Shi-Jie Chen

List of Publications by Citations

120 papers	4,004 citations	34 h-index	59 g-index
127 ext. papers	4,679 ext. citations	5.5 avg, IF	6.06 L-index

#	Paper	IF	Citations
120	RNA folding: conformational statistics, folding kinetics, and ion electrostatics. *Annual Review of Biophysics*, **2008**, 37, 197-214	21.1	237
119	Nucleic acid helix stability: effects of salt concentration, cation valence and size, and chain length. *Biophysical Journal*, **2006**, 90, 1175-90	2.9	235
118	RNA-Puzzles: a CASP-like evaluation of RNA three-dimensional structure prediction. *Rna*, **2012**, 18, 610-25	5.8	181
117	RNA folding energy landscapes. *Proceedings of the National Academy of Sciences of the United States of America*, **2000**, 97, 646-51	11.5	178
116	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. *Rna*, **2015**, 21, 1066-84	5.8	122
115	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. *Rna*, **2017**, 23, 655-672	5.8	118
114	Predicting RNA pseudoknot folding thermodynamics. *Nucleic Acids Research*, **2006**, 34, 2634-52	20.1	115
113	Electrostatic correlations and fluctuations for ion binding to a finite length polyelectrolyte. *Journal of Chemical Physics*, **2005**, 122, 44903	3.9	114
112	RNA hairpin-folding kinetics. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 1931-6	11.5	111
111	Physics-based de novo prediction of RNA 3D structures. *Journal of Physical Chemistry B*, **2011**, 115, 4216-26	3.4	103
110	Vfold: a web server for RNA structure and folding thermodynamics prediction. *PLoS ONE*, **2014**, 9, e107504	3.7	103
109	Predicting RNA folding thermodynamics with a reduced chain representation model. *Rna*, **2005**, 11, 1884-97	5.8	93
108	Rational truncation of an RNA aptamer to prostate-specific membrane antigen using computational structural modeling. *Nucleic Acid Therapeutics*, **2011**, 21, 299-314	4.8	86
107	RNA helix stability in mixed Na+/Mg2+ solution. *Biophysical Journal*, **2007**, 92, 3615-32	2.9	82
106	Designing a polycationic probe for simultaneous enrichment and detection of microRNAs in a nanopore. *ACS Nano*, **2013**, 7, 3962-9	16.7	80
105	Salt dependence of nucleic acid hairpin stability. *Biophysical Journal*, **2008**, 95, 738-52	2.9	78
104	Theory and Modeling of RNA Structure and Interactions with Metal Ions and Small Molecules. *Annual Review of Biophysics*, **2017**, 46, 227-246	21.1	77

103	Predicting structures and stabilities for H-type pseudoknots with interhelix loops. *Rna*, **2009**, 15, 696-706	5.8	77
102	Ion-mediated nucleic acid helix-helix interactions. *Biophysical Journal*, **2006**, 91, 518-36	2.9	77
101	Salt contribution to RNA tertiary structure folding stability. *Biophysical Journal*, **2011**, 101, 176-87	2.9	66
100	Predicting ion binding properties for RNA tertiary structures. *Biophysical Journal*, **2010**, 99, 1565-76	2.9	58
99	Exploring the complex folding kinetics of RNA hairpins: I. General folding kinetics analysis. *Biophysical Journal*, **2006**, 90, 765-77	2.9	57
98	AAV CRISPR editing rescues cardiac and muscle function for 18 months in dystrophic mice. *JCI Insight*, **2018**, 3,	9.9	56
97	CRISPR-Cas9 cleavage efficiency correlates strongly with target-sgRNA folding stability: from physical mechanism to off-target assessment. *Scientific Reports*, **2017**, 7, 143	4.9	43
96	Electrostatic free energy landscapes for nucleic acid helix assembly. *Nucleic Acids Research*, **2006**, 34, 6629-39	20.1	42
95	Statistical thermodynamics of double-stranded polymer molecules. *Journal of Chemical Physics*, **1995**, 103, 5802-5813	3.9	41
94	Predicting secondary structural folding kinetics for nucleic acids. *Biophysical Journal*, **2010**, 98, 1617-25	2.9	39
93	Theory for the conformational changes of double-stranded chain molecules. *Journal of Chemical Physics*, **1998**, 109, 4602-4616	3.9	39
92	Nanopore electric snapshots of an RNA tertiary folding pathway. *Nature Communications*, **2017**, 8, 1458	17.4	38
91	Ion-mediated RNA structural collapse: effect of spatial confinement. *Biophysical Journal*, **2012**, 103, 827-36	2.9	38
90	Electrostatic free energy landscapes for DNA helix bending. *Biophysical Journal*, **2008**, 94, 3137-49	2.9	38
89	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. *Rna*, **2020**, 26, 982-995	5.8	37
88	Mimicking Ribosomal Unfolding of RNA Pseudoknot in a Protein Channel. *Journal of the American Chemical Society*, **2015**, 137, 15742-52	16.4	36
87	Biphasic folding kinetics of RNA pseudoknots and telomerase RNA activity. *Journal of Molecular Biology*, **2007**, 367, 909-24	6.5	35
86	Cotranscriptional folding kinetics of ribonucleic acid secondary structures. *Journal of Chemical Physics*, **2011**, 135, 245101	3.9	34

