Li-Wei Hung

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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	PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 213-21		16067
47	PHENIX: building new software for automated crystallographic structure determination. *Acta Crystallographica Section D: Biological Crystallography*, **2002**, 58, 1948-54		3477
46	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 861-877	5.5	1527
45	Iterative model building, structure refinement and density modification with the PHENIX AutoBuild wizard. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 61-9		1042
44	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		657
43	Protein production and purification. *Nature Methods*, **2008**, 5, 135-46	21.6	655
42	The Phenix software for automated determination of macromolecular structures. *Methods*, **2011**, 55, 94-106	4.6	580
41	Automated structure solution with the PHENIX suite. *Methods in Molecular Biology*, **2008**, 426, 419-35	1.4	421
40	Recent developments in the PHENIX software for automated crystallographic structure determination. *Journal of Synchrotron Radiation*, **2004**, 11, 53-5	2.4	273
39	Iterative-build OMIT maps: map improvement by iterative model building and refinement without model bias. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, 64, 515-24		130
38	Crystal Structure of AhpE from Mycobacterium tuberculosis, a 1-Cys peroxiredoxin. *Journal of Molecular Biology*, **2005**, 346, 1035-46	6.5	70
37	Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. *Cell Research*, **2014**, 24, 344-58	24.7	66
36	Domain orientation in the inactive response regulator Mycobacterium tuberculosis MtrA provides a barrier to activation. *Biochemistry*, **2007**, 46, 6733-43	3.2	64
35	Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. *Acta Crystallographica Section D: Biological Crystallography*, **2007**, 63, 597-610		56
34	Functional and structural characterization of a thiol peroxidase from Mycobacterium tuberculosis. *Journal of Molecular Biology*, **2006**, 361, 850-63	6.5	39
33	Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. *Structure*, **2015**, 23, 1858-1865	5.2	37
32	Structure and function of Bacillus subtilis YphP, a prokaryotic disulfide isomerase with a CXC catalytic motif. *Biochemistry*, **2009**, 48, 8664-71	3.2	35

(2014-2012)

31	Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 861-70		33
30	The TB Structural Genomics Consortium: a decade of progress. *Tuberculosis*, **2011**, 91, 155-72	2.6	33
29	Crystal structure of AcrB complexed with linezolid at 3.5 Å resolution. *Journal of Structural and Functional Genomics*, **2013**, 14, 71-5		32
28	Structural basis for termination of AIM2-mediated signaling by p202. *Cell Research*, **2013**, 23, 855-8	24.7	30
27	Structure of Thermotoga maritima TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn2+-binding FCD domains. *Acta Crystallographica Section D: Biological Crystallography*, **2009**, 65, 356-65		28
26	Can I solve my structure by SAD phasing? Anomalous signal in SAD phasing. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 346-58	5.5	26
25	Structural basis for DNA recognition by STAT6. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13015-13020	11.5	26
24	Model morphing and sequence assignment after molecular replacement. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2244-50		24
23	Split green fluorescent protein as a modular binding partner for protein crystallization. *Acta Crystallographica Section D: Biological Crystallography*, **2013**, 69, 2513-23		24
22	Can I solve my structure by SAD phasing? Planning an experiment, scaling data and evaluating the useful anomalous correlation and anomalous signal. *Acta Crystallographica Section D: Structural Biology*, **2016**, 72, 359-74	5.5	23
21	Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from Burkholderia pseudomallei. *Journal of Biological Chemistry*, **2016**, 291, 19387-400	5.4	23
20	Mechanism of the Rpn13-induced activation of Uch37. *Protein and Cell*, **2014**, 5, 616-30	7.2	22
19	S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 521-30		22
18	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. *Nature Methods*, **2021**, 18, 156-164	21.6	22
17	An extracellular disulfide bond forming protein (DsbF) from Mycobacterium tuberculosis: structural, biochemical, and gene expression analysis. *Journal of Molecular Biology*, **2010**, 396, 1211-26	6.5	20
16	Crystal structure of a putative pyridoxine 5′-phosphate oxidase (Rv2607) from Mycobacterium tuberculosis. *Proteins: Structure, Function and Bioinformatics*, **2006**, 62, 563-9	4.2	18
15	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. *Medicine (United States)*, **2017**, 96, e7618	1.8	17
14	High short-term and long-term excess mortality in geriatric patients after hip fracture: a prospective cohort study in Taiwan. *BMC Musculoskeletal Disorders*, **2014**, 15, 151	2.8	16

13	Lovastatin promotes redifferentiation of human nucleus pulposus cells during expansion in monolayer culture. *Artificial Organs*, **2011**, 35, 411-6	2.6	14
12	Hip fracture risk assessment: artificial neural network outperforms conditional logistic regression in an age- and sex-matched case control study. *BMC Musculoskeletal Disorders*, **2013**, 14, 207	2.8	13
11	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		11
10	Structure of Mycobacterium tuberculosis RuvA, a protein involved in recombination. *Acta Crystallographica Section F: Structural Biology Communications*, **2006**, 62, 731-4		11
9	Structure of Rv1848 (UreA), the Mycobacterium tuberculosis urease gamma subunit. *Acta Crystallographica Section F: Structural Biology Communications*, **2010**, 66, 781-6		10
8	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*, **2006**, 7, 139-47		5
7	Time orientation and visual construction subdomains of the MMSE as independent risk factors for hip fractures. *Orthopedics*, **2013**, 36, e869-76	1.5	5
6	Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. *Journal of Structural and Functional Genomics*, **2012**, 13, 71-9		4
5	Subfamily-specific adaptations in the structures of two penicillin-binding proteins from Mycobacterium tuberculosis. *PLoS ONE*, **2014**, 9, e116249	3.7	4
4	Chronic kidney disease predicts a lower probability of improvement in patient-reported experience measures among patients with fractures: a prospective multicenter cohort study. *Archives of Osteoporosis*, **2018**, 13, 126	2.9	3
3	Automated structure determination with phenix. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 101-109		2
2	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. *Journal of Shoulder and Elbow Surgery*, **2021**, 30, e636-e645	4.3	0
1	BpeB, a major resistance-nodulation-cell division transporter from Burkholderia cenocepacia: construct design, crystallization and preliminary structural analysis. *Acta Crystallographica Section F, Structural Biology Communications*, **2018**, 74, 710-716	1.1	