Peng Sang

List of Publications by Year
in descending order

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23	1,305	759055	580701
papers	citations	12 h-index	25 g-index

26	26	26	2161
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Insights into Proteinâ€“Ligand Interactions: Mechanisms, Models, and Methods. International Journal of Molecular Sciences, 2016, 17, 144.	1.8	885
2	Protein dynamics and motions in relation to their functions: several case studies and the underlying mechanisms. Journal of Biomolecular Structure and Dynamics, 2014, 32, 372-393.	2.0	95
3	Anti-HIV drug repurposing against SARS-CoV-2. RSC Advances, 2020, 10, 15775-15783.	1.7	76
4	Molecular motions and free-energy landscape of serine proteinase K in relation to its cold-adaptation: a comparative molecular dynamics simulation study and the underlying mechanisms. RSC Advances, 2017, 7, 28580-28590.	1.7	31
5	Substrate-induced changes in dynamics and molecular motions of cuticle-degrading serine protease PL646: a molecular dynamics study. RSC Advances, 2017, 7, 42094-42104.	1.7	20
6	Insights into the role of electrostatics in temperature adaptation: a comparative study of psychrophilic, mesophilic, and thermophilic subtilisin-like serine proteases. RSC Advances, 2018, 8, 29698-29713.	1.7	20
7	Comparative thermal unfolding study of psychrophilic and mesophilic subtilisin-like serine proteases by molecular dynamics simulations. Journal of Biomolecular Structure and Dynamics, 2017, 35, 1500-1517.	2.0	19
8	Effect of the Solvent Temperatures on Dynamics of Serine Protease Proteinase K. International Journal of Molecular Sciences, 2016, 17, 254.	1.8	18
9	New Insight into Mechanisms of Protein Adaptation to High Temperatures: A Comparative Molecular Dynamics Simulation Study of Thermophilic and Mesophilic Subtilisin-Like Serine Proteases. International Journal of Molecular Sciences, 2020, 21, 3128.	1.8	18
10	Expression and Characteristics of Two Glucose-Tolerant GH1 Î²-glucosidases From Actinomadura amylolytica YIM 77502T for Promoting Cellulose Degradation. Frontiers in Microbiology, 2018, 9, 3149.	1.5	17
11	Expression and characterization of a cold-adapted, salt- and glucose-tolerant GH1 Î²-glucosidase obtained from Thermobifida halotolerans and its use in sugarcane bagasse hydrolysis. Biomass Conversion and Biorefinery, 2021, 11, 1245-1253.	2.9	14
12	Insight Derived from Molecular Dynamics Simulations into Molecular Motions, Thermodynamics and Kinetics of HIV-1 gp120. PLoS ONE, 2014, 9, e104714.	1.1	12
13	In silico screening, molecular docking, and molecular dynamics studies of SNP-derived human P5CR mutants. Journal of Biomolecular Structure and Dynamics, 2017, 35, 2441-2453.	2.0	12
14	Effects of CD4 Binding on Conformational Dynamics, Molecular Motions, and Thermodynamics of HIV-1 gp120. International Journal of Molecular Sciences, 2019, 20, 260.	1.8	10
15	Insights into the molecular mechanism underlying CD4-dependency and neutralization sensitivity of HIV-1: a comparative molecular dynamics study on gp120s from isolates with different phenotypes. RSC Advances, 2018, 8, 14355-14368.	1.7	9
16	Characterization of a Cu2+, SDS, alcohol and glucose tolerant GH1 Î²-glucosidase from Bacillus sp. CGMCC 1.16541. Antonie Van Leeuwenhoek, 2020, 113, 1467-1477.	0.7	7
17	Insight derived from molecular dynamics simulation into dynamics and molecular motions of cuticle-degrading serine protease Ver112. Journal of Biomolecular Structure and Dynamics, 2019, 37, 2004-2016.	2.0	6
18	CD4-binding obstacles in conformational transitions and allosteric communications of HIV gp120. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183217.	1.4	6

#	Article	IF	Citations
19	Deciphering gp120 sequence variation and structural dynamics in <scp>HIV</scp> neutralization phenotype by molecular dynamics simulations and graph machine learning. Proteins: Structure, Function and Bioinformatics, 2022, 90, 1413-1424.	1.5	5
20	Effect of the R119G mutation on human P5CR structure and its interactions with NAD: Insights derived from molecular dynamics simulation and free energy analysis. Computational Biology and Chemistry, 2017, 67, 141-149.	1.1	4
21	Characterization of an alkali-tolerant, thermostable, and multifunctional GH5 family endoglucanase from Thermoactinospora rubra YIM 77501T for prebiotic production. Biomass Conversion and Biorefinery, 2022, 12, 3399-3408.	2.9	4
22	Probing intrinsic dynamics and conformational transition of HIV gp120 by molecular dynamics simulation. RSC Advances, 2020, 10, 30499-30507.	1.7	3
23	Insight derived from molecular dynamics simulation into cold-adaptation mechanism of trypsins. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2768-2776.	2.0	2