32
26	Oxidative Stress in Autoimmune Diseases: An Under Dealt Malice. Current Protein and Peptide Science, 2020, 21, 611-621.	0.7	40
27	i In-silico i approach to identify novel potent inhibitors against GraR of i S aureus i. Frontiers in Bioscience - Landmark, 2020, 25, 1337-1360.	3.0	39
28	Phthalatesâ€"A class of ubiquitous pollutant: Microbial and enzymatic degradation perspectives. , 2020, , 487-513.		0
29	Bioremediation of synthetic dyes: Dye decolorizing peroxidases (DyPs). , 2020, , 453-486.		1
30	Nanoscience: Convergence with Biomedical and Biological Applications. Nanotechnology in the Life Sciences, 2020, , 1-25.	0.4	3
31	Repurposing an Ancient Protein Core Structure: Structural Studies on FmtA, a Novel Esterase of Staphylococcus aureus. Journal of Molecular Biology, 2019, 431, 3107-3123.	2.0	51
32	Molecular docking and dynamic approach to virtual screen inhibitors against Esbp of Candidatus Liberibacter asiaticus. Journal of Molecular Graphics and Modelling, 2019, 92, 329-340.	1.3	28
33	Structural insights into EntamoebaÂhistolytica arginase and structureâ€based identification of novel nonâ€amino acid based inhibitors as potential antiamoebic molecules. FEBS Journal, 2019, 286, 4135-4155.	2.2	39
34	Characterization of phthalate reductase from Ralstonia eutropha CH34 and in silico study of phthalate dioxygenase and phthalate reductase interaction. Journal of Molecular Graphics and Modelling, 2019, 90, 161-170.	1.3	23
35	Nanoparticle-Mediated Oxidative Stress Monitoring and Role of Nanoparticle for Treatment of Inflammatory Diseases. , 2019, , 97-112.		2
36	Structure based mimicking of Phthalic acid esters (PAEs) and inhibition of hACMSD, an important enzyme of the tryptophan kynurenine metabolism pathway. International Journal of Biological Macromolecules, 2018, 108, 214-224.	3.6	38

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37	Identification of novel phosphatidic acid binding domain on sphingosine kinase 1 of Arabidopsis thaliana. Plant Physiology and Biochemistry, 2018, 128, 178-184.	2.8	23
38	The analysis of subtle internal communications through mutation studies in periplasmic metal uptake protein CLas-ZnuA2. Journal of Structural Biology, 2018, 204, 228-239.	1.3	6
39	Biodegradation of phthalic acid esters (PAEs) and in silico structural characterization of mono-2-ethylhexyl phthalate (MEHP) hydrolase on the basis of close structural homolog. Journal of Hazardous Materials, 2017, 338, 11-22.	6.5	96
40	Oxidative Stress: Diagnostic Methods and Application in Medical Science. , 2017, , 23-45.		5