

Li-Wei Hung

List of Publications by Year in descending order

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Version: 2024-02-01

50
papers

34,372
citations

201385

27
h-index

197535

49
g-index

52
all docs

52
docs citations

52
times ranked

43655
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | <i>PHENIX</i>: a comprehensive Python-based system for macromolecular structure solution. Acta Crystallographica Section D: Biological Crystallography, 2010, 66, 213-221. | 2.5 | 20,564 |
| 2 | Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in <i>Phenix</i>. Acta Crystallographica Section D: Structural Biology, 2019, 75, 861-877. | 1.1 | 4,060 |
| 3 | PHENIX: building new software for automated crystallographic structure determination. Acta Crystallographica Section D: Biological Crystallography, 2002, 58, 1948-1954. | 2.5 | 3,979 |
| 4 | Iterative model building, structure refinement and density modification with the <i>PHENIX AutoBuild</i> wizard. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 61-69. | 2.5 | 1,319 |
| 5 | Decision-making in structure solution using Bayesian estimates of map quality: the <i>PHENIX AutoSol</i> wizard. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 582-601. | 2.5 | 804 |
| 6 | The Phenix software for automated determination of macromolecular structures. Methods, 2011, 55, 94-106. | 1.9 | 764 |
| 7 | Protein production and purification. Nature Methods, 2008, 5, 135-146. | 9.0 | 763 |
| 8 | Automated Structure Solution with the PHENIX Suite. Methods in Molecular Biology, 2008, 426, 419-435. | 0.4 | 492 |
| 9 | Recent developments in the PHENIX software for automated crystallographic structure determination. Journal of Synchrotron Radiation, 2004, 11, 53-55. | 1.0 | 319 |
| 10 | 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 |
| 11 | Structural analysis of asparaginyl endopeptidase reveals the activation mechanism and a reversible intermediate maturation stage. Cell Research, 2014, 24, 344-358. | 5.7 | 86 |
| 12 | Crystal Structure of AhpE from Mycobacterium tuberculosis, a 1-Cys Peroxiredoxin. Journal of Molecular Biology, 2005, 346, 1035-1046. | 2.0 | 77 |
| 13 | Domain Orientation in the Inactive Response Regulator Mycobacterium tuberculosis MtrA Provides a Barrier to Activation. Biochemistry, 2007, 46, 6733-6743. | 1.2 | 76 |
| 14 | Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. Nature Methods, 2021, 18, 156-164. | 9.0 | 73 |
| 15 | Interpretation of ensembles created by multiple iterative rebuilding of macromolecular models. Acta Crystallographica Section D: Biological Crystallography, 2007, 63, 597-610. | 2.5 | 60 |
| 16 | Functional and Structural Characterization of a Thiol Peroxidase from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 361, 850-863. | 2.0 | 58 |
| 17 | Structure of Ribosomal Silencing Factor Bound to Mycobacterium tuberculosis Ribosome. Structure, 2015, 23, 1858-1865. | 1.6 | 50 |
| 18 | Structural basis for DNA recognition by STAT6. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13015-13020. | 3.3 | 46 |

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|----|--|-----|-----------|
| 19 | The TB Structural Genomics Consortium: A decade of progress. <i>Tuberculosis</i> , 2011, 91, 155-172. | 0.8 | 39 |
| 20 | Crystal structure of AcrB complexed with linezolid at 3.5Å... resolution. <i>Journal of Structural and Functional Genomics</i> , 2013, 14, 71-75. | 1.2 | 38 |
| 21 | Structural basis for termination of AIM2-mediated signaling by p202. <i>Cell Research</i> , 2013, 23, 855-858. | 5.7 | 38 |
| 22 | Structure and Function of Bacillus subtilis YphP, a Prokaryotic Disulfide Isomerase with a CXC Catalytic Motif. <i>Biochemistry</i> , 2009, 48, 8664-8671. | 1.2 | 37 |
| 23 | Improved crystallographic models through iterated local density-guided model deformation and reciprocal-space refinement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 861-870. | 2.5 | 37 |
| 24 | Model morphing and sequence assignment after molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2244-2250. | 2.5 | 37 |
| 25 | Structure of <i>Thermotoga maritima</i> TM0439: implications for the mechanism of bacterial GntR transcription regulators with Zn ²⁺ -binding FCD domains. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 356-365. | 2.5 | 31 |
| 26 | 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 |
| 27 | Split green fluorescent protein as a modular binding partner for protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 2513-2523. | 2.5 | 29 |
| 28 | 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 |
| 29 | Functional Diversity of Cytotoxic tRNase/Immunity Protein Complexes from Burkholderia pseudomallei. <i>Journal of Biological Chemistry</i> , 2016, 291, 19387-19400. | 1.6 | 28 |
| 30 | Mechanism of the Rpn13-induced activation of Uch37. <i>Protein and Cell</i> , 2014, 5, 616-630. | 4.8 | 27 |
| 31 | S-SAD phasing study of death receptor 6 and its solution conformation revealed by SAXS. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2012, 68, 521-530. | 2.5 | 24 |
| 32 | An Extracellular Disulfide Bond Forming Protein (DsbF) from Mycobacterium tuberculosis: Structural, Biochemical, and Gene Expression Analysis. <i>Journal of Molecular Biology</i> , 2010, 396, 1211-1226. | 2.0 | 23 |
| 33 | 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 |
| 34 | Crystal structure of a putative pyridoxine 5-phosphate oxidase (Rv2607) from Mycobacterium tuberculosis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 62, 563-569. | 1.5 | 19 |
| 35 | 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 |
| 36 | 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 |

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|----|--|-----|-----------|
| 37 | Lovastatin Promotes Redifferentiation of Human Nucleus Pulposus Cells During Expansion in Monolayer Culture. <i>Artificial Organs</i> , 2011, 35, 411-416. | 1.0 | 14 |
| 38 | 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> , 2009, 10, 291-301. | 1.2 | 13 |
| 39 | Structure of <i>Mycobacterium tuberculosis</i> RuvA, a protein involved in recombination. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 731-734. | 0.7 | 12 |
| 40 | Structure of Rv1848 (UreA), the <i>Mycobacterium tuberculosis</i> urease \hat{I}^3 subunit. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 781-786. | 0.7 | 10 |
| 41 | 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> , 2007, 7, 139-147. | 1.2 | 7 |
| 42 | 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 |
| 43 | 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 |
| 44 | Time Orientation and Visual Construction Subdomains of the MMSE as Independent Risk Factors for Hip Fractures. <i>Orthopedics</i> , 2013, 36, e869-76. | 0.5 | 6 |
| 45 | Enhancement of crystallization with nucleotide ligands identified by dye-ligand affinity chromatography. <i>Journal of Structural and Functional Genomics</i> , 2012, 13, 71-79. | 1.2 | 5 |
| 46 | Construction, characterization and crystal structure of a fluorescent single-chain Fv chimera. <i>Protein Engineering, Design and Selection</i> , 2021, 34, . | 1.0 | 4 |
| 47 | Automated structure determination with phenix. <i>NATO Science Series Series II, Mathematics, Physics and Chemistry</i> , 2007, , 101-109. | 0.1 | 4 |
| 48 | 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 |
| 49 | BpeB, a major resistance-nodulation-cell division transporter from <i>Burkholderia cenocepacia</i> : construct design, crystallization and preliminary structural analysis. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2018, 74, 710-716. | 0.4 | 1 |
| 50 | Combining Crystallographic and Structure-Modeling Approaches in Macromolecular Crystallography. <i>Biophysical Journal</i> , 2014, 106, 34a. | 0.2 | 0 |