85	Exploring the complex folding kinetics of RNA hairpins: II. Effect of sequence, length, and misfolded states. *Biophysical Journal*, **2006**, 90, 778-87	2.9	33
84	3:Importance of Diffuse Metal Ion Binding to RNA. *Metal Ions in Life Sciences*, **2011**, 101-124		33
83	AAV9 Edits Muscle Stem Cells in Normal and Dystrophic Adult Mice. *Molecular Therapy*, **2019**, 27, 1568-1585	10.7	32
82	Predicting loop-helix tertiary structural contacts in RNA pseudoknots. *Rna*, **2010**, 16, 538-52	5.8	32
81	Understanding the kinetic mechanism of RNA single base pair formation. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 116-21	11.5	30
80	Structure and stability of RNA/RNA kissing complex: with application to HIV dimerization initiation signal. *Rna*, **2011**, 17, 2130-43	5.8	30
79	Free energy landscapes of RNA/RNA complexes: with applications to snRNA complexes in spliceosomes. *Journal of Molecular Biology*, **2006**, 357, 292-312	6.5	30
78	Monte Carlo Tightly Bound Ion Model: Predicting Ion-Binding Properties of RNA with Ion Correlations and Fluctuations. *Journal of Chemical Theory and Computation*, **2016**, 12, 3370-81	6.4	29
77	Predicting electrostatic forces in RNA folding. *Methods in Enzymology*, **2009**, 469, 465-87	1.7	28
76	Predicting kissing interactions in microRNA-target complex and assessment of microRNA activity. *Nucleic Acids Research*, **2012**, 40, 4681-90	20.1	28
75	IsRNA: An Iterative Simulated Reference State Approach to Modeling Correlated Interactions in RNA Folding. *Journal of Chemical Theory and Computation*, **2018**, 14, 2230-2239	6.4	27
74	A conserved RNA pseudoknot in a putative molecular switch domain of the 3′untranslated region of coronaviruses is only marginally stable. *Rna*, **2011**, 17, 1747-59	5.8	26
73	Unified energetics analysis unravels SpCas9 cleavage activity for optimal gRNA design. *Proceedings of the National Academy of Sciences of the United States of America*, **2019**, 116, 8693-8698	11.5	24
72	Predicting RNA Structure with Vfold. *Methods in Molecular Biology*, **2017**, 1654, 3-15	1.4	23
71	Predicting ribosomal frameshifting efficiency. *Physical Biology*, **2008**, 5, 016002	3	22
70	Kinetic mechanism of conformational switch between bistable RNA hairpins. *Journal of the American Chemical Society*, **2012**, 134, 12499-507	16.4	21
69	Hierarchical Assembly of RNA Three-Dimensional Structures Based on Loop Templates. *Journal of Physical Chemistry B*, **2018**, 122, 5327-5335	3.4	20
68	Computing the conformational entropy for RNA folds. *Journal of Chemical Physics*, **2010**, 132, 235104	3.9	19

