Shi-Jie Chen

List of Publications by Year
in descending order

126	5,243	87888	102487
papers	citations	38 h-index	66 g-index

127	127	127	3442
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nucleic Acid Helix Stability: Effects of Salt Concentration, Cation Valence and Size, and Chain Length. Biophysical Journal, 2006, 90, 1175-1190.	0.5	284
2	RNA Folding: Conformational Statistics, Folding Kinetics, and Ion Electrostatics. Annual Review of Biophysics, 2008, 37, 197-214.	10.0	272
3	RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction. Rna, 2012, 18, 610-625.	3.5	241
4	RNA folding energy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 646-651.	7.1	203
5	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	3.5	161
6	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
7	Physics-Based De Novo Prediction of RNA 3D Structures. Journal of Physical Chemistry B, 2011, 115, 4216-4226.	2.6	142
8	Vfold: A Web Server for RNA Structure and Folding Thermodynamics Prediction. PLoS ONE, 2014, 9, e107504.	2.5	139
9	Electrostatic correlations and fluctuations for ion binding to a finite length polyelectrolyte. Journal of Chemical Physics, 2005, 122, 044903.	3.0	138
10	Predicting RNA pseudoknot folding thermodynamics. Nucleic Acids Research, 2006, 34, 2634-2652.	14.5	135
11	RNA hairpin-folding kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1931-1936.	7.1	122
12	Predicting RNA folding thermodynamics with a reduced chain representation model. Rna, 2005, 11, 1884-1897.	3.5	117
13	Theory and Modeling of RNA Structure and Interactions with Metal Ions and Small Molecules. Annual Review of Biophysics, 2017, 46, 227-246.	10.0	112
14	Rational Truncation of an RNA Aptamer to Prostate-Specific Membrane Antigen Using Computational Structural Modeling. Nucleic Acid Therapeutics, 2011, 21, 299-314.	3.6	106
15	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
16	RNA Helix Stability in Mixed Na+/Mg2+ Solution. Biophysical Journal, 2007, 92, 3615-3632.	0.5	94
17	Designing a Polycationic Probe for Simultaneous Enrichment and Detection of MicroRNAs in a Nanopore. ACS Nano, 2013, 7, 3962-3969.	14.6	94
18	Predicting structures and stabilities for H-type pseudoknots with interhelix loops. Rna, 2009, 15, 696-706.	3.5	89

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19	Salt Dependence of Nucleic Acid Hairpin Stability. Biophysical Journal, 2008, 95, 738-752.	0.5	87
20	Salt Contribution to RNA Tertiary Structure Folding Stability. Biophysical Journal, 2011, 101, 176-187.	0.5	86
21	Ion-Mediated Nucleic Acid Helix-Helix Interactions. Biophysical Journal, 2006, 91, 518-536.	0.5	84
22	AAV CRISPR editing rescues cardiac and muscle function for 18 months in dystrophic mice. JCI Insight, 2018, 3, .	5.0	79
23	Cas9-specific immune responses compromise local and systemic AAV CRISPR therapy in multiple dystrophic canine models. Nature Communications, 2021, 12, 6769.	12.8	73
24	Predicting Ion Binding Properties for RNA Tertiary Structures. Biophysical Journal, 2010, 99, 1565-1576.	0.5	66
25	Exploring the Complex Folding Kinetics of RNA Hairpins: I. General Folding Kinetics Analysis. Biophysical Journal, 2006, 90, 765-777.	0.5	61
26	CRISPR-Cas9 cleavage efficiency correlates strongly with target-sgRNA folding stability: from physical mechanism to off-target assessment. Scientific Reports, 2017, 7, 143.	3.3	59
27	AAV9 Edits Muscle Stem Cells in Normal and Dystrophic Adult Mice. Molecular Therapy, 2019, 27, 1568-1585.	8.2	54
28	Nanopore electric snapshots of an RNA tertiary folding pathway. Nature Communications, 2017, 8, 1458.	12.8	50
29	Electrostatic free energy landscapes for nucleic acid helix assembly. Nucleic Acids Research, 2006, 34, 6629-6639.	14.5	49
30	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.	7.1	46
31	Mimicking Ribosomal Unfolding of RNA Pseudoknot in a Protein Channel. Journal of the American Chemical Society, 2015, 137, 15742-15752.	13.7	45
32	IsRNA: An Iterative Simulated Reference State Approach to Modeling Correlated Interactions in RNA Folding. Journal of Chemical Theory and Computation, 2018, 14, 2230-2239.	5.3	45
33	Predicting RNA Structure with Vfold. Methods in Molecular Biology, 2017, 1654, 3-15.	0.9	44
34	Statistical thermodynamics of doubleâ€stranded polymer molecules. Journal of Chemical Physics, 1995, 103, 5802-5813.	3.0	43
35	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, 3370-3381.	5.3	43
36	Ion-Mediated RNA Structural Collapse: Effect of Spatial Confinement. Biophysical Journal, 2012, 103, 827-836.	0.5	42

