Yongqi Huang

List of Publications by Year
in descending order

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47	1,139	471509	414414
papers	citations	17 h-index	32 g-index

47	47	47	1585
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Kinetic Advantage of Intrinsically Disordered Proteins in Coupled Foldingâ€“Binding Process: A Critical Assessment of the â€œFly-Castingâ€•Mechanism. Journal of Molecular Biology, 2009, 393, 1143-1159.	4.2	246
2	Advantages of proteins being disordered. Protein Science, 2014, 23, 539-550.	7.6	140
3	Cryptic sequence features within the disordered protein p27 ^{Kip1} regulate cell cycle signaling. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 5616-5621.	7.1	109
4	Features of molecular recognition of intrinsically disordered proteins via coupled folding and binding. Protein Science, 2019, 28, 1952-1965.	7.6	55
5	Bacterial cupredoxin azurin hijacks cellular signaling networks: Proteinâ€“protein interactions and cancer therapy. Protein Science, 2017, 26, 2334-2341.	7.6	45
6	Do Intrinsically Disordered Proteins Possess High Specificity in Proteinâ€“Protein Interactions?. Chemistry - A European Journal, 2013, 19, 4462-4467.	3.3	41
7	Binding of Two Intrinsically Disordered Peptides to a Multi-Specific Protein: A Combined Monte Carlo and Molecular Dynamics Study. PLoS Computational Biology, 2012, 8, e1002682.	3.2	37
8	Nonnative Interactions in Coupled Folding and Binding Processes of Intrinsically Disordered Proteins. PLoS ONE, 2010, 5, e15375.	2.5	36
9	Smoothing molecular interactions: The â€œkinetic bufferâ€•effect of intrinsically disordered proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3251-3259.	2.6	31
10	The Activity and Stability of the Intrinsically Disordered Cip/Kip Protein Family AreRegulated by Non-Receptor TyrosineKinases. Journal of Molecular Biology, 2015, 427, 371-386.	4.2	31
11	Threeâ€dimensional domain swapping in the protein structure space. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1610-1619.	2.6	29
12	14-3-3/Tau Interaction and Tau Amyloidogenesis. Journal of Molecular Neuroscience, 2019, 68, 620-630.	2.3	24
13	Anchoring Intrinsically Disordered Proteins to Multiple Targets: Lessons from N-Terminus of the p53 Protein. International Journal of Molecular Sciences, 2011, 12, 1410-1430.	4.1	21
14	Tanshinones: First-in-Class Inhibitors of the Biogenesis of the Type 3 Secretion System Needle of Pseudomonas aeruginosa for Antibiotic Therapy. ACS Central Science, 2019, 5, 1278-1288.	11.3	21
15	The structure and phase of tau: from monomer to amyloid filament. Cellular and Molecular Life Sciences, 2021, 78, 1873-1886.	5.4	21
16	Anticancer Actions of Azurin and Its Derived Peptide p28. Protein Journal, 2020, 39, 182-189.	1.6	19
17	Recombinant Butelase-Mediated Cyclization of the p53-Binding Domain of the Oncoprotein MdmX-Stabilized Protein Conformation as a Promising Model for Structural Investigation. Biochemistry, 2019, 58, 3005-3015.	2.5	18
18	Electrostatic interactions in molecular recognition of intrinsically disordered proteins. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4883-4894.	3.5	18

