

Ji-Long Zhang

List of Publications by Year in descending order

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papers

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23
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319
citing authors

#	ARTICLE	IF	CITATIONS
1	Lacking of ESIPT Band of Aromatic ortho-Aminoaldehyde Derivatives Triggered by the N-H Vibration. <i>Physical Chemistry Chemical Physics</i> , 2022, , .	2.8	0
2	<i>In Silico</i> Investigation on KAR Signaling Reveals the Significant Dynamic Change of Its Receptor's Structure. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1933-1941.	5.4	4
3	Molecular Dynamics Simulation Investigation of the Binding and Interaction of the EphA6-Odin Protein Complex. <i>Journal of Physical Chemistry B</i> , 2022, 126, 4914-4924.	2.6	7
4	Dearomatization of Benzenoid Arenes Triggered by Triplet Excited State Intramolecular Proton Transfer. <i>Journal of Physical Chemistry A</i> , 2022, 126, 4424-4431.	2.5	1
5	Molecular dynamics investigation on the interaction of human angiotensin-converting enzyme with tetrapeptide inhibitors. <i>Physical Chemistry Chemical Physics</i> , 2021, 23, 6685-6694.	2.8	6
6	Interaction Mechanism of the Germination Stimulants Karrikins and Their Receptor ShKAI2iB. <i>Journal of Physical Chemistry B</i> , 2020, 124, 9812-9819.	2.6	8
7	MD Simulation Investigation on the Binding Process of Smoke-Derived Germination Stimulants to Its Receptor. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1554-1562.	5.4	17
8	Effect of External Electric Field on Substrate Transport of a Secondary Active Transporter. <i>Journal of Chemical Information and Modeling</i> , 2016, 56, 1539-1546.	5.4	5
9	Exploring the interaction between human focal adhesion kinase and inhibitors: a molecular dynamic simulation and free energy calculations. <i>Journal of Biomolecular Structure and Dynamics</i> , 2016, 34, 2351-2366.	3.5	11
10	Structural features and dynamic investigations of the membrane-bound cytochrome P450 17A1. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2015, 1848, 2013-2021.	2.6	20
11	How mutations affecting the ligand-receptor interactions: a combined MD and QM/MM calculation on CYP2E1 and its two mutants. <i>Chemical Research in Chinese Universities</i> , 2015, 31, 1029-1038.	2.6	6
12	Theoretical investigation on binding process of allophanate to allophanate hydrolase. <i>Chemical Research in Chinese Universities</i> , 2015, 31, 1023-1028.	2.6	2
13	Insights into the epimerization activities of RaCE and pAGE: the quantum mechanics/molecular mechanics simulations. <i>RSC Advances</i> , 2015, 5, 102284-102293.	3.6	10
14	Theoretical evaluation and improvement on the potency of the rhodanine-based inhibitors for human serotonin N-acetyltransferase. <i>Molecular Simulation</i> , 2014, 40, 1201-1208.	2.0	1
15	Molecular simulation investigation on the interaction between barrier-to-autointegration factor dimer or its Gly25Glu mutant and LEM domain of emerin. <i>Computational Biology and Chemistry</i> , 2014, 53, 184-190.	2.3	1
16	Mutation and low pH effect on the stability as well as unfolding kinetics of transthyretin dimer. <i>Biophysical Chemistry</i> , 2014, 189, 8-15.	2.8	7
17	Molecular dynamics (MD) simulations and binding free energy calculation studies between inhibitors and type II dehydroquinase (DHQ2). <i>Molecular Simulation</i> , 2013, 39, 137-144.	2.0	5
18	How Does (E)-2-(Acetamidomethylene)succinate Bind to Its Hydrolase? From the Binding Process to the Final Result. <i>PLoS ONE</i> , 2013, 8, e53811.	2.5	12

#	ARTICLE	IF	CITATIONS
19	Drug Design Benefits from Molecular Dynamics: Some Examples. <i>Current Computer-Aided Drug Design</i> , 2013, 9, 532-546.	1.2	11
20	Molecular Dynamics Simulations Suggest Ligand's Binding to Nicotinamidase/Pyrazinamidase. <i>PLoS ONE</i> , 2012, 7, e39546.	2.5	28
21	Theoretical improvement of the specific inhibitor of human carbonic anhydrase VII. <i>Computational Biology and Chemistry</i> , 2011, 35, 50-56.	2.3	9
22	Unbinding of glucose from human pulmonary surfactant protein D studied by steered molecular dynamics simulations. <i>Chemical Physics Letters</i> , 2010, 484, 338-343.	2.6	27
23	Insight into the Dynamic Interaction of Different Carbohydrates with Human Surfactant Protein D: Molecular Dynamics Simulations. <i>Journal of Physical Chemistry B</i> , 2010, 114, 7383-7390.	2.6	12