

# Lee-Wei Yang

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Global Dynamics of Proteins: Bridging Between Structure and Function. Annual Review of Biophysics, 2010, 39, 23-42.	10.0	536
2	Coupling between Catalytic Site and Collective Dynamics: A Requirement for Mechanochemical Activity of Enzymes. Structure, 2005, 13, 893-904.	3.3	257
3	Elastic network models for understanding biomolecular machinery: from enzymes to supramolecular assemblies. Physical Biology, 2005, 2, S173-S180.	1.8	159
4	oGNM: online computation of structural dynamics using the Gaussian Network Model. Nucleic Acids Research, 2006, 34, W24-W31.	14.5	140
5	DynOmics: dynamics of structural proteome and beyond. Nucleic Acids Research, 2017, 45, W374-W380.	14.5	135
6	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
7	Principal component analysis of native ensembles of biomolecular structures (PCA_NEST): insights into functional dynamics. Bioinformatics, 2009, 25, 606-614.	4.1	120
8	iGNM: a database of protein functional motions based on Gaussian Network Model. Bioinformatics, 2005, 21, 2978-2987.	4.1	115
9	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
10	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
11	<i>i</i>GNM 2.0: the Gaussian network model database for biomolecular structural dynamics. Nucleic Acids Research, 2016, 44, D415-D422.	14.5	71
12	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
13	Coarse-Grained Models Reveal Functional Dynamics - I. Elastic Network Models “ Theories, Comparisons and Perspectives. Bioinformatics and Biology Insights, 2008, 2, BBI.S460.	2.0	47
14	Ligand-Induced Protein Responses and Mechanical Signal Propagation Described by Linear Response Theories. Biophysical Journal, 2014, 107, 1415-1425.	0.5	23
15	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
16	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
17	ZHX2 promotes HIF1 $\alpha$ oncogenic signaling in triple-negative breast cancer. ELife, 2021, 10, .	6.0	21
18	S100B as an antagonist to block the interaction between S100A1 and the RAGE V domain. PLoS ONE, 2018, 13, e0190545.	2.5	16

#	ARTICLE	IF	CITATIONS
19	Models with Energy Penalty on Interresidue Rotation Address Insufficiencies of Conventional Elastic Network Models. <i>Biophysical Journal</i> , 2011, 100, 1784-1793.	0.5	14
20	Helical structure motifs made searchable for functional peptide design. <i>Nature Communications</i> , 2022, 13, 102.	12.8	10
21	Protein Dynamics and Contact Topology Reveal Proteinâ€™DNA Binding Orientation. <i>Journal of Chemical Theory and Computation</i> , 2016, 12, 5269-5277.	5.3	9
22	Resolution-exchanged structural modeling and simulations jointly unravel that subunit rolling underlies the mechanism of programmed ribosomal frameshifting. <i>Bioinformatics</i> , 2019, 35, 945-952.	4.1	9
23	Structure and function of chicken interleukin-1 beta mutants: uncoupling of receptor binding and in vivo biological activity. <i>Scientific Reports</i> , 2016, 6, 27729.	3.3	7
24	The N-terminal substrate-recognition domain of a LonC protease exhibits structural and functional similarity to cytosolic chaperones. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1789-1797.	2.5	6
25	Functional Importance of Mobile Ribosomal Proteins. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	5
26	Structural Insights into Substrate Recognition by <i>Clostridium difficile</i> Sortase. <i>Frontiers in Cellular and Infection Microbiology</i> , 2016, 6, 160.	3.9	4
27	An Efficient Timer and Sizer of Biomacromolecular Motions. <i>Structure</i> , 2020, 28, 259-269.e8.	3.3	4
28	Molecular dynamics simulations and linear response theories jointly describe biphasic responses of myoglobin relaxation and reveal evolutionarily conserved frequent communicators. <i>Biophysics and Physicobiology</i> , 2019, 16, 473-484.	1.0	3
29	An Effective and Safe Enkephalin Analog for Antinociception. <i>Pharmaceutics</i> , 2021, 13, 927.	4.5	3
30	DR-SIP: protocols for higher order structure modeling with distance restraints- and cyclic symmetry-imposed packing. <i>Bioinformatics</i> , 2020, 36, 449-461.	4.1	1