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	Topological frustration leading to backtracking in a coupled foldingâ€“binding process. Physical Chemistry Chemical Physics, 2022, 24, 2630-2637.	2.8	1
2	14-3-3 Proteins are Potential Regulators of Liquidâ€“Liquid Phase Separation. Cell Biochemistry and Biophysics, 2022, 80, 277-293.	1.8	16
3	Leveraging the multivalent p53 peptide-MdmX interaction to guide the improvement of small molecule inhibitors. Nature Communications, 2022, 13, 1087.	12.8	9
4	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
5	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
6	PrematureÂterminationÂcodon: a tunable protein translation approach. BioTechniques, 2022, 73, 80-89.	1.8	3
7	The structure and phase of tau: from monomer to amyloid filament. Cellular and Molecular Life Sciences, 2021, 78, 1873-1886.	5.4	21
8	The Structure Biology of Tau and Clue for Aggregation Inhibitor Design. Protein Journal, 2021, 40, 656-668.	1.6	9
9	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
10	Introducing intrinsic disorder reduces electrostatic steering in protein-protein interactions. Biophysical Journal, 2021, 120, 2998-3007.	0.5	3
11	Electrostatic interactions in molecular recognition of intrinsically disordered proteins. Journal of Biomolecular Structure and Dynamics, 2020, 38, 4883-4894.	3.5	18
12	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
13	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
14	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
15	Anticancer Actions of Azurin and Its Derived Peptide p28. Protein Journal, 2020, 39, 182-189.	1.6	19
16	Intrinsically Disordered Transactivation Domains Bind to TAZ1 Domain of CBP via Diverse Mechanisms. Biophysical Journal, 2019, 117, 1301-1310.	0.5	10
17	Features of molecular recognition of intrinsically disordered proteins via coupled folding and binding. Protein Science, 2019, 28, 1952-1965.	7.6	55
18	Polyamines Disrupt the KaiABC Oscillator by Inducing Protein Denaturation. Molecules, 2019, 24, 3351.	3.8	9

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19	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
20	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
21	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
22	14-3-3/Tau Interaction and Tau Amyloidogenesis. Journal of Molecular Neuroscience, 2019, 68, 620-630.	2.3	24
23	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
24	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
25	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
26	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
27	Mechanism of An Anticancer Peptide Rescuing p53 from Degradation by COP1. FASEB Journal, 2018, 32, lb28.	0.5	0
28	Characterizing the Interactions between Intrinsically Disordered Transactivation Domains and the KIX Domain. FASEB Journal, 2018, 32, lb29.	0.5	0
29	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
30	Bacterial cupredoxin azurin hijacks cellular signaling networks: Proteinâ€“protein interactions and cancer therapy. Protein Science, 2017, 26, 2334-2341.	7.6	45
31	Effect of the Flexible Regions of the Oncoprotein Mouse Double Minute X on Inhibitor Binding Affinity. Biochemistry, 2017, 56, 5943-5954.	2.5	3
32	A novel strategy to prepare the precursor peptide of liraglutide. Process Biochemistry, 2017, 62, 10-15.	3.7	2
33	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
34	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
35	Model-Guided Interface Probe Arrangement for Sensitive Protein Detection. Analytical Chemistry, 2016, 88, 9885-9889.	6.5	12
36	Interplay between binding affinity and kinetics in proteinâ€“protein interactions. Proteins: Structure, Function and Bioinformatics, 2016, 84, 920-933.	2.6	11

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37	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
38	Advantages of proteins being disordered. Protein Science, 2014, 23, 539-550.	7.6	140
39	Evidences for the unfolding mechanism of threeâ€dimensional domain swapping. Protein Science, 2013, 22, 280-286.	7.6	13
40	Do Intrinsically Disordered Proteins Possess High Specificity in Proteinâ€“Protein Interactions?. Chemistry - A European Journal, 2013, 19, 4462-4467.	3.3	41
41	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
42	Threeâ€dimensional domain swapping in the protein structure space. Proteins: Structure, Function and Bioinformatics, 2012, 80, 1610-1619.	2.6	29
43	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
44	Smoothing molecular interactions: The â€œkinetic bufferâ€•effect of intrinsically disordered proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3251-3259.	2.6	31
45	Nonnative Interactions in Coupled Folding and Binding Processes of Intrinsically Disordered Proteins. PLoS ONE, 2010, 5, e15375.	2.5	36
46	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
47	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