Xianyang Fang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Long-range distance determination in fully deuterated RNA with pulsed EPR spectroscopy. Biophysical Journal, 2022, 121, 37-43.	0.5	12
2	Recent advances in RNA structurome. Science China Life Sciences, 2022, 65, 1285-1324.	4.9	22
3	A novel partially open state of SHP2 points to a "multiple gear―regulation mechanism. Journal of Biological Chemistry, 2021, 296, 100538.	3.4	18
4	Structural mechanism for modulation of functional amyloid and biofilm formation by Staphylococcal Bap protein switch. EMBO Journal, 2021, 40, e107500.	7.8	22
5	Pseudoknot length modulates the folding, conformational dynamics, and robustness of Xrn1 resistance of flaviviral xrRNAs. Nature Communications, 2021, 12, 6417.	12.8	15
6	Structure and regulation of human epithelial cell transforming 2 protein. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1027-1035.	7.1	37
7	Short Direct Repeats in the 3′ Untranslated Region Are Involved in Subgenomic Flaviviral RNA Production. Journal of Virology, 2020, 94, .	3.4	11
8	Molecular mechanisms underlying the extreme mechanical anisotropy of the flaviviral exoribonuclease-resistant RNAs (xrRNAs). Nature Communications, 2020, 11, 5496.	12.8	9
9	Posttranscriptional site-directed spin labeling of large RNAs with an unnatural base pair system under non-denaturing conditions. Chemical Science, 2020, 11, 9655-9664.	7.4	16
10	Site-specific covalent labeling of large RNAs with nanoparticles empowered by expanded genetic alphabet transcription. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 22823-22832.	7.1	13
11	Revisiting Bap Multidomain Protein: More Than Sticking Bacteria Together. Frontiers in Microbiology, 2020, 11, 613581.	3.5	15
12	The dimeric organization that enhances the microtubule end-binding affinity of EB1 is susceptible to phosphorylation. Journal of Cell Science, 2020, 133, .	2.0	9
13	The MLL1 trimeric catalytic complex is a dynamic conformational ensemble stabilized by multiple weak interactions. Nucleic Acids Research, 2019, 47, 9433-9447.	14.5	8
14	Characterization of the FMN-Dependent Cysteine Decarboxylase from Thioviridamide Biosynthesis. Organic Letters, 2019, 21, 4676-4679.	4.6	25
15	The effect of phosphate ion on the ssDNA binding mode of MoSub1, a Sub1/PC4 homolog from rice blast fungus. Proteins: Structure, Function and Bioinformatics, 2019, 87, 257-264.	2.6	5
16	Long non oding subgenomic flavivirus RNAs have extended 3D structures and are flexible in solution. EMBO Reports, 2019, 20, e47016.	4.5	33
17	Visualizing the long non-coding subgenomic flavivirus RNAs in solution. Acta Crystallographica Section A: Foundations and Advances, 2019, 75, a176-a176.	0.1	0
18	Structural basis of ubiquitin modification by the Legionella effector SdeA. Nature, 2018, 557, 674-678.	27.8	69

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19	Staphylococcus epidermidis small basic protein (Sbp) forms amyloid fibrils, consistent with its function as a scaffolding protein in biofilms. Journal of Biological Chemistry, 2018, 293, 14296-14311.	3.4	23
20	Structural Definition of a Unique Neutralization Epitope on the Receptor-Binding Domain of MERS-CoV Spike Glycoprotein. Cell Reports, 2018, 24, 441-452.	6.4	57
21	The Functional Cycle of Rnt1p: Five Consecutive Steps of Double-Stranded RNA Processing by a Eukaryotic RNase III. Structure, 2017, 25, 353-363.	3.3	15
22	Capture and Release of tRNA by the T-Loop Receptor in the Function of the T-Box Riboswitch. Biochemistry, 2017, 56, 3549-3558.	2.5	18
23	Topological Structure Determination of RNA Using Small-Angle X-Ray Scattering. Journal of Molecular Biology, 2017, 429, 3635-3649.	4.2	12
24	Topological structure determination of RNA using small-angle X-ray scattering. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, a104-a104.	0.1	0
25	Structure of chromatin remodeler Swi2/Snf2 in the resting state. Nature Structural and Molecular Biology, 2016, 23, 722-729.	8.2	55
26	Small-angle X-ray scattering: a bridge between RNA secondary structures and three-dimensional topological structures. Current Opinion in Structural Biology, 2015, 30, 147-160.	5.7	40
27	A Mechanism of Global Shape-dependent Recognition and Phosphorylation of Filamin by Protein Kinase A. Journal of Biological Chemistry, 2015, 290, 8527-8538.	3.4	14
28	Hydrodynamic and Membrane Binding Properties of Purified Rous Sarcoma Virus Gag Protein. Journal of Virology, 2015, 89, 10371-10382.	3.4	17
29	Allosteric Activation of Bacterial Swi2/Snf2 (Switch/Sucrose Non-fermentable) Protein RapA by RNA Polymerase. Journal of Biological Chemistry, 2015, 290, 23656-23669.	3.4	8
30	Cu(I)-mediated Allosteric Switching in a Copper-sensing Operon Repressor (CsoR). Journal of Biological Chemistry, 2014, 289, 19204-19217.	3.4	50
31	Structural Characterization of a Flexible Two-Domain Protein in Solution Using Small Angle X-Ray Scattering and NMR Data. Structure, 2014, 22, 1862-1874.	3.3	9
32	Structural model of an mRNA in complex with the bacterial chaperone Hfq. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17134-17139.	7.1	70
33	An Unusual Topological Structure of the HIV-1 Rev Response Element. Cell, 2013, 155, 594-605.	28.9	109
34	G503 Is Obligatory for Coupling of Regulatory Domains in NCX Proteins. Biochemistry, 2012, 51, 7313-7320.	2.5	14
35	Two ZnF-UBP Domains in Isopeptidase T (USP5). Biochemistry, 2012, 51, 1188-1198.	2.5	49
36	A Common Ca2+-Driven Interdomain Module Governs Eukaryotic NCX Regulation. PLoS ONE, 2012, 7, e39985.	2.5	36

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37	Favorable contribution of the C-terminal residue K97 to the stability of a hyperthermophilic archaeal [P62A]Ssh10b. Archives of Biochemistry and Biophysics, 2009, 481, 52-58.	3.0	4
38	A Stabilizing α/β-Hydrophobic Core Greatly Contributes to Hyperthermostability of Archaeal [P62A]Ssh10b. Biochemistry, 2008, 47, 11212-11221.	2.5	12