67	In vitro RNA SELEX for the generation of chemically-optimized therapeutic RNA drugs. *Methods*, **2016**, 103, 167-74	4.6	18
66	Salt-dependent folding energy landscape of RNA three-way junction. *Biophysical Journal*, **2010**, 98, 111-20	3.9	18
65	Predicting ion-nucleic acid interactions by energy landscape-guided sampling. *Journal of Chemical Theory and Computation*, **2012**, 8, 2095-2101	6.4	17
64	Folding thermodynamics of pseudoknotted chain conformations. *Journal of Chemical Physics*, **2006**, 124, 154903	3.9	17
63	Master equation approach to finding the rate-limiting steps in biopolymer folding. *Journal of Chemical Physics*, **2003**, 118, 3413-3420	3.9	17
62	A three-dimensional statistical mechanical model of folding double-stranded chain molecules. *Journal of Chemical Physics*, **2001**, 114, 7669-7681	3.9	17
61	Physics-based RNA structure prediction. *Biophysics Reports*, **2015**, 1, 2-13	3.5	16
60	Binding interface and impact on protease cleavage for an RNA aptamer to HIV-1 reverse transcriptase. *Nucleic Acids Research*, **2020**, 48, 2709-2722	20.1	16
59	Predicting structure and stability for RNA complexes with intermolecular loop-loop base-pairing. *Rna*, **2014**, 20, 835-45	5.8	16
58	Symmetries in proteins: A knot theory approach. *Journal of Chemical Physics*, **1996**, 104, 5964-5973	3.9	15
57	Importance of diffuse metal ion binding to RNA. *Metal Ions in Life Sciences*, **2011**, 9, 101-24	2.6	15
56	Quantifying Coulombic and solvent polarization-mediated forces between DNA helices. *Journal of Physical Chemistry B*, **2013**, 117, 7221-7	3.4	14
55	VfoldLA: A web server for loop assembly-based prediction of putative 3D RNA structures. *Journal of Structural Biology*, **2019**, 207, 235-240	3.4	13
54	Structural computational modeling of RNA aptamers. *Methods*, **2016**, 103, 175-9	4.6	13
53	Analyzing the biopolymer folding rates and pathways using kinetic cluster method. *Journal of Chemical Physics*, **2003**, 119, 8716-8729	3.9	13
52	Duchenne muscular dystrophy animal models for high-throughput drug discovery and precision medicine. *Expert Opinion on Drug Discovery*, **2020**, 15, 443-456	6.2	12
51	Cas9-specific immune responses compromise local and systemic AAV CRISPR therapy in multiple dystrophic canine models. *Nature Communications*, **2021**, 12, 6769	17.4	12
50	Many-body effect in ion binding to RNA. *Journal of Chemical Physics*, **2014**, 141, 055101	3.9	11

49	RNA Folding Transitions and Cooperativity. *Journal of Physical Chemistry B*, **2001**, 105, 1618-1630	3.4	11
48	MCTBI: a web server for predicting metal ion effects in RNA structures. *Rna*, **2017**, 23, 1155-1165	5.8	10
47	Predicting RNA-Metal Ion Binding with Ion Dehydration Effects. *Biophysical Journal*, **2019**, 116, 184-195	2.9	10
46	Quantitative Understanding of SHAPE Mechanism from RNA Structure and Dynamics Analysis. *Journal of Physical Chemistry B*, **2018**, 122, 4771-4783	3.4	10
45	Predicting Cotranscriptional Folding Kinetics For Riboswitch. *Journal of Physical Chemistry B*, **2018**, 122, 7484-7496	3.4	10
44	Nuclear Magnetic Resonance Study of RNA Structures at the 3′-End of the Hepatitis C Virus Genome. *Biochemistry*, **2017**, 56, 4972-4984	3.2	10
43	Coarse-grained prediction of RNA loop structures. *PLoS ONE*, **2012**, 7, e48460	3.7	10
42	A new computational approach for mechanical folding kinetics of RNA hairpins. *Biophysical Journal*, **2009**, 96, 4024-34	2.9	10
41	Statistical thermodynamics for chain molecules with simple RNA tertiary contacts. *Journal of Chemical Physics*, **2005**, 122, 094909	3.9	10
40	A Method to Predict the 3D Structure of an RNA Scaffold. *Methods in Molecular Biology*, **2015**, 1316, 1-11	1.4	10
39	Folding kinetics for the conformational switch between alternative RNA structures. *Journal of Physical Chemistry B*, **2010**, 114, 13609-15	3.4	9
38	VfoldCPX Server: Predicting RNA-RNA Complex Structure and Stability. *PLoS ONE*, **2016**, 11, e0163454	3.7	9
37	RLDOCK: A New Method for Predicting RNA-Ligand Interactions. *Journal of Chemical Theory and Computation*, **2020**, 16, 7173-7183	6.4	8
36	Questions Answered and Unanswered by the First CRISPR Editing Study in a Canine Model of Duchenne Muscular Dystrophy. *Human Gene Therapy*, **2019**, 30, 535-543	4.8	8
35	Exploring the electrostatic energy landscape for tetraloop-receptor docking. *Physical Chemistry Chemical Physics*, **2014**, 16, 6367-75	3.6	7
34	Predicting free energy landscapes for complexes of double-stranded chain molecules. *Journal of Chemical Physics*, **2001**, 114, 4253-4266	3.9	7
33	TBI server: a web server for predicting ion effects in RNA folding. *PLoS ONE*, **2015**, 10, e0119705	3.7	7
32	IsRNA1: Prediction and Blind Screening of RNA 3D Structures. *Journal of Chemical Theory and Computation*, **2021**, 17, 1842-1857	6.4	7

