Zhuqing Zhang

List of Publications by Year
in descending order

19 papers	927 citations	686830 13 h-index	839053 18 g-index
21 all docs	21 docs citations	21 times ranked	930 citing authors

#	Article	IF	Citations
1	LLPSDB v2.0: an updated database of proteins undergoing liquidâ€“liquid phase separation in vitro. Bioinformatics, 2022, 38, 2010-2014.	1.8	23
2	Prediction of liquidâ€“liquid phase separating proteins using machine learning. BMC Bioinformatics, 2022, 23, 72.	1.2	74
3	Modulation of p53 N-terminal transactivation domain 2 conformation ensemble and kinetics by phosphorylation. Journal of Biomolecular Structure and Dynamics, 2020, 38, 2613-2623.	2.0	9
4	LLPSDB: a database of proteins undergoing liquidâ€“liquid phase separation in vitro. Nucleic Acids Research, 2020, 48, D320-D327.	6.5	130
5	Protein Databases Related to Liquidâ€“Liquid Phase Separation. International Journal of Molecular Sciences, 2020, 21, 6796.	1.8	27
6	How calcium ion binding induces the conformational transition of the calmodulin N-terminal domainâ€”an atomic level characterization. Physical Chemistry Chemical Physics, 2019, 21, 19795-19804.	1.3	7
7	Characterization of the structural ensembles of p53 TAD2 by molecular dynamics simulations with different force fields. Physical Chemistry Chemical Physics, 2018, 20, 8676-8684.	1.3	24
8	A critical comparison of coarse-grained structure-based approaches and atomic models of protein folding. Physical Chemistry Chemical Physics, 2017, 19, 13629-13639.	1.3	24
9	The low populated folding intermediate of a mutant of the Fyn SH3 domain identified by a simple model. Physical Chemistry Chemical Physics, 2017, 19, 22321-22328.	1.3	9
10	The Folding of de Novo Designed Protein DS119 via Molecular Dynamics Simulations. International Journal of Molecular Sciences, 2016, 17, 612.	1.8	2
11	Influences of heterogeneous native contact energy and many-body interactions on the prediction of protein folding mechanisms. Physical Chemistry Chemical Physics, 2016, 18, 31304-31311.	1.3	5
12	Transition paths, diffusive processes, and preequilibria of protein folding. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 20919-20924.	3.3	38
13	Kinetic consequences of native state optimization of surfaceâ€exposed electrostatic interactions in the Fyn SH3 domain. Proteins: Structure, Function and Bioinformatics, 2012, 80, 858-870.	1.5	42
14	Cooperativity, Local-Nonlocal Coupling, and Nonnative Interactions: Principles of Protein Folding from Coarse-Grained Models. Annual Review of Physical Chemistry, 2011, 62, 301-326.	4.8	187
15	Competition between native topology and nonnative interactions in simple and complex folding kinetics of natural and designed proteins. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 2920-2925.	3.3	91
16	Native Topology of the Designed Protein Top7 is Not Conducive to Cooperative Folding. Biophysical Journal, 2009, 96, L25-L27.	0.2	31
17	Identification of amyloid fibril-forming segments based on structure and residue-based statistical potential. Bioinformatics, 2007, 23, 2218-2225.	1.8	106
18	Molecular Dynamics Simulations on the Oligomer-Formation Process of the GNNQQNY Peptide from Yeast Prion Protein Sup35. Biophysical Journal, 2007, 93, 1484-1492.	0.2	80

#	ARTICLE	IF	CITATIONS
19	Prediction of Liquid-Liquid Phase Separation Proteins Using Machine Learning. SSRN Electronic Journal, 0, , .	0.4	7