Yuan Xiaohui

List of Publications by Year
in descending order

18 papers	321 citations	840776 11 h-index	839539 18 g-index
19 all docs	19 docs citations	19 times ranked	299 citing authors

#	Article	IF	Citations
1	Molecular modeling and epitopes mapping of human adenovirus type 3 hexon protein. Vaccine, 2009, 27, 5103-5110.	3.8	53
2	Assessing the performance of the g_mmpbsa tools to simulate the inhibition of oseltamivir to influenza virus neuraminidase by molecular mechanics Poissonâ€“Boltzmann surface area methods. Journal of the Chinese Chemical Society, 2020, 67, 46-53.	1.4	43
3	Organophosphorus insecticide interacts with the pheromone-binding proteins of Athetis lepigone: Implication for olfactory dysfunction. Journal of Hazardous Materials, 2020, 397, 122777.	12.4	30
4	Molecular Docking and Molecular Dynamics (MD) Simulation of Human Anti-Complement Factor H (CFH) Antibody Ab42 and CFH Polypeptide. International Journal of Molecular Sciences, 2019, 20, 2568.	4.1	27
5	Novel binding patterns between ganoderic acids and neuraminidase: Insights from docking, molecular dynamics and MM/PBSA studies. Journal of Molecular Graphics and Modelling, 2016, 65, 27-34.	2.4	24
6	A Novel Antibody Humanization Method Based on Epitopes Scanning and Molecular Dynamics Simulation. PLoS ONE, 2013, 8, e80636.	2.5	24
7	Structure-Based High-Throughput Epitope Analysis of Hexon Proteins in B and C Species Human Adenoviruses (HAdVs). PLoS ONE, 2012, 7, e32938.	2.5	19
8	Computational and Experimental Approaches to Decipher the Binding Mechanism of General Odorant-Binding Protein 2 from Athetis lepigone to Chlorpyrifos and Phoxim. Journal of Agricultural and Food Chemistry, 2021, 69, 88-100.	5.2	18
9	Key Amino Acid Residues Influencing Binding Affinities of Pheromone-Binding Protein from Athetis lepigone to Two Sex Pheromones. Journal of Agricultural and Food Chemistry, 2020, 68, 6092-6103.	5.2	17
10	The Antiadenovirus Activities of Cinnamaldehyde In Vitro. Laboratory Medicine, 2009, 40, 669-674.	1.2	14
11	Rapid Structure-Based Screening Informs Potential Agents for Coronavirus Disease (COVID-19) Outbreak*. Chinese Physics Letters, 2020, 37, 058701.	3.3	11
12	Mechanistic Insights to the Binding of Antibody CR3022 Against RBD from SARS-CoV and HCoV-19/SARS-CoV-2: A Computational Study. Combinatorial Chemistry and High Throughput Screening, 2021, 24, 1069-1082.	1.1	10
13	Computational Interaction Analysis of Sirex noctilio Odorant-Binding Protein (SnocOBP7) Combined with Female Sex Pheromones and Symbiotic Fungal Volatiles. Agronomy, 2021, 11, 2461.	3.0	6
14	Structure Based Affinity Maturation and Characterizing of SARS-CoV Antibody CR3022 against SARS-CoV-2 by Computational and Experimental Approaches. Viruses, 2022, 14, 186.	3.3	6
15	Computational Simulation of HIV Protease Inhibitors to the Main Protease (Mpro) of SARS-CoV-2: Implications for COVID-19 Drugs Design. Molecules, 2021, 26, 7385.	3.8	6
16	Phylogenetic and structural analysis of major surface proteins hemagglutinin and neuraminidase of novel avian influenza virus A H7N9 from chinese patient. Chemical Research in Chinese Universities, 2013, 29, 934-940.	2.6	5
17	Computational identification of potential chemoprophylactic agents according to dynamic behavior of peroxisome proliferator-activated receptor gamma. RSC Advances, 2021, 11, 147-159.	3.6	5
18	Interaction Analysis of Odorant-Binding Protein 12 from Sirex noctilio and Volatiles from Host Plants and Symbiotic Fungi Based on Molecule Dynamics Simulation. Agronomy, 2022, 12, 861.	3.0	2