

# Li-Wei Hung

## List of Publications by Year in descending order

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Version: 2024-02-01

50  
papers

34,372  
citations

230014

27  
h-index

223390

49  
g-index

52  
all docs

52  
docs citations

52  
times ranked

48001  
citing authors

#	ARTICLE	IF	CITATIONS
1	Construction, characterization and crystal structure of a fluorescent single-chain Fv chimera. <i>Protein Engineering, Design and Selection</i> , 2021, 34, .	1.0	4
2	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. <i>Nature Methods</i> , 2021, 18, 156-164.	9.0	73
3	Teres minor muscle hypertrophy is a negative predictor of outcomes after reverse total shoulder arthroplasty: an evaluation of preoperative magnetic resonance imaging and postoperative implant position. <i>Journal of Shoulder and Elbow Surgery</i> , 2021, 30, e636-e645.	1.2	3
4	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>&lt;i&gt;Phenix&lt;/i&gt;</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2019, 75, 861-877.	1.1	4,060
5	BpeB, a major resistance-nodulation-cell division transporter from <i>&lt;i&gt;Burkholderia cenocepacia&lt;/i&gt;</i> : construct design, crystallization and preliminary structural analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 710-716.	0.4	1
6	Chronic kidney disease predicts a lower probability of improvement in patient-reported experience measures among patients with fractures: a prospective multicenter cohort study. <i>Archives of Osteoporosis</i> , 2018, 13, 126.	1.0	6
7	The influence of renal dialysis and hip fracture sites on the 10-year mortality of elderly hip fracture patients. <i>Medicine (United States)</i> , 2017, 96, e7618.	0.4	19
8	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 359-374.	1.1	29
9	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from <i>Burkholderia pseudomallei</i> . <i>Journal of Biological Chemistry</i> , 2016, 291, 19387-19400.	1.6	28
10	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 346-358.	1.1	31
11	Structural basis for DNA recognition by STAT6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13015-13020.	3.3	46
12	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. <i>Structure</i> , 2015, 23, 1858-1865.	1.6	50
13	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630.	4.8	27
14	High short-term and long-term excess mortality in geriatric patients after hip fracture: a prospective cohort study in Taiwan. <i>BMC Musculoskeletal Disorders</i> , 2014, 15, 151.	0.8	21
15	Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. <i>Biophysical Journal</i> , 2014, 106, 34a.	0.2	0
16	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , 2014, 24, 344-358.	5.7	86
17	Subfamily-Specific Adaptations in the Structures of Two Penicillin-Binding Proteins from <i>Mycobacterium tuberculosis</i> . <i>PLoS ONE</i> , 2014, 9, e116249.	1.1	6
18	Hip fracture risk assessment: artificial neural network outperforms conditional logistic regression in an age- and sex-matched case control study. <i>BMC Musculoskeletal Disorders</i> , 2013, 14, 207.	0.8	18

#	ARTICLE	IF	CITATIONS
19	Crystal structure of AcrB complexed with linezolid at 3.5Å... resolution. Journal of Structural and Functional Genomics, 2013, 14, 71-75.	1.2	38
20	Structural basis for termination of AIM2-mediated signaling by p202. Cell Research, 2013, 23, 855-858.	5.7	38
21	Model morphing and sequence assignment after molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2244-2250.	2.5	37
22	Split green fluorescent protein as a modular binding partner for protein crystallization. Acta Crystallographica Section D: Biological Crystallography, 2013, 69, 2513-2523.	2.5	29
23	Time Orientation and Visual Construction Subdomains of the MMSE as Independent Risk Factors for Hip Fractures. Orthopedics, 2013, 36, e869-76.	0.5	6
24	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. Journal of Structural and Functional Genomics, 2012, 13, 71-79.	1.2	5
25	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 521-530.	2.5	24
26	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. Acta Crystallographica Section D: Biological Crystallography, 2012, 68, 861-870.	2.5	37
27	The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106.	1.9	764
28	Lovastatin Promotes Redifferentiation of Human Nucleus Pulposus Cells During Expansion in Monolayer Culture. Artificial Organs, 2011, 35, 411-416.	1.0	14
29	The TB Structural Genomics Consortium: A decade of progress. Tuberculosis, 2011, 91, 155-172.	0.8	39
30	PHENIX: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221.	2.5	20,564
31	Structure of Rv1848 (UreA), the Mycobacterium tuberculosis urease $\hat{3}$ subunit. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 781-786.	0.7	10
32	An Extracellular Disulfide Bond Forming Protein (DsbF) from Mycobacterium tuberculosis: Structural, Biochemical, and Gene Expression Analysis. Journal of Molecular Biology, 2010, 396, 1211-1226.	2.0	23
33	Analysis of nucleoside-binding proteins by ligand-specific elution from dye resin: application to Mycobacterium tuberculosis aldehyde dehydrogenases. Journal of Structural and Functional Genomics, 2009, 10, 291-301.	1.2	13
34	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn <sup>2+</sup> -binding FCD domains. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 356-365.	2.5	31
35	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601.	2.5	804
36	Structure and Function of Bacillus subtilis YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. Biochemistry, 2009, 48, 8664-8671.	1.2	37

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37	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 61-69.	2.5	1,319
38	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 515-524.	2.5	165
39	Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435.	0.4	492
40	Protein production and purification. Nature Methods, 2008, 5, 135-146.	9.0	763
41	Domain Orientation in the Inactive Response Regulator Mycobacterium tuberculosis MtrA Provides a Barrier to Activation. Biochemistry, 2007, 46, 6733-6743.	1.2	76
42	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610.	2.5	60
43	An automated high-throughput screening method for the identification of high-yield, soluble protein variants using cell-free expression and systematic truncation. Journal of Structural and Functional Genomics, 2007, 7, 139-147.	1.2	7
44	Automated structure determination with phenix. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 101-109.	0.1	4
45	Functional and Structural Characterization of a Thiol Peroxidase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 361, 850-863.	2.0	58
46	Structure of Mycobacterium tuberculosis RuvA, a protein involved in recombination. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 731-734.	0.7	12
47	Crystal structure of a putative pyridoxine 5-phosphate oxidase (Rv2607) from Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2005, 62, 563-569.	1.5	19
48	Crystal Structure of AhpE from Mycobacterium tuberculosis, a 1-Cys Peroxiredoxin. Journal of Molecular Biology, 2005, 346, 1035-1046.	2.0	77
49	Recent developments in the PHENIX software for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55.	1.0	319
50	PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954.	2.5	3,979