Kuen-Phon Wu

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3125868/publications.pdf

Version: 2024-02-01

430874 454955 1,735 32 18 30 citations h-index g-index papers 33 33 33 2847 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Structural basis for the helical filament formation of <i>Escherichia coli</i> glutamine synthetase. Protein Science, 2022, 31, e4304.	7.6	5
2	Tumor suppressor BAP1 nuclear import is governed by transportin-1. Journal of Cell Biology, 2022, 221,	5.2	5
3	VPS34 K29/K48 branched ubiquitination governed by UBE3C and TRABID regulates autophagy, proteostasis and liver metabolism. Nature Communications, 2021, 12, 1322.	12.8	43
4	Direct Visualization of a 26 kDa Protein by Cryo-Electron Microscopy Aided by a Small Scaffold Protein. Biochemistry, 2021, 60, 1075-1079.	2.5	8
5	Simeprevir Potently Suppresses SARS-CoV-2 Replication and Synergizes with Remdesivir. ACS Central Science, 2021, 7, 792-802.	11.3	59
6	Identification of disease-linked hyperactivating mutations in UBE3A through large-scale functional variant analysis. Nature Communications, 2021, 12, 6809.	12.8	10
7	Cryo-EM analysis of a feline coronavirus spike protein reveals a unique structure and camouflaging glycans. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1438-1446.	7.1	94
8	Branched Ubiquitination: Detection Methods, Biological Functions and Chemical Synthesis. Molecules, 2020, 25, 5200.	3.8	18
9	Insights Into Dynamics of Inhibitor and Ubiquitin-Like Protein Binding in SARS-CoV-2 Papain-Like Protease. Frontiers in Molecular Biosciences, 2020, 7, 174.	3.5	51
10	Insights into links between autophagy and the ubiquitin system from the structure of LC3B bound to the LIR motif from the E3 ligase NEDD4. Protein Science, 2017, 26, 1674-1680.	7.6	18
11	Deubiquitinase activity is required for the proteasomal degradation of misfolded cytosolic proteins upon heat-stress. Nature Communications, 2016, 7, 12907.	12.8	45
12	A cascading activity-based probe sequentially targets E1–E2–E3 ubiquitin enzymes. Nature Chemical Biology, 2016, 12, 523-530.	8.0	122
13	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	28.9	126
14	System-Wide Modulation of HECT E3 Ligases with Selective Ubiquitin Variant Probes. Molecular Cell, 2016, 62, 121-136.	9.7	142
15	Unveiling transient protein-protein interactions that modulate inhibition of alpha-synuclein aggregation by beta-synuclein, a pre-synaptic protein that co-localizes with alpha-synuclein. Scientific Reports, 2015, 5, 15164.	3.3	53
16	Itch WW Domains Inhibit Its E3 Ubiquitin Ligase Activity by Blocking E2-E3 Ligase Trans-thiolation. Journal of Biological Chemistry, 2015, 290, 23875-23887.	3.4	56
17	Fast hydrogen exchange affects 15N relaxation measurements in intrinsically disordered proteins. Journal of Biomolecular NMR, 2013, 55, 249-256.	2.8	18
18	ACAâ€specific RNA sequence recognition is acquired via the loop 2 region of MazF mRNA interferase. Proteins: Structure, Function and Bioinformatics, 2013, 81, 874-883.	2.6	8

#	Article	IF	CITATIONS
19	Investigation of the Polymeric Properties of \hat{l}_{\pm} -Synuclein and Comparison with NMR Experiments: A Replica Exchange Molecular Dynamics Study. Journal of Chemical Theory and Computation, 2012, 8, 3929-3942.	5. 3	31
20	Segmental isotope labeling of proteins for NMR structural study using a protein S tag for higher expression and solubility. Journal of Biomolecular NMR, 2012, 52, 303-313.	2.8	16
21	YeeU enhances the bundling of cytoskeletal polymers of MreB and FtsZ, antagonizing the CbtA (YeeV) toxicity in <i>Escherichia coli</i> i>. Molecular Microbiology, 2012, 84, 979-989.	2.5	204
22	The A53T Mutation is Key in Defining the Differences in the Aggregation Kinetics of Human and Mouse \hat{l}_{\pm} -Synuclein. Journal of the American Chemical Society, 2011, 133, 13465-13470.	13.7	45
23	Transient Protein-Protein Interactions in the IDP Alpha-Synuclein Detected by NMR: Implications for Protein Aggregation. Biophysical Journal, 2011, 100, 519a.	0.5	O
24	Backbone assignment and dynamics of human α-synuclein in viscous 2ÂM glucose solution. Biomolecular NMR Assignments, 2011, 5, 43-46.	0.8	13
25	Detection of Transient Interchain Interactions in the Intrinsically Disordered Protein α-Synuclein by NMR Paramagnetic Relaxation Enhancement. Journal of the American Chemical Society, 2010, 132, 5546-5547.	13.7	93
26	Structural Reorganization of \hat{l}_{\pm} -Synuclein at Low pH Observed by NMR and REMD Simulations. Journal of Molecular Biology, 2009, 391, 784-796.	4.2	170
27	Backbone NMR assignments of DFP-inhibited mature subtilisin E. Biomolecular NMR Assignments, 2008, 2, 131-133.	0.8	5
28	Characterization of Conformational and Dynamic Properties of Natively Unfolded Human and Mouse \hat{l}_{\pm} -Synuclein Ensembles by NMR: Implication for Aggregation. Journal of Molecular Biology, 2008, 378, 1104-1115.	4.2	112
29	Distinguishing among Structural Ensembles of the GB1 Peptide:Â REMD Simulations and NMR Experiments. Journal of the American Chemical Society, 2007, 129, 4858-4859.	13.7	24
30	Letter to the Editor: 1H, 13C and 15N resonance assignments and secondary structure of murine angiogenin 4. Journal of Biomolecular NMR, 2005, 31, 175-176.	2.8	3
31	Novel Solution Structure of Porcine \hat{l}^2 -Microseminoprotein. Journal of Molecular Biology, 2005, 346, 1071-1082.	4.2	11
32	Structural Basis of a Flavivirus Recognized by Its Neutralizing Antibody. Journal of Biological Chemistry, 2003, 278, 46007-46013.	3.4	108