

# Yu-Wei Chen

## List of Publications by Year in descending order

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51  
papers

1,431  
citations

567281

15  
h-index

330143

37  
g-index

55  
all docs

55  
docs citations

55  
times ranked

2170  
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of the SARS-CoV-2 (2019-nCoV) 3C-like protease (3CLpro) structure: virtual screening reveals velpatasvir, ledipasvir, and other drug repurposing candidates. <i>F1000Research</i> , 2020, 9, 129.	1.6	368
2	Prediction of the SARS-CoV-2 (2019-nCoV) 3C-like protease (3CLpro) structure: virtual screening reveals velpatasvir, ledipasvir, and other drug repurposing candidates. <i>F1000Research</i> , 2020, 9, 129.	1.6	242
3	Structure of UreG/UreF/UreH Complex Reveals How Urease Accessory Proteins Facilitate Maturation of <i>Helicobacter pylori</i> Urease. <i>PLoS Biology</i> , 2013, 11, e1001678.	5.6	104
4	Contribution of Buried Hydrogen Bonds to Protein Stability The Crystal Structures of Two Barnase Mutants. <i>Journal of Molecular Biology</i> , 1993, 234, 1158-1170.	4.2	71
5	Rational Design of a Novel Fluorescent Biosensor for $\beta$ -Lactam Antibiotics from a Class A $\beta$ -Lactamase. <i>Journal of the American Chemical Society</i> , 2004, 126, 4074-4075.	13.7	65
6	Crystal structure of a dimeric chymotrypsin inhibitor 2 mutant containing an inserted glutamine repeat. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 1257-1261.	7.1	59
7	Simeprevir Potently Suppresses SARS-CoV-2 Replication and Synergizes with Remdesivir. <i>ACS Central Science</i> , 2021, 7, 792-802.	11.3	59
8	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. <i>Journal of Biological Chemistry</i> , 2004, 279, 3758-3765.	3.4	55
9	Assembly of Preactivation Complex for Urease Maturation in <i>Helicobacter pylori</i> . <i>Journal of Biological Chemistry</i> , 2011, 286, 43241-43249.	3.4	42
10	Does NMR Mean "Not for Molecular Replacement"? Using NMR-Based Search Models to Solve Protein Crystal Structures. <i>Structure</i> , 2000, 8, R213-R220.	3.3	31
11	First Glimpse of the Peptide Presentation by Rhesus Macaque MHC Class I: Crystal Structures of Mamu-A*01 Complexed with Two Immunogenic SIV Epitopes and Insights into CTL Escape. <i>Journal of Immunology</i> , 2007, 178, 944-952.	0.8	31
12	Structure of the C-terminal sterile $\alpha$ -motif (SAM) domain of human p73 $\Delta$ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 545-551.	2.5	28
13	Phosphorylation of FE65 Ser610 by serum- and glucocorticoid-induced kinase 1 modulates Alzheimer's disease amyloid precursor protein processing. <i>Biochemical Journal</i> , 2015, 470, 303-317.	3.7	22
14	Self-Assembly and Conformational Heterogeneity of the AXH Domain of Ataxin-1: An Unusual Example of a Chameleon Fold. <i>Biophysical Journal</i> , 2013, 104, 1304-1313.	0.5	19
15	Solution Model of the Intrinsically Disordered Polyglutamine Tract-Binding Protein-1. <i>Biophysical Journal</i> , 2012, 102, 1608-1616.	0.5	16
16	Crystal Structure of Ribosomal Protein L30e from the Extreme Thermophile <i>Thermococcus celer</i> : Thermal Stability and RNA Binding. <i>Biochemistry</i> , 2003, 42, 2857-2865.	2.5	15
17	Conformational Dynamics of the Helix 10 Region as an Allosteric Site in Class A $\beta$ -Lactamase Inhibitory Binding. <i>Journal of the American Chemical Society</i> , 2020, 142, 13756-13767.	13.7	15
18	A systematic case study on using NMR models for molecular replacement: p53 tetramerization domain revisited. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1535-1540.	2.5	13

