Rishikesh S Parulekar

List of Publications by Year
in descending order

15 papers	259 citations	1040056 9 h-index	996975 15 g-index
15 all docs	15 docs citations	15 times ranked	247 citing authors

#	Article	IF	Citations
1	In silico evaluation of NO donor heterocyclic vasodilators as SARS-CoV-2 M^{pro} protein inhibitor. Journal of Biomolecular Structure and Dynamics, 2023, 41, 280-297.	3.5	3
2	Design and in silico investigation of novel Maraviroc analogues as dual inhibition of CCR-5/SARS-CoV-2 M^{pro}. Journal of Biomolecular Structure and Dynamics, 2022, 40, 11095-11110.	3.5	7
3	In silico exploration of binding potentials of anti SARS-CoV-1 phytochemicals against main protease of SARS-CoV-2. Journal of Saudi Chemical Society, 2022, 26, 101453.	5.2	5
4	Interrogating the substrate specificity landscape of UvrC reveals novel insights into its non-canonical function. Biophysical Journal, 2022, 121, 3103-3125.	0.5	4
5	Potential of NO donor furoxan as SARS-CoV-2 main protease (M^{pro}) inhibitors:in silicoanalysis. Journal of Biomolecular Structure and Dynamics, 2021, 39, 5804-5818.	3.5	21
6	Peptide Similarity Search Based and Virtual Screening Based Strategies to Identify Small Molecules to Inhibit CarDâ€“RNAP Interaction in M. tuberculosis. International Journal of Peptide Research and Therapeutics, 2019, 25, 697-709.	1.9	11
7	Antibiotic resistance and inhibition mechanism of novel aminoglycoside phosphotransferase APH(5) from B. subtilis subsp. subtilis strain RK. Brazilian Journal of Microbiology, 2019, 50, 887-898.	2.0	9
8	Molecular Insights into Destabilization of Alzheimerâ€™s AÎ² Protofibril by Arginine Containing Short Peptides: A Molecular Modeling Approach. ACS Omega, 2019, 4, 892-903.	3.5	38
9	Biofilm inhibition mechanism from extract of Hymenocallis littoralis leaves. Journal of Ethnopharmacology, 2018, 222, 121-132.	4.1	28
10	Molecular modeling studies to explore the binding affinity of virtually screened inhibitor toward different aminoglycoside kinases from diverse MDR strains. Journal of Cellular Biochemistry, 2018, 119, 2679-2695.	2.6	21
11	Insights into the antibiotic resistance and inhibition mechanism of aminoglycoside phosphotransferase from Bacillus cereus : In silico and in vitro perspective. Journal of Cellular Biochemistry, 2018, 119, 9444-9461.	2.6	17
12	Role of Trace Elements as Cofactor: An Efficient Strategy toward Enhanced Biobutanol Production. ACS Sustainable Chemistry and Engineering, 2018, 6, 9304-9313.	6.7	31
13	Molecular modeling approach to explore the role of cathepsin B from Hordeum vulgare in the degradation of AÎ² peptides. Molecular BioSystems, 2016, 12, 162-168.	2.9	33
14	Homology modeling and molecular docking studies of ArnA protein from Erwinia amylovora: role in polymyxin antibiotic resistance. Journal of Plant Biochemistry and Biotechnology, 2015, 24, 425-432.	1.7	6
15	Homology Modeling, Molecular Docking and DNA Binding Studies of Nucleotide Excision Repair UvrC Protein from M. tuberculosis. Protein Journal, 2013, 32, 467-476.	1.6	25