31	Structural basis of prostate-specific membrane antigen recognition by the A9g RNA aptamer. *Nucleic Acids Research*, **2020**, 48, 11130-11145	20.1	6
30	Hexahydrated Mg Binding and Outer-Shell Dehydration on RNA Surface. *Biophysical Journal*, **2018**, 114, 1274-1284	2.9	6
29	Predicting Monovalent Ion Correlation Effects in Nucleic Acids. *ACS Omega*, **2019**, 4, 13435-13446	3.9	6
28	Quantitative analysis of the ion-dependent folding stability of DNA triplexes. *Physical Biology*, **2011**, 8, 066006	3	6
27	A domain-based model for predicting large and complex pseudoknotted structures. *RNA Biology*, **2012**, 9, 200-11	4.8	6
26	Development and application of a droplet digital polymerase chain reaction (ddPCR) for detection and investigation of African swine fever virus. *Canadian Journal of Veterinary Research*, **2018**, 82, 70-74	0.5	6
25	A Method to Predict the Structure and Stability of RNA/RNA Complexes. *Methods in Molecular Biology*, **2016**, 1490, 63-72	1.4	6
24	Site-Specific Binding of Non-Site-Specific Ions. *Biophysical Journal*, **2019**, 116, 2237-2239	2.9	5
23	Modeling Loop Composition and Ion Concentration Effects in RNA Hairpin Folding Stability. *Biophysical Journal*, **2020**, 119, 1439-1455	2.9	5
22	Predicting Molecular Crowding Effects in Ion-RNA Interactions. *Journal of Physical Chemistry B*, **2016**, 120, 8837-44	3.4	5
21	Predicting Ion Effects in an RNA Conformational Equilibrium. *Journal of Physical Chemistry B*, **2017**, 121, 8026-8036	3.4	4
20	Topological constraints of RNA pseudoknotted and loop-kissing motifs: applications to three-dimensional structure prediction. *Nucleic Acids Research*, **2020**, 48, 6503-6512	20.1	4
19	Deciphering nucleotide modification-induced structure and stability changes. *RNA Biology*, **2021**, 18, 1920-1930	4.8	4
18	RNA 3D Structure Prediction Using Coarse-Grained Models. *Frontiers in Molecular Biosciences*, **2021**, 8, 720937	5.6	4
17	RNA□gand molecular docking: Advances and challenges. *Wiley Interdisciplinary Reviews: Computational Molecular Science*,e1571	7.9	4
16	Theory Meets Experiment: Metal Ion Effects in HCV Genomic RNA Kissing Complex Formation. *Frontiers in Molecular Biosciences*, **2017**, 4, 92	5.6	3
15	A New Method to Predict Ion Effects in RNA Folding. *Methods in Molecular Biology*, **2017**, 1632, 1-17	1.4	2
14	Graph, pseudoknot, and SARS-CoV-2 genomic RNA: A biophysical synthesis. *Biophysical Journal*, **2021**, 120, 980-982	2.9	2

13	The three-way junction structure of the HIV-1 PBS-segment binds host enzyme important for viral infectivity. *Nucleic Acids Research*, **2021**, 49, 5925-5942	20.1	2
12	Kinetic Mechanism of RNA Helix-Terminal Basepairing-A Kinetic Minima Network Analysis. *Biophysical Journal*, **2019**, 117, 1674-1683	2.9	2
11	RLDOCK method for predicting RNA-small molecule binding modes. *Methods*, **2021**,	4.6	2
10	A Bayes-inspired theory for optimally building an efficient coarse-grained folding force field. *Communications in Information and Systems*, **2021**, 21, 65-83	0.8	2
9	Statistical mechanical modeling of RNA folding: from free energy landscape to tertiary structural prediction. *Nucleic Acids and Molecular Biology*, **2012**, 27, 185-212		1
8	Analytical modeling and deep learning approaches to estimating RNA SHAPE reactivity from 3D structure. *Communications in Information and Systems*, **2019**, 19, 299-319	0.8	1
7	Modeling Noncanonical RNA Base Pairs by a Coarse-Grained IsRNA2 Model. *Journal of Physical Chemistry B*, **2021**, 125, 11907-11915	3.4	1
6	Sieving RNA 3D Structures with SHAPE and Evaluating Mechanisms Driving Sequence-Dependent Reactivity Bias. *Journal of Physical Chemistry B*, **2021**, 125, 1156-1166	3.4	1
5	SHAPER: A Web Server for Fast and Accurate SHAPE Reactivity Prediction. *Frontiers in Molecular Biosciences*, **2021**, 8, 721955	5.6	0
4	Vfold2D-MC: A Physics-Based Hybrid Model for Predicting RNA Secondary Structure Folding. *Journal of Physical Chemistry B*, **2021**, 125, 10108-10118	3.4	0
3	Predicting RNA Scaffolds with a Hybrid Method of Vfold3D and VfoldLA. *Methods in Molecular Biology*, **2021**, 2323, 1-11	1.4	0
2	3 Importance of Diffuse Metal Ion Binding to RNA **2015**, 101-124		
1	Designing RNA folding cooperativity **1999**, 56-61		