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19	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeon <i>Thermococcus celer</i> . <i>Protein Science</i> , 2003, 12, 1483-1495.	7.6	13
20	Local protein unfolding and pathogenesis of polyglutamine-expansion diseases. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 51, 68-73.	2.6	13
21	Mono-PEGylation of a Thermostable Arginine-Depleting Enzyme for the Treatment of Lung Cancer. <i>International Journal of Molecular Sciences</i> , 2020, 21, 4234.	4.1	13
22	Design of a structure-based fluorescent biosensor from bioengineered arginine deiminase for rapid determination of L-arginine. <i>International Journal of Biological Macromolecules</i> , 2020, 165, 472-482.	7.5	12
23	Design and Characterization of Human Respiratory Syncytial Virus Entry Inhibitors. <i>Antiviral Therapy</i> , 2005, 10, 833-840.	1.0	12
24	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73 $\Delta$ . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 769-771.	2.5	11
25	Solution solution: using NMR models for molecular replacement. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 1457-1461.	2.5	11
26	Discovery of FtsZ inhibitors by virtual screening as antibacterial agents and study of the inhibition mechanism. <i>RSC Medicinal Chemistry</i> , 2022, 13, 79-89.	3.9	10
27	Hydrophobic substituents on isatin derivatives enhance their inhibition against bacterial peptidoglycan glycosyltransferase activity. <i>Bioorganic Chemistry</i> , 2020, 97, 103710.	4.1	9
28	Stability and solvation of Thr/Ser to Ala and Gly mutations at the N-cap of $\alpha$ -helices. <i>FEBS Letters</i> , 1994, 347, 304-309.	2.8	8
29	Frameshift PQBP-1 mutants K192Sfs*7 and R153Sfs*41 implicated in X-linked intellectual disability form stable dimers. <i>Journal of Structural Biology</i> , 2019, 206, 305-313.	2.8	7
30	High-Quality Macromolecular Graphics on Mobile Devices: A Quick Starter's Guide. <i>Methods in Molecular Biology</i> , 2014, 1091, 343-352.	0.9	7
31	From Disorder to Mis-Order: Structural Aspects of Pathogenic Oligomerization in Conformational Diseases. <i>Protein and Peptide Letters</i> , 2017, 24, 307-314.	0.9	7
32	Insoluble Protein Purification with Sarkosyl: Facts and Precautions. <i>Methods in Molecular Biology</i> , 2014, 1091, 179-186.	0.9	6
33	Crystallographic analysis of Phe $\rightarrow$ Leu substitution in the hydrophobic core of barnase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 220-231.	2.5	4
34	Computational Resources for Protein Modelling and Drug Discovery Applications. <i>Infectious Disorders - Drug Targets</i> , 2009, 9, 557-562.	0.8	4
35	The crystal structure of the ubiquitin-like (UbL) domain of human homologue A of Rad23 (hHR23A) protein. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 131-138.	2.1	4
36	Site-specific mutagenesis in a homogeneous polyglutamine tract: application to spinocerebellar ataxin-3. <i>Protein Engineering, Design and Selection</i> , 2003, 16, 1-4.	2.1	3

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37	Refolding, crystallization and preliminary X-ray structural studies of the West Nile virus envelope (E) protein domain III. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 421-423.	0.7	3
38	BADAN-conjugated $\beta$ -lactamases as biosensors for $\beta$ -lactam antibiotic detection. <i>PLoS ONE</i> , 2020, 15, e0241594.	2.5	3
39	Crystallization and preliminary crystallographic studies of a ribosomal protein L30e from the hyperthermophilic archaeon <i>Thermococcus celer</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2001, 57, 865-866.	2.5	2
40	Interdomain flexibility and interfacial integrity of $\beta$ -lactamase inhibitory protein (BLIP) modulate its binding to class A $\beta$ -lactamases. <i>Journal of Biological Chemistry</i> , 2021, 297, 100980.	3.4	2
41	Molecular Data Visualization with Augmented Reality (AR) on Mobile Devices. <i>Methods in Molecular Biology</i> , 2021, 2199, 347-356.	0.9	2
42	Fatal Attraction: The Case of Toxic Soluble Dimers of Truncated PQBP-1 Mutants in X-Linked Intellectual Disability. <i>International Journal of Molecular Sciences</i> , 2021, 22, 2240.	4.1	1
43	Virtual screening on the web for drug repurposing: a primer. <i>Journal of Biological Methods</i> , 2021, 8, e148.	0.6	1
44	Parameterization of Large Ligands for Gromacs Molecular Dynamics Simulation with LigParGen. <i>Methods in Molecular Biology</i> , 2021, 2199, 277-288.	0.9	1
45	Molecular Data Visualization on Mobile Devices: A Quick Starter's Guide. <i>Methods in Molecular Biology</i> , 2021, 2199, 337-346.	0.9	1
46	How to prepare a DNA sequencing chromatogram for publication. <i>Technical Tips Online</i> , 2001, 6, 37-38.	0.2	0
47	Internet Resources for the Antibody Engineer. , 2004, , 3-10.		0
48	Crystallization and preliminary X-ray diffraction studies of the ubiquitin-like (Ubl) domain of the human homologue A of Rad23 (hHR23A) protein. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 930-932.	0.7	0
49	Crystallization and preliminary crystallographic analysis of the central domain of <i>Drosophila</i> Dribble, a protein that is essential for ribosome biogenesis. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 546-548.	0.7	0
50	Strong, non-local interactions: the Hong Kong bond. <i>Protein Engineering, Design and Selection</i> , 2011, 24, 235-239.	2.1	0
51	Characterization of chemically synthesized hybrid CXC chemokines. <i>Acta Crystallographica Section A: Foundations and Advances</i> , 1996, 52, C219-C220.	0.3	0