Wookyung Yu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2315804/publications.pdf

Version: 2024-02-01

18	317	1163117	888059
papers	citations	8 h-index	17 g-index

19	19	19	536
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Computational design of a thermolabile uracil-DNA glycosylase of Escherichia coli. Biophysical Journal, 2022, 121, 1276-1288.	0.5	2
2	Unveiling OASIS family as a key player in hypoxiaâ€“ischemia cases induced by cocaine using generative adversarial networks. Scientific Reports, 2022, 12, 6734.	3.3	1
3	Conformational switch that induces GDP release from Gi. Journal of Structural Biology, 2021, 213, 107694.	2.8	9
4	Coevolution underlies GPCR-G protein selectivity and functionality. Scientific Reports, 2021, 11, 7858.	3.3	7
5	Aggregation-Prone Structural Ensembles of Transthyretin Collected With Regression Analysis for NMR Chemical Shift. Frontiers in Molecular Biosciences, 2021, 8, 766830.	3.5	2
6	Understanding the role of the CB1 toggle switch in interaction networks using molecular dynamics simulation. Scientific Reports, 2021, 11, 22369.	3.3	2
7	Sibe: a computation tool to apply protein sequence statistics to predict folding and design in silico. BMC Bioinformatics, 2019, 20, 455.	2.6	6
8	Atomic insights into the effects of pathological mutants through the disruption of hydrophobic core in the prion protein. Scientific Reports, 2019, 9, 19144.	3.3	6
9	Exploring the Ligand Efficacy of Cannabinoid Receptor 1 (CB1) using Molecular Dynamics Simulations. Scientific Reports, 2018, 8, 13787.	3.3	25
10	De novo protein structure prediction using ultra-fast molecular dynamics simulation. PLoS ONE, 2018, 13, e0205819.	2.5	21
11	Perplexing cooperative folding and stability of a low-sequence complexity, polyproline 2 protein lacking a hydrophobic core. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 2241-2246.	7.1	29
12	Cooperative folding near the downhill limit determined with amino acid resolution by hydrogen exchange. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4747-4752.	7.1	6
13	Even with nonnative interactions, the updated folding transition states of the homologs Proteins G & L are extensive and similar. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8302-8307.	7.1	21
14	Benchmarking all-atom simulations using hydrogen exchange. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15975-15980.	7.1	67
15	PACSY, a relational database management system for protein structure and chemical shift analysis. Journal of Biomolecular NMR, 2012, 54, 169-179.	2.8	33
16	Uncovering symmetry-breaking vector and reliability order for assigning secondary structures of proteins from atomic NMR chemical shifts in amino acids. Journal of Biomolecular NMR, 2011, 51, 411-424.	2.8	5
17	Functional Implications of an Intermeshing Cogwheel-like Interaction between TolC and MacA in the Action of Macrolide-specific Efflux Pump MacAB-TolC. Journal of Biological Chemistry, 2011, 286, 13541-13549.	3.4	49
18	Cooperative folding kinetics of BBL protein and peripheral subunit-binding domain homologues. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2397-2402.	7.1	26