

# Li-Wei Hung

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48  
papers

25,719  
citations

24  
h-index

52  
g-index

52  
ext. papers

30,594  
ext. citations

6.2  
avg, IF

5.97  
L-index

#	Paper	IF	Citations
48	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDDataResource challenge. <i>Nature Methods</i> , <b>2021</b> , 18, 156-164	21.6	22
47	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> , <b>2021</b> , 30, e636-e645	4.3	0
46	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2019</b> , 75, 861-877	5.5	1527
45	BpeB, a major resistance-nodulation-cell division transporter from Burkholderia cenocepacia: construct design, crystallization and preliminary structural analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2018</b> , 74, 710-716	1.1	
44	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> , <b>2018</b> , 13, 126	2.9	3
43	The influence of renal dialysis and hip fracture sites on the 10-year mortality of elderly hip fracture patients: A nationwide population-based observational study. <i>Medicine (United States)</i> , <b>2017</b> , 96, e7618	1.8	17
42	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 346-58	5.5	26
41	Structural basis for DNA recognition by STAT6. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 13015-13020	11.5	26
40	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> , <b>2016</b> , 72, 359-74	5.5	23
39	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from Burkholderia pseudomallei. <i>Journal of Biological Chemistry</i> , <b>2016</b> , 291, 19387-400	5.4	23
38	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. <i>Structure</i> , <b>2015</b> , 23, 1858-1865	5.2	37
37	Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , <b>2014</b> , 5, 616-30	7.2	22
36	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> , <b>2014</b> , 15, 151	2.8	16
35	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. <i>Cell Research</i> , <b>2014</b> , 24, 344-58	24.7	66
34	Subfamily-specific adaptations in the structures of two penicillin-binding proteins from Mycobacterium tuberculosis. <i>PLoS ONE</i> , <b>2014</b> , 9, e116249	3.7	4
33	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> , <b>2013</b> , 14, 207	2.8	13
32	Crystal structure of AcrB complexed with linezolid at 3.5 Å resolution. <i>Journal of Structural and Functional Genomics</i> , <b>2013</b> , 14, 71-5		32

31	Structural basis for termination of AIM2-mediated signaling by p202. <i>Cell Research</i> , <b>2013</b> , 23, 855-8	24.7	30
30	Model morphing and sequence assignment after molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2244-50		24
29	Split green fluorescent protein as a modular binding partner for protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2013</b> , 69, 2513-23		24
28	Time orientation and visual construction subdomains of the MMSE as independent risk factors for hip fractures. <i>Orthopedics</i> , <b>2013</b> , 36, e869-76	1.5	5
27	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 521-30		22
26	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2012</b> , 68, 861-70		33
25	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. <i>Journal of Structural and Functional Genomics</i> , <b>2012</b> , 13, 71-9		4
24	The Phenix software for automated determination of macromolecular structures. <i>Methods</i> , <b>2011</b> , 55, 94-106	4.6	580
23	Lovastatin promotes redifferentiation of human nucleus pulposus cells during expansion in monolayer culture. <i>Artificial Organs</i> , <b>2011</b> , 35, 411-6	2.6	14
22	The TB Structural Genomics Consortium: a decade of progress. <i>Tuberculosis</i> , <b>2011</b> , 91, 155-72	2.6	33
21	An extracellular disulfide bond forming protein (DsbF) from <i>Mycobacterium tuberculosis</i> : structural, biochemical, and gene expression analysis. <i>Journal of Molecular Biology</i> , <b>2010</b> , 396, 1211-26	6.5	20
20	PHENIX: a comprehensive Python-based system for macromolecular structure solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2010</b> , 66, 213-21		16067
19	Structure of Rv1848 (UreA), the <i>Mycobacterium tuberculosis</i> urease gamma subunit. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2010</b> , 66, 781-6		10
18	Analysis of nucleoside-binding proteins by ligand-specific elution from dye resin: application to <i>Mycobacterium tuberculosis</i> aldehyde dehydrogenases. <i>Journal of Structural and Functional Genomics</i> , <b>2009</b> , 10, 291-301		11
17	Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn <sup>2+</sup> -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 356-65		28
16	Decision-making in structure solution using Bayesian estimates of map quality: the PHENIX AutoSol wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2009</b> , 65, 582-601		657
15	Structure and function of <i>Bacillus subtilis</i> YphP, a prokaryotic disulfide isomerase with a CXC catalytic motif. <i>Biochemistry</i> , <b>2009</b> , 48, 8664-71	3.2	35
14	Protein production and purification. <i>Nature Methods</i> , <b>2008</b> , 5, 135-46	21.6	655

13	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 61-9		1042
12	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2008</b> , 64, 515-24		130
11	Automated structure solution with the PHENIX suite. <i>Methods in Molecular Biology</i> , <b>2008</b> , 426, 419-35	1.4	421
10	Domain orientation in the inactive response regulator Mycobacterium tuberculosis MtrA provides a barrier to activation. <i>Biochemistry</i> , <b>2007</b> , 46, 6733-43	3.2	64
9	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2007</b> , 63, 597-610		56
8	Automated structure determination with phenix. <i>NATO Science Series Series II, Mathematics, Physics and Chemistry</i> , <b>2007</b> , 101-109		2
7	An automated high-throughput screening method for the identification of high-yield, soluble protein variants using cell-free expression and systematic truncation. <i>Journal of Structural and Functional Genomics</i> , <b>2006</b> , 7, 139-47		5
6	Functional and structural characterization of a thiol peroxidase from Mycobacterium tuberculosis. <i>Journal of Molecular Biology</i> , <b>2006</b> , 361, 850-63	6.5	39
5	Structure of Mycobacterium tuberculosis RuvA, a protein involved in recombination. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , <b>2006</b> , 62, 731-4		11
4	Crystal structure of a putative pyridoxine 5-phosphate oxidase (Rv2607) from Mycobacterium tuberculosis. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2006</b> , 62, 563-9	4.2	18
3	Crystal Structure of AhpE from Mycobacterium tuberculosis, a 1-Cys peroxiredoxin. <i>Journal of Molecular Biology</i> , <b>2005</b> , 346, 1035-46	6.5	70
2	Recent developments in the PHENIX software for automated crystallographic structure determination. <i>Journal of Synchrotron Radiation</i> , <b>2004</b> , 11, 53-5	2.4	273
1	PHENIX: building new software for automated crystallographic structure determination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2002</b> , 58, 1948-54		3477