

Jinwei Zhang

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

2,401
citations

257450

24
h-index

254184

43
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47
all docs

47
docs citations

47
times ranked

2451
citing authors

#	ARTICLE	IF	CITATIONS
1	Rational engineering enables co-crystallization and structural determination of the HIV-1 matrix-tRNA complex. STAR Protocols, 2022, 3, 101056.	1.2	1
2	Structural basis of R-loop recognition by the S9.6 monoclonal antibody. Nature Communications, 2022, 13, 1641.	12.8	32
3	Lineage-specific insertions in T-box riboswitches modulate antibiotic binding and action. Nucleic Acids Research, 2022, , .	14.5	2
4	Improving RNA Crystal Diffraction Quality by Postcrystallization Treatment. Methods in Molecular Biology, 2021, 2323, 25-37.	0.9	1
5	HIV-1 matrix-tRNA complex structure reveals basis for host control of Gag localization. Cell Host and Microbe, 2021, 29, 1421-1436.e7.	11.0	22
6	Interplay between Host tRNAs and HIV-1: A Structural Perspective. Viruses, 2021, 13, 1819.	3.3	6
7	Human cell based directed evolution of adenine base editors with improved efficiency. Nature Communications, 2021, 12, 5897.	12.8	15
8	The long and short of it: long noncoding RNAs in neural development and diseases. Frontiers in Bioscience, 2021, 26, 258.	2.1	0
9	Cooperativity and Interdependency between RNA Structure and RNA-RNA Interactions. Non-coding RNA, 2021, 7, 81.	2.6	5
10	Unboxing the T-box riboswitches: A glimpse into multivalent and multimodal <sc>RNA-RNA</sc> interactions. Wiley Interdisciplinary Reviews RNA, 2020, 11, e1600.	6.4	23
11	High-fidelity SaCas9 identified by directional screening in human cells. PLoS Biology, 2020, 18, e3000747.	5.6	38
12	Structural Insights into RNA Dimerization: Motifs, Interfaces and Functions. Molecules, 2020, 25, 2881.	3.8	28
13	Crystal structure of an adenovirus virus-associated RNA. Nature Communications, 2019, 10, 2871.	12.8	36
14	An evolving tale of two interacting RNAs: themes and variations of the T-box riboswitch mechanism. IUBMB Life, 2019, 71, 1167-1180.	3.4	15
15	The search for a PKR code: differential regulation of protein kinase R activity by diverse RNA and protein regulators. Rna, 2019, 25, 539-556.	3.5	48
16	Structural basis of amino acid surveillance by higher-order tRNA-mRNA interactions. Nature Structural and Molecular Biology, 2019, 26, 1094-1105.	8.2	52
17	High-affinity recognition of specific tRNAs by an mRNA anticodon-binding groove. Nature Structural and Molecular Biology, 2019, 26, 1114-1122.	8.2	28
18	Brothers in arms: emerging roles of RNA epigenetics in DNA damage repair. Cell and Bioscience, 2017, 7, 24.	4.8	12

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19	Structures of riboswitch RNA reaction states by mix-and-inject XFEL serial crystallography. <i>Nature</i> , 2017, 541, 242-246.	27.8	251
20	Direct modulation of T-box riboswitch-controlled transcription by protein synthesis inhibitors. <i>Nucleic Acids Research</i> , 2017, 45, 10242-10258.	14.5	21
21	Trying on tRNA for Size: RNase P and the T-box Riboswitch as Molecular Rulers. <i>Biomolecules</i> , 2016, 6, 18.	4.0	17
22	The tRNA Elbow in Structure, Recognition and Evolution. <i>Life</i> , 2016, 6, 3.	2.4	63
23	A Two-Way Street: Regulatory Interplay between RNA Polymerase and Nascent RNA Structure. <i>Trends in Biochemical Sciences</i> , 2016, 41, 293-310.	7.5	113
24	Structure and mechanism of the T-box riboswitches. <i>Wiley Interdisciplinary Reviews RNA</i> , 2015, 6, 419-433.	6.4	38
25	Interaction between the tRNA-Binding and C-Terminal Domains of Yeast Gcn2 Regulates Kinase Activity In Vivo. <i>PLoS Genetics</i> , 2015, 11, e1004991.	3.5	35
26	Synthesis and applications of RNAs with position-selective labelling and mosaic composition. <i>Nature</i> , 2015, 522, 368-372.	27.8	95
27	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	3.5	161
28	Post-crystallization Improvement of RNA Crystal Diffraction Quality. <i>Methods in Molecular Biology</i> , 2015, 1316, 13-24.	0.9	2
29	Post-crystallization Improvement of RNA Crystals by Synergistic Ion Exchange and Dehydration. <i>Bio-protocol</i> , 2015, 5, .	0.4	1
30	Post-crystallization Improvement of RNA Crystals by Synergistic Ion Exchange and Dehydration. <i>Bio-protocol</i> , 2015, 5, .	0.4	1
31	A Flexible, Scalable Method for Preparation of Homogeneous Aminoacylated tRNAs. <i>Methods in Enzymology</i> , 2014, 549, 105-113.	1.0	9
32	Trigger-helix folding pathway and S13 mediate catalysis and hairpin-stabilized pausing by Escherichia coli RNA polymerase. <i>Nucleic Acids Research</i> , 2014, 42, 12707-12721.	14.5	43
33	Global analysis of riboswitches by small-angle X-ray scattering and calorimetry. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2014, 1839, 1020-1029.	1.9	34
34	Dramatic Improvement of Crystals of Large RNAs by Cation Replacement and Dehydration. <i>Structure</i> , 2014, 22, 1363-1371.	3.3	52
35	New molecular engineering approaches for crystallographic studies of large RNAs. <i>Current Opinion in Structural Biology</i> , 2014, 26, 9-15.	5.7	46
36	Direct Evaluation of tRNA Aminoacylation Status by the T-Box Riboswitch Using tRNA-mRNA Stacking and Steric Readout. <i>Molecular Cell</i> , 2014, 55, 148-155.	9.7	49

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37	Co-crystal structure of a T-box riboswitch stem I domain in complex with its cognate tRNA. <i>Nature</i> , 2013, 500, 363-366.	27.8	136
38	YbxF and YlxQ are bacterial homologs of L7Ae and bind K-turns but not K-loops. <i>Rna</i> , 2012, 18, 759-770.	3.5	49
39	Role of the RNA polymerase trigger loop in catalysis and pausing. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 99-104.	8.2	138
40	Ribozymes and Riboswitches: Modulation of RNA Function by Small Molecules. <i>Biochemistry</i> , 2010, 49, 9123-9131.	2.5	140
41	Substrate Loading, Nucleotide Addition, and Translocation by RNA Polymerase. <i>RSC Biomolecular Sciences</i> , 2009, , 206-235.	0.4	12
42	A Central Role of the RNA Polymerase Trigger Loop in Active-Site Rearrangement during Transcriptional Pausing. <i>Molecular Cell</i> , 2007, 27, 406-419.	9.7	189
43	Structural basis for substrate loading in bacterial RNA polymerase. <i>Nature</i> , 2007, 448, 163-168.	27.8	333
44	Inhibition of RNA Polymerase by Streptolydigin: No Cycling Allowed. <i>Cell</i> , 2005, 122, 494-496.	28.9	7