Yu-Wei Chen

List of Publications by Year in descending order

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567281 330143 1,431 51 15 37 citations h-index g-index papers 55 55 55 2170 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Discovery of FtsZ inhibitors by virtual screening as antibacterial agents and study of the inhibition mechanism. RSC Medicinal Chemistry, 2022, 13, 79-89.	3.9	10
2	Fatal Attraction: The Case of Toxic Soluble Dimers of Truncated PQBP-1 Mutants in X-Linked Intellectual Disability. International Journal of Molecular Sciences, 2021, 22, 2240.	4.1	1
3	Simeprevir Potently Suppresses SARS-CoV-2 Replication and Synergizes with Remdesivir. ACS Central Science, 2021, 7, 792-802.	11.3	59
4	Virtual screening on the web for drug repurposing: a primer. Journal of Biological Methods, 2021, 8, e148.	0.6	1
5	Interdomain flexibility and interfacial integrity of \hat{l}^2 -lactamase inhibitory protein (BLIP) modulate its binding to class A \hat{l}^2 -lactamases. Journal of Biological Chemistry, 2021, 297, 100980.	3.4	2
6	Parameterization of Large Ligands for Gromacs Molecular Dynamics Simulation with LigParGen. Methods in Molecular Biology, 2021, 2199, 277-288.	0.9	1
7	Molecular Data Visualization with Augmented Reality (AR) on Mobile Devices. Methods in Molecular Biology, 2021, 2199, 347-356.	0.9	2
8	Molecular Data Visualization on Mobile Devices: A Quick Starter's Guide. Methods in Molecular Biology, 2021, 2199, 337-346.	0.9	1
9	Design of a structure-based fluorescent biosensor from bioengineered arginine deiminase for rapid determination of L-arginine. International Journal of Biological Macromolecules, 2020, 165, 472-482.	7.5	12
10	Conformational Dynamics of the Helix 10 Region as an Allosteric Site in Class A \hat{I}^2 -Lactamase Inhibitory Binding. Journal of the American Chemical Society, 2020, 142, 13756-13767.	13.7	15
11	Mono-PEGylation of a Thermostable Arginine-Depleting Enzyme for the Treatment of Lung Cancer. International Journal of Molecular Sciences, 2020, 21, 4234.	4.1	13
12	Hydrophobic substituents on isatin derivatives enhance their inhibition against bacterial peptidoglycan glycosyltransferase activity. Bioorganic Chemistry, 2020, 97, 103710.	4.1	9
13	Prediction of the SARS-CoV-2 (2019-nCoV) 3C-like protease (3CLpro) structure: virtual screening reveals velpatasvir, ledipasvir, and other drug repurposing candidates. F1000Research, 2020, 9, 129.	1.6	242
14	Prediction of the SARS-CoV-2 (2019-nCoV) 3C-like protease (3CLpro) structure: virtual screening reveals velpatasvir, ledipasvir, and other drug repurposing candidates. F1000Research, 2020, 9, 129.	1.6	368
15	BADAN-conjugated \hat{l}^2 -lactamases as biosensors for \hat{l}^2 -lactam antibiotic detection. PLoS ONE, 2020, 15, e0241594.	2.5	3
16	Frameshift PQBP-1 mutants K192Sfs*7 and R153Sfs*41 implicated in X-linked intellectual disability form stable dimers. Journal of Structural Biology, 2019, 206, 305-313.	2.8	7
17	From Disorder to Mis-Order: Structural Aspects of Pathogenic Oligomerization in Conformational Diseases. Protein and Peptide Letters, 2017, 24, 307-314.	0.9	7
18	Phosphorylation of FE65 Ser610 by serum- and glucocorticoid-induced kinase 1 modulates Alzheimer's disease amyloid precursor protein processing. Biochemical Journal, 2015, 470, 303-317.	3.7	22

