Pu Tian

List of Publications by Year
in descending order

21 papers	242 citations	1307366 7 h-index	996849 15 g-index
36 all docs	36 docs citations	36 times ranked	318 citing authors

#	Article	IF	Citations
1	Labelâ€Free and In Situ Identification of Cells via Combinational Machine Learning Models. Small Methods, 2022, 6, e2101405.	4.6	2
2	Molecular free energy optimization on a computational graph. RSC Advances, 2021, 11, 12929-12937.	1.7	5
3	â€œDividing and Conqueringâ€•and â€œCachingâ€•in Molecular Modeling. International Journal of Molecular Sciences, 2021, 22, 5053.	1.8	5
4	Fundamental asymmetry of insertions and deletions in genomes size evolution. Journal of Theoretical Biology, 2019, 482, 109983.	0.8	4
5	Significance of triple torsional correlations in proteins. RSC Advances, 2019, 9, 13949-13958.	1.7	3
6	A simple neural network implementation of generalized solvation free energy for assessment of protein structural models. RSC Advances, 2019, 9, 36227-36233.	1.7	7
7	Protein secondary structure prediction with context convolutional neural network. RSC Advances, 2019, 9, 38391-38396.	1.7	17
8	Prevention of Bacterial Contamination of a Silica Matrix Containing Entrapped Î²-Galactosidase through the Action of Covalently Bound Lysozymes. Molecules, 2017, 22, 377.	1.7	15
9	Investigating the substrate binding mechanism of sulfotransferase 2A1 based on substrate tunnel analysis: a molecular dynamics simulation study. Journal of Molecular Modeling, 2016, 22, 176.	0.8	2
10	Nonlinear backbone torsional pair correlations in proteins. Scientific Reports, 2016, 6, 34481.	1.6	8
11	Configurational space discretization and free energy calculation in complex molecular systems. Scientific Reports, 2016, 6, 22217.	1.6	1
12	Impact of stable protein-protein interaction on protein conformational space. Chemical Research in Chinese Universities, 2015, 31, 149-155.	1.3	3
13	The effect of ligands on the thermal stability of sulfotransferases: a molecular dynamics simulation study. Journal of Molecular Modeling, 2015, 21, 72.	0.8	2
14	The impact of ligands on the structure and flexibility of sulfotransferases: a molecular dynamics simulation study. Journal of Molecular Modeling, 2015, 21, 190.	0.8	4
15	Hierarchical Conformational Analysis of Native Lysozyme Based on Sub-Millisecond Molecular Dynamics Simulations. PLoS ONE, 2015, 10, e0129846.	1.1	4
16	Reconciling Mediating and Slaving Roles of Water in Protein Conformational Dynamics. PLoS ONE, 2013, 8, e60553.	1.1	14
17	Molecular Basis for the Structural Stability of an Enclosed Î²-Barrel Loop. Journal of Molecular Biology, 2010, 402, 475-489.	2.0	12
18	Computational protein design, from single domain soluble proteins to membrane proteins. Chemical Society Reviews, 2010, 39, 2071.	18.7	29

#	Article	IF	Citations
19	Size, Motion, and Function of the SecY Translocon Revealed by Molecular Dynamics Simulations with Virtual Probes. Biophysical Journal, 2006, 90, 2718-2730.	0.2	48
20	Repetitive Pulling Catalyzes Co-translocational Unfolding of Barnase During Import Through a Mitochondrial Pore. Journal of Molecular Biology, 2005, 350, 1017-1034.	2.0	53
21	The repetitive local sampling and the local distribution theory. Wiley Interdisciplinary Reviews: Computational Molecular Science, 0, , e1588.	6.2	2