Akshay Uttarkar

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/2072360/publications.pdf

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15	199	1163117 8	1125743 13
papers	citations	h-index	g-index

18	18	18	143
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Coumarin derivative as a potent drug candidate against triple negative breast cancer targeting the frizzled receptor of wingless-related integration site signaling pathway. Journal of Biomolecular Structure and Dynamics, 2023, 41, 1561-1573.	3.5	18
2	Understanding the Xylooligosaccharides Utilization Mechanism of Lactobacillus brevis and Bifidobacterium adolescentis: Proteins Involved and Their Conformational Stabilities for Effectual Binding. Molecular Biotechnology, 2022, 64, 75-89.	2.4	6
3	Novel small molecules targeting bZIP23 TF improve stomatal conductance and photosynthesis under mild drought stress by regulating ABA. FEBS Journal, 2022, 289, 6058-6077.	4.7	17
4	Carbon fullerene acts as potential lead molecule against prospective molecular targets of biofilm-producing multidrug-resistant Acinetobacter baumanni and Pseudomonas aerugenosa: computational modeling and MD simulation studies. Journal of Biomolecular Structure and Dynamics, 2021, 39, 1121-1137.	3.5	3
5	Stress-Induced Detoxification Enzymes in Rice Have Broad Substrate Affinity. ACS Omega, 2021, 6, 3399-3410.	3.5	9
6	Spiro Benzodiazepine Substituted Fluorocoumarins as Potent Anti-Anxiety Agents. Russian Journal of Bioorganic Chemistry, 2021, 47, 390-398.	1.0	10
7	Structural insights on the interaction potential of natural leads against major protein targets of SARS-CoV-2: Molecular modelling, docking and dynamic simulation studies. Computers in Biology and Medicine, 2021, 132, 104325.	7.0	18
8	Study of SARS-nCoV2 Indian Isolates Gaining Insights into Mutation Frequencies, Protein Stability and Prospective Effect on Pathogenicity. Coronaviruses, 2021, 2, .	0.3	3
9	Carbon fullerene and nanotube are probable binders to multiple targets of SARS-CoV-2: Insights from computational modeling and molecular dynamic simulation studies. Infection, Genetics and Evolution, 2021, 96, 105155.	2.3	21
10	Molecular Docking and Interaction Studies of Identified Abscisic Acid Receptors in Oryza sativa: An In-Silico Perspective on Comprehending Stress Tolerance Mechanisms. Current Genomics, 2021, 22, 607-619.	1.6	8
11	Mitogen activated protein kinase-1 and cell division control protein-42 are putative targets for the binding of novel natural lead molecules: a therapeutic intervention against Candida albicans. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4584-4599.	3.5	10
12	Structural and molecular basis of the interaction mechanism of selected drugs towards multiple targets of SARS-CoV-2 by molecular docking and dynamic simulation studies- deciphering the scope of repurposed drugs. Computers in Biology and Medicine, 2020, 126, 104054.	7.0	30
13	Response regulator GacA and transcriptional activator RhlR proteins involved in biofilm formation of Pseudomonas aeruginosa are prospective targets for natural lead molecules: Computational modelling, molecular docking and dynamic simulation studies. Infection, Genetics and Evolution, 2020, 85, 104448.	2.3	13
14	Natural epiestriol-16 act as potential lead molecule against prospective molecular targets of multidrug resistant Acinetobacter baumannii-Insight from in silico modelling and in vitro investigations. Infection, Genetics and Evolution, 2020, 82, 104314.	2.3	16
15	Genome Resequencing Reveals Single Nucleotide Polymorphism and Repeat Regions in Giardia lamblia Indian Isolate. Journal of Next Generation Sequencing & Applications, 2017, 04, .	0.3	1