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	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
2	Characterization of dye-decolorizing peroxidase from Bacillus subtilis. Archives of Biochemistry and Biophysics, 2020, 693, 108590.	1.4	61
3	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
4	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
5	Oxidative Stress in Autoimmune Diseases: An Under Dealt Malice. Current Protein and Peptide Science, 2020, 21, 611-621.	0.7	40
6	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
7	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
8	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
9	Structural characterization and in-silico analysis of Momordica charantia 7S globulin for stability and ACE inhibition. Scientific Reports, 2020, 10, 1160.	1.6	32
10	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
11	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
12	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
13	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
14	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
15	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
16	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
17	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
18	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

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19	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
20	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
21	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
22	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
23	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
24	A molecular docking and dynamic approach to screen inhibitors against ZnuA1 ofCandidatusLiberibacter asiaticus. Molecular Simulation, 2021, 47, 510-525.	0.9	18
25	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
26	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
27	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
28	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
29	Characterization of the heavy metal binding properties of periplasmic metal uptake protein CLas-ZnuA2. Metallomics, 2020, 12, 280-289.	1.0	11
30	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
31	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
32	Oxidative Stress: Diagnostic Methods and Application in Medical Science. , 2017, , 23-45.		5
33	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
34	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
35	Nanoscience: Convergence with Biomedical and Biological Applications. Nanotechnology in the Life Sciences, 2020, , 1-25.	0.4	3
36	Nanoparticle-Mediated Oxidative Stress Monitoring and Role of Nanoparticle for Treatment of Inflammatory Diseases. , 2019, , 97-112.		2

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37	Bioremediation of synthetic dyes: Dye decolorizing peroxidases (DyPs). , 2020, , 453-486.		1
38	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
39	Phthalatesâ€"A class of ubiquitous pollutant: Microbial and enzymatic degradation perspectives. , 2020, , 487-513.		0
40	Erythrocytes model for oxidative stress analysis. , 2022, , 363-390.		0