## Peng Sang

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6489908/publications.pdf

Version: 2024-02-01

759055 580701 1,305 25 23 12 citations h-index g-index papers 26 26 26 2161 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	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
2	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
3	Expression and characterization of a cold-adapted, salt- and glucose-tolerant GH1 $\hat{l}^2$ -glucosidase obtained from Thermobifida halotolerans and its use in sugarcane bagasse hydrolysis. Biomass Conversion and Biorefinery, 2021, 11, 1245-1253.	2.9	14
4	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
5	Characterization of a Cu2+, SDS, alcohol and glucose tolerant GH1 $\hat{l}^2$ -glucosidase from Bacillus sp. CGMCC 1.16541. Antonie Van Leeuwenhoek, 2020, 113, 1467-1477.	0.7	7
6	Probing intrinsic dynamics and conformational transition of HIV gp120 by molecular dynamics simulation. RSC Advances, 2020, 10, 30499-30507.	1.7	3
7	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
8	CD4-binding obstacles in conformational transitions and allosteric communications of HIV gp120. Biochimica Et Biophysica Acta - Biomembranes, 2020, 1862, 183217.	1.4	6
9	Anti-HIV drug repurposing against SARS-CoV-2. RSC Advances, 2020, 10, 15775-15783.	1.7	76
10	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
11	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
12	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
13	Expression and Characteristics of Two Glucose-Tolerant GH1 $\hat{l}^2$ -glucosidases From Actinomadura amylolytica YIM 77502T for Promoting Cellulose Degradation. Frontiers in Microbiology, 2018, 9, 3149.	1.5	17
14	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
15	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
16	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
17	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
18	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

#	Article	IF	CITATIONS
19	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
20	Insights into Protein–Ligand Interactions: Mechanisms, Models, and Methods. International Journal of Molecular Sciences, 2016, 17, 144.	1.8	885
21	Effect of the Solvent Temperatures on Dynamics of Serine Protease Proteinase K. International Journal of Molecular Sciences, 2016, 17, 254.	1.8	18
22	Insight Derived from Molecular Dynamics Simulations into Molecular Motions, Thermodynamics and Kinetics of HIV-1 gp120. PLoS ONE, 2014, 9, e104714.	1.1	12
23	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