

Jun Zhang

List of Publications by Year in descending order

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papers

951
citations

567281

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1269
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#	ARTICLE	IF	CITATIONS
1	Poly(<i>N</i> -vinylpyrrolidone)- <i>b</i> -Poly(dimethylsiloxane)- <i>b</i> -Poly(<i>N</i> -vinylpyrrolidone) Triblock Copolymer Polymersomes for Delivery of PARP1 siRNA to Breast Cancers. <i>ACS Applied Bio Materials</i> , 2022, 5, 1670-1682.	4.6	13
2	Intrinsically disordered electronegative clusters improve stability and binding specificity of RNA-binding proteins. <i>Journal of Biological Chemistry</i> , 2021, 297, 100945.	3.4	18
3	Nop9 recognizes structured and single-stranded RNA elements of preribosomal RNA. <i>Rna</i> , 2020, 26, 1049-1059.	3.5	3
4	Amide additives improve RDC measurements in polyacrylamide. <i>Journal of Biomolecular NMR</i> , 2020, 74, 119-124.	2.8	4
5	Application of tyrosine-tryptophan fluorescence resonance energy transfer in monitoring protein size changes. <i>Analytical Biochemistry</i> , 2018, 557, 142-150.	2.4	26
6	Native State Volume Fluctuations in Proteins as a Mechanism for Dynamic Allostery. <i>Journal of the American Chemical Society</i> , 2017, 139, 3599-3602.	13.7	33
7	U7 snRNP is recruited to histone pre-mRNA in a FLASH-dependent manner by two separate regions of the stem-loop binding protein. <i>Rna</i> , 2017, 23, 938-951.	3.5	26
8	Nop9 is a PUF-like protein that prevents premature cleavage to correctly process pre-18S rRNA. <i>Nature Communications</i> , 2016, 7, 13085.	12.8	34
9	Structural analysis reveals the flexible C-terminus of Nop15 undergoes rearrangement to recognize a pre-ribosomal RNA folding intermediate. <i>Nucleic Acids Research</i> , 2016, 45, gkw961.	14.5	4
10	Alpha-1-antitrypsin interacts with gp41 to block HIV-1 entry into CD4+ T lymphocytes. <i>BMC Microbiology</i> , 2016, 16, 172.	3.3	21
11	The molecular basis for ANE syndrome revealed by the large ribosomal subunit processome interactome. <i>ELife</i> , 2016, 5, .	6.0	11
12	Molecular mechanisms for the regulation of histone mRNA stem-loop binding protein by phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E2937-46.	7.1	29
13	Supertertiary Structure of the MAGUK Core from PSD-95. <i>Structure</i> , 2013, 21, 402-413.	3.3	61
14	Phosphorylation of a PDZ Domain Extension Modulates Binding Affinity and Interdomain Interactions in Postsynaptic Density-95 (PSD-95) Protein, a Membrane-associated Guanylate Kinase (MAGUK). <i>Journal of Biological Chemistry</i> , 2011, 286, 41776-41785.	3.4	61
15	Crystallographic and Nuclear Magnetic Resonance Evaluation of the Impact of Peptide Binding to the Second PDZ Domain of Protein Tyrosine Phosphatase 1E. <i>Biochemistry</i> , 2010, 49, 9280-9291.	2.5	64
16	Hidden dynamic allostery in a PDZ domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18249-18254.	7.1	296
17	Reshaping the folding energy landscape of human carbonic anhydrase II by a single point genetic mutation Pro237His. <i>International Journal of Biochemistry and Cell Biology</i> , 2008, 40, 776-788.	2.8	10
18	Hydrophobic Core Mutations in CI2 Globally Perturb Fast Side-Chain Dynamics Similarly without Regard to Position. <i>Biochemistry</i> , 2008, 47, 8566-8576.	2.5	18

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19	Oligomerization and Aggregation of Bovine Pancreatic Ribonuclease A: Backbone Hydration Probed by Infrared Band-Shift. <i>Protein and Peptide Letters</i> , 2008, 15, 650-657.	0.9	5
20	Oligomerization and Aggregation of Bovine Pancreatic Ribonuclease A: Characteristic Events Observed by FTIR Spectroscopy. <i>Biophysical Journal</i> , 2006, 90, 2525-2533.	0.5	35
21	Assisting the Reactivation of Guanidine Hydrochloride-Denatured Aminoacylase by Hydroxypropyl Cyclodextrins. <i>Biophysical Journal</i> , 2006, 91, 686-693.	0.5	18
22	Sequential Events in Ribonuclease A Thermal Unfolding Characterized by Two-Dimensional Infrared Correlation Spectroscopy. <i>Protein and Peptide Letters</i> , 2006, 13, 33-40.	0.9	10
23	Probing conformational changes of proteins by quantitative second-derivative infrared spectroscopy. <i>Analytical Biochemistry</i> , 2005, 340, 89-98.	2.4	75
24	Conformational Change in the C-Terminal Domain Is Responsible for the Initiation of Creatine Kinase Thermal Aggregation. <i>Biophysical Journal</i> , 2005, 89, 2650-2658.	0.5	76