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37	Predicting Secondary Structural Folding Kinetics for Nucleic Acids. Biophysical Journal, 2010, 98, 1617-1625.	0.5	41
38	Cotranscriptional folding kinetics of ribonucleic acid secondary structures. Journal of Chemical Physics, 2011, 135, 245101.	3.0	41
39	Theory for the conformational changes of double-stranded chain molecules. Journal of Chemical Physics, 1998, 109, 4602-4616.	3.0	40
40	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, 116-121.	7.1	40
41	Electrostatic Free Energy Landscapes for DNA Helix Bending. Biophysical Journal, 2008, 94, 3137-3149.	0.5	39
42	Predicting loopâ€“helix tertiary structural contacts in RNA pseudoknots. Rna, 2010, 16, 538-552.	3.5	38
43	Structure and stability of RNA/RNA kissing complex: with application to HIV dimerization initiation signal. Rna, 2011, 17, 2130-2143.	3.5	38
44	Biphasic Folding Kinetics of RNA Pseudoknots and Telomerase RNA Activity. Journal of Molecular Biology, 2007, 367, 909-924.	4.2	37
45	IsRNA1: De Novo Prediction and Blind Screening of RNA 3D Structures. Journal of Chemical Theory and Computation, 2021, 17, 1842-1857.	5.3	37
46	Importance of Diffuse Metal Ion Binding to RNA. Metal Ions in Life Sciences, 2011, , 101-124.	1.0	37
47	Free Energy Landscapes of RNA/RNA Complexes: With Applications to snRNA Complexes in Spliceosomes. Journal of Molecular Biology, 2006, 357, 292-312.	4.2	36
48	Exploring the Complex Folding Kinetics of RNA Hairpins: II. Effect of Sequence, Length, and Misfolded States. Biophysical Journal, 2006, 90, 778-787.	0.5	35
49	Predicting Electrostatic Forces in RNA Folding. Methods in Enzymology, 2009, 469, 465-487.	1.0	33
50	A conserved RNA pseudoknot in a putative molecular switch domain of the 3â€²-untranslated region of coronaviruses is only marginally stable. Rna, 2011, 17, 1747-1759.	3.5	33
51	Hierarchical Assembly of RNA Three-Dimensional Structures Based on Loop Templates. Journal of Physical Chemistry B, 2018, 122, 5327-5335.	2.6	33
52	Predicting kissing interactions in microRNAâ€“target complex and assessment of microRNA activity. Nucleic Acids Research, 2012, 40, 4681-4690.	14.5	31
53	RLDOCK: A New Method for Predicting RNAâ€“Ligand Interactions. Journal of Chemical Theory and Computation, 2020, 16, 7173-7183.	5.3	30
54	RNA 3D Structure Prediction Using Coarse-Grained Models. Frontiers in Molecular Biosciences, 2021, 8, 720937.	3.5	30