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19	Insoluble Protein Purification with Sarkosyl: Facts and Precautions. Methods in Molecular Biology, 2014, 1091, 179-186.	0.9	6
20	High-Quality Macromolecular Graphics on Mobile Devices: A Quick Starter's Guide. Methods in Molecular Biology, 2014, 1091, 343-352.	0.9	7
21	Self-Assembly and Conformational Heterogeneity of the AXH Domain ofÂAtaxin-1: An Unusual Example of a Chameleon Fold. Biophysical Journal, 2013, 104, 1304-1313.	0.5	19
22	Structure of UreG/UreF/UreH Complex Reveals How Urease Accessory Proteins Facilitate Maturation of Helicobacter pylori Urease. PLoS Biology, 2013, 11, e1001678.	5.6	104
23	Solution Model of the Intrinsically Disordered Polyglutamine Tract-Binding Protein-1. Biophysical Journal, 2012, 102, 1608-1616.	0.5	16
24	Assembly of Preactivation Complex for Urease Maturation in Helicobacter pylori. Journal of Biological Chemistry, 2011, 286, 43241-43249.	3.4	42
25	The crystal structure of the ubiquitin-like (UbL) domain of human homologue A of Rad23 (hHR23A) protein. Protein Engineering, Design and Selection, 2011, 24, 131-138.	2.1	4
26	Strong, non-local interactions: the Hong Kong bond. Protein Engineering, Design and Selection, 2011, 24, 235-239.	2.1	0
27	Crystallization and preliminary crystallographic analysis of the central domain ofDrosophilaDribble, a protein that is essential for ribosome biogenesis. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 546-548.	0.7	0
28	Computational Resources for Protein Modelling and Drug Discovery Applications. Infectious Disorders - Drug Targets, 2009, 9, 557-562.	0.8	4
29	Crystallization and preliminary X-ray diffraction studies of the ubiquitin-like (UbL) domain of the human homologue A of Rad23 (hHR23A) protein. Acta Crystallographica Section F: Structural Biology Communications, 2009, 65, 930-932.	0.7	0
30	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. Journal of Immunology, 2007, 178, 944-952.	0.8	31
31	Refolding, crystallization and preliminary X-ray structural studies of the West Nile virus envelope (E) protein domain III. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 421-423.	0.7	3
32	Design and Characterization of Human Respiratory Syncytial Virus Entry Inhibitors. Antiviral Therapy, 2005, 10, 833-840.	1.0	12
33	Internet Resources for the Antibody Engineer. , 2004, , 3-10.		0
34	The Structure of the AXH Domain of Spinocerebellar Ataxin-1. Journal of Biological Chemistry, 2004, 279, 3758-3765.	3.4	55
35	Rational Design of a Novel Fluorescent Biosensor for \hat{l}^2 -Lactam Antibiotics from a Class A \hat{l}^2 -Lactamase. Journal of the American Chemical Society, 2004, 126, 4074-4075.	13.7	65
36	Solution structure and thermal stability of ribosomal protein L30e from hyperthermophilic archaeonThermococcus celer. Protein Science, 2003, 12, 1483-1495.	7.6	13

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37	Local protein unfolding and pathogenesis of polyglutamine-expansion diseases. Proteins: Structure, Function and Bioinformatics, 2003, 51, 68-73.	2.6	13
38	Crystal Structure of Ribosomal Protein L30e from the Extreme ThermophileThermococcus celer: Thermal Stability and RNA Bindingâ€,‡. Biochemistry, 2003, 42, 2857-2865.	2.5	15
39	Site-specific mutagenesis in a homogeneous polyglutamine tract: application to spinocerebellar ataxin-3. Protein Engineering, Design and Selection, 2003, 16 , 1 -4.	2.1	3
40	Structure of the C-terminal sterile α-motif (SAM) domain of human p73α. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 545-551.	2.5	28
41	Crystallization and preliminary crystallographic studies of a ribosomal protein L30e from the hyperthermophilic archaeonThermococcus celer. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 865-866.	2.5	2
42	Solution solution: using NMR models for molecular replacement. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1457-1461.	2.5	11
43	How to prepare a DNA sequencing chromatogram for publication. Technical Tips Online, 2001, 6, 37-38.	0.2	0
44	Crystallization and preliminary crystallographic studies of a SAM domain at the C-terminus of human p73α. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 769-771.	2.5	11
45	A systematic case study on using NMR models for molecular replacement: p53 tetramerization domain revisited. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1535-1540.	2.5	13
46	Does NMR Mean "Not for Molecular Replacement� Using NMR-Based Search Models to Solve Protein Crystal Structures. Structure, 2000, 8, R213-R220.	3.3	31
47	Crystal structure of a dimeric chymotrypsin inhibitor 2 mutant containing an inserted glutamine repeat. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 1257-1261.	7.1	59
48	Characterization of chemically synthesized hybrid CXC chemokines. Acta Crystallographica Section A: Foundations and Advances, 1996, 52, C219-C220.	0.3	0
49	Crystallographic analysis of Pheâ†'Leu substitution in the hydrophobic core of barnase. Acta Crystallographica Section D: Biological Crystallography, 1995, 51, 220-231.	2.5	4
50	Stability and solvation of Thr/Ser to Ala and Gly mutations at the N-cap of \hat{l} ±-helices. FEBS Letters, 1994, 347, 304-309.	2.8	8
51	Contribution of Buried Hydrogen Bonds to Protein Stability The Crystal Structures of Two Barnase Mutants. Journal of Molecular Biology, 1993, 234, 1158-1170.	4.2	71