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19	The Role of Post-Translational Modifications on the Structure and Function of Tau Protein. Journal of Molecular Neuroscience, 2022, 72, 1557-1571.	2.3	17
20	14-3-3 Proteins are Potential Regulators of Liquidâ€“Liquid Phase Separation. Cell Biochemistry and Biophysics, 2022, 80, 277-293.	1.8	16
21	Molecular dynamics simulation exploration of cooperative migration mechanism of calcium ions in sarcoplasmic reticulum Ca²⁺â€ATPase. Journal of Computational Chemistry, 2009, 30, 2136-2145.	3.3	13
22	Evidences for the unfolding mechanism of threeâ€dimensional domain swapping. Protein Science, 2013, 22, 280-286.	7.6	13
23	Model-Guided Interface Probe Arrangement for Sensitive Protein Detection. Analytical Chemistry, 2016, 88, 9885-9889.	6.5	12
24	Whole-genome and enzymatic analyses of an androstenedione-producing Mycobacterium strain with residual phytosterol-degrading pathways. Microbial Cell Factories, 2020, 19, 187.	4.0	12
25	Interplay between binding affinity and kinetics in proteinâ€“protein interactions. Proteins: Structure, Function and Bioinformatics, 2016, 84, 920-933.	2.6	11
26	Intrinsically Disordered Transactivation Domains Bind to TAZ1 Domain of CBP via Diverse Mechanisms. Biophysical Journal, 2019, 117, 1301-1310.	0.5	10
27	Efficient conversion of phytosterols into 4-androstene-3,17-dione and its C1,2-dehydrogenized and 9Î±-hydroxylated derivatives by engineered Mycobacteria. Microbial Cell Factories, 2021, 20, 158.	4.0	10
28	Polyamines Disrupt the KaiABC Oscillator by Inducing Protein Denaturation. Molecules, 2019, 24, 3351.	3.8	9
29	The Structure Biology of Tau and Clue for Aggregation Inhibitor Design. Protein Journal, 2021, 40, 656-668.	1.6	9
30	Leveraging the multivalent p53 peptide-MdmX interaction to guide the improvement of small molecule inhibitors. Nature Communications, 2022, 13, 1087.	12.8	9
31	Deciphering the promiscuous interactions between intrinsically disordered transactivation domains and the KIX domain. Proteins: Structure, Function and Bioinformatics, 2017, 85, 2088-2095.	2.6	8
32	Exploring the Roles of Proline in Three-Dimensional Domain Swapping from Structure Analysis and Molecular Dynamics Simulations. Protein Journal, 2018, 37, 13-20.	1.6	8
33	In vitro characterization and molecular dynamics simulation reveal mechanism of 14-3-3Î¶ regulated phase separation of the tau protein. International Journal of Biological Macromolecules, 2022, 208, 1072-1081.	7.5	8
34	A Fusion Protein of the p53 Transaction Domain and the p53-Binding Domain of the Oncoprotein MdmX as an Efficient System for High-Throughput Screening of MdmX Inhibitors. Biochemistry, 2017, 56, 3273-3282.	2.5	7
35	Exploring the sequenceâ€“structureâ€“function relationship for the intrinsically disordered Î²Î³-crystallin Hahellin. Journal of Biomolecular Structure and Dynamics, 2018, 36, 1171-1181.	3.5	4
36	Effect of the Flexible Regions of the Oncoprotein Mouse Double Minute X on Inhibitor Binding Affinity. Biochemistry, 2017, 56, 5943-5954.	2.5	3

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37	A Protein Biosynthesis Machinery Strategy for Identifying P53^{PTC}â€Rescuing Compounds as Synergic Antiâ€Tumor Drugs. ChemistrySelect, 2018, 3, 11048-11053.	1.5	3
38	Introducing intrinsic disorder reduces electrostatic steering in protein-protein interactions. Biophysical Journal, 2021, 120, 2998-3007.	0.5	3
39	PrematureÂterminationÂcodon: a tunable protein translation approach. BioTechniques, 2022, 73, 80-89.	1.8	3
40	A novel strategy to prepare the precursor peptide of liraglutide. Process Biochemistry, 2017, 62, 10-15.	3.7	2
41	Structure-based reconstruction of a Mycobacterium hypothetical protein into an active Î”5â€“3-ketosteroid isomerase. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2019, 1867, 821-830.	2.3	2
42	The influence of intrinsic folding mechanism of an unfolded protein on the coupled foldingâ€binding process during target recognition. Proteins: Structure, Function and Bioinformatics, 2019, 87, 265-275.	2.6	2
43	P55PIK Regulates P53-Dependent Apoptosis in Cancer Cells by Interacting with P53 DNA-Specific Domain . OncoTargets and Therapy, 2020, Volume 13, 5177-5190.	2.0	1
44	The recovery of KaiAâ€™s activity depends on its N-terminal domain and KaiB in the cyanobacterial circadian clock. Biochemical and Biophysical Research Communications, 2020, 524, 123-128.	2.1	1
45	Topological frustration leading to backtracking in a coupled foldingâ€“binding process. Physical Chemistry Chemical Physics, 2022, 24, 2630-2637.	2.8	1
46	Mechanism of An Anticancer Peptide Rescuing p53 from Degradation by COP1. FASEB Journal, 2018, 32, lb28.	0.5	0
47	Characterizing the Interactions between Intrinsically Disordered Transactivation Domains and the KIX Domain. FASEB Journal, 2018, 32, lb29.	0.5	0