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55	Minimizing off-target effects in CRISPR-Cas9 genome editing. Cell Biology and Toxicology, 2019, 35, 399-401.	5.3	28
56	In vitro RNA SELEX for the generation of chemically-optimized therapeutic RNA drugs. Methods, 2016, 103, 167-174.	3.8	26
57	Kinetic Mechanism of Conformational Switch between Bistable RNA Hairpins. Journal of the American Chemical Society, 2012, 134, 12499-12507.	13.7	25
58	Predicting ribosomal frameshifting efficiency. Physical Biology, 2008, 5, 016002.	1.8	24
59	Predicting Cotranscriptional Folding Kinetics For Riboswitch. Journal of Physical Chemistry B, 2018, 122, 7484-7496.	2.6	23
60	Binding interface and impact on protease cleavage for an RNA aptamer to HIV-1 reverse transcriptase. Nucleic Acids Research, 2020, 48, 2709-2722.	14.5	22
61	Physics-based RNA structure prediction. Biophysics Reports, 2015, 1, 2-13.	0.8	21
62	Duchenne muscular dystrophy animal models for high-throughput drug discovery and precision medicine. Expert Opinion on Drug Discovery, 2020, 15, 443-456.	5.0	21
63	A three-dimensional statistical mechanical model of folding double-stranded chain molecules. Journal of Chemical Physics, 2001, 114, 7669-7681.	3.0	20
64	Predicting structure and stability for RNA complexes with intermolecular loopâ€“loop base-pairing. Rna, 2014, 20, 835-845.	3.5	20
65	Quantitative Understanding of SHAPE Mechanism from RNA Structure and Dynamics Analysis. Journal of Physical Chemistry B, 2018, 122, 4771-4783.	2.6	20
66	<scp>RNA</scp>â€“ligand molecular docking: Advances and challenges. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1571.	14.6	20
67	Computing the conformational entropy for RNA folds. Journal of Chemical Physics, 2010, 132, 235104.	3.0	19
68	Predicting Ionâ€“Nucleic Acid Interactions by Energy Landscape-Guided Sampling. Journal of Chemical Theory and Computation, 2012, 8, 2095-2102.	5.3	19
69	Master equation approach to finding the rate-limiting steps in biopolymer folding. Journal of Chemical Physics, 2003, 118, 3413-3420.	3.0	18
70	Salt-Dependent Folding Energy Landscape of RNA Three-Way Junction. Biophysical Journal, 2010, 98, 111-120.	0.5	18
71	Structural computational modeling of RNA aptamers. Methods, 2016, 103, 175-179.	3.8	18
72	VfoldLA: A web server for loop assembly-based prediction of putative 3D RNA structures. Journal of Structural Biology, 2019, 207, 235-240.	2.8	18

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73	Symmetries in proteins: A knot theory approach. Journal of Chemical Physics, 1996, 104, 5964-5973.	3.0	17
74	Folding thermodynamics of pseudoknotted chain conformations. Journal of Chemical Physics, 2006, 124, 154903.	3.0	17
75	MCTBI: a web server for predicting metal ion effects in RNA structures. Rna, 2017, 23, 1155-1165.	3.5	17
76	Importance of diffuse metal ion binding to RNA. Metal Ions in Life Sciences, 2011, 9, 101-24.	2.8	17
77	Hexahydrated Mg2+ Binding and Outer-Shell Dehydration on RNA Surface. Biophysical Journal, 2018, 114, 1274-1284.	0.5	16
78	Predicting RNA-Metal Ion Binding with Ion Dehydration Effects. Biophysical Journal, 2019, 116, 184-195.	0.5	15
79	Structural basis of prostate-specific membrane antigen recognition by the A9g RNA aptamer. Nucleic Acids Research, 2020, 48, 11130-11145.	14.5	15
80	Analyzing the biopolymer folding rates and pathways using kinetic cluster method. Journal of Chemical Physics, 2003, 119, 8716-8729.	3.0	14
81	Quantifying Coulombic and Solvent Polarization-Mediated Forces Between DNA Helices. Journal of Physical Chemistry B, 2013, 117, 7221-7227.	2.6	14
82	Modeling Noncanonical RNA Base Pairs by a Coarse-Grained IsRNA2 Model. Journal of Physical Chemistry B, 2021, 125, 11907-11915.	2.6	13
83	Many-body effect in ion binding to RNA. Journal of Chemical Physics, 2014, 141, 055101.	3.0	12
84	VfoldCPX Server: Predicting RNA-RNA Complex Structure and Stability. PLoS ONE, 2016, 11, e0163454.	2.5	12
85	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.	2.7	12
86	Deciphering nucleotide modification-induced structