Lee-Wei Yang

List of Publications by Year
in descending order

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30 papers	2,118 citations	567281 15 h-index	454955 30 g-index
38 all docs	38 docs citations	38 times ranked	2328 citing authors

#	Article	IF	Citations
1	Helical structure motifs made searchable for functional peptide design. Nature Communications, 2022, 13, 102.	12.8	10
2	An Effective and Safe Enkephalin Analog for Antinociception. Pharmaceutics, 2021, 13, 927.	4.5	3
3	ZHX2 promotes HIF1Î± oncogenic signaling in triple-negative breast cancer. ELife, 2021, 10, .	6.0	21
4	DR-SIP: protocols for higher order structure modeling with distance restraints- and cyclic symmetry-imposed packing. Bioinformatics, 2020, 36, 449-461.	4.1	1
5	An Efficient Timer and Sizer of Biomacromolecular Motions. Structure, 2020, 28, 259-269.e8.	3.3	4
6	Molecular dynamics simulations and linear response theories jointly describe biphasic responses of myoglobin relaxation and reveal evolutionarily conserved frequent communicators. Biophysics and Physicobiology, 2019, 16, 473-484.	1.0	3
7	Resolution-exchanged structural modeling and simulations jointly unravel that subunit rolling underlies the mechanism of programmed ribosomal frameshifting. Bioinformatics, 2019, 35, 945-952.	4.1	9
8	Drug Repurposing Screening Identifies Tioconazole as an ATG4 Inhibitor that Suppresses Autophagy and Sensitizes Cancer Cells to Chemotherapy. Theranostics, 2018, 8, 830-845.	10.0	106
9	S100B as an antagonist to block the interaction between S100A1 and the RAGE V domain. PLoS ONE, 2018, 13, e0190545.	2.5	16
10	DynOmics: dynamics of structural proteome and beyond. Nucleic Acids Research, 2017, 45, W374-W380.	14.5	135
11	Structural Insights into Substrate Recognition by Clostridium difficile Sortase. Frontiers in Cellular and Infection Microbiology, 2016, 6, 160.	3.9	4
12	Structure and function of chicken interleukin-1 beta mutants: uncoupling of receptor binding and in vivo biological activity. Scientific Reports, 2016, 6, 27729.	3.3	7
13	Protein Dynamics and Contact Topology Reveal Proteinâ€“DNA Binding Orientation. Journal of Chemical Theory and Computation, 2016, 12, 5269-5277.	5.3	9
14	Blocking the interaction between S100A9 and RAGE V domain using CHAPS molecule: A novel route to drug development against cell proliferation. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2016, 1864, 1558-1569.	2.3	51
15	iGNM 2.0: the Gaussian network model database for biomolecular structural dynamics. Nucleic Acids Research, 2016, 44, D415-D422.	14.5	71
16	Functional Importance of Mobile Ribosomal Proteins. BioMed Research International, 2015, 2015, 1-11.	1.9	5
17	Ligand-Induced Protein Responses and Mechanical Signal Propagation Described by Linear Response Theories. Biophysical Journal, 2014, 107, 1415-1425.	0.5	23
18	Molecular Binding Sites Are Located Near the Interface of Intrinsic Dynamics Domains (IDDs). Journal of Chemical Information and Modeling, 2014, 54, 2275-2285.	5.4	23

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19	Structural insights into the interaction of human S100B and basic fibroblast growth factor (FGF2): Effects on FGFR1 receptor signaling. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 2606-2619.	2.3	21
20	The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 1789-1797.	2.5	6
21	Models with Energy Penalty on Interresidue Rotation Address Insufficiencies of Conventional Elastic Network Models. Biophysical Journal, 2011, 100, 1784-1793.	0.5	14
22	Global Dynamics of Proteins: Bridging Between Structure and Function. Annual Review of Biophysics, 2010, 39, 23-42.	10.0	536
23	Principal component analysis of native ensembles of biomolecular structures (PCA_NEST): insights into functional dynamics. Bioinformatics, 2009, 25, 606-614.	4.1	120
24	Coarse-Grained Models Reveal Functional Dynamics - I. Elastic Network Models â€“ Theories, Comparisons and Perspectives. Bioinformatics and Biology Insights, 2008, 2, BBI.S460.	2.0	47
25	Anisotropic fluctuations of amino acids in protein structures: insights from X-ray crystallography and elastic network models. Bioinformatics, 2007, 23, i175-i184.	4.1	73
26	Insights into Equilibrium Dynamics of Proteins from Comparison of NMR and X-Ray Data with Computational Predictions. Structure, 2007, 15, 741-749.	3.3	124
27	o GNM: online computation of structural dynamics using the Gaussian Network Model. Nucleic Acids Research, 2006, 34, W24-W31.	14.5	140
28	Coupling between Catalytic Site and Collective Dynamics: A Requirement for Mechanochemical Activity of Enzymes. Structure, 2005, 13, 893-904.	3.3	257
29	iGNM: a database of protein functional motions based on Gaussian Network Model. Bioinformatics, 2005, 21, 2978-2987.	4.1	115
30	Elastic network models for understanding biomolecular machinery: from enzymes to supramolecular assemblies. Physical Biology, 2005, 2, S173-S180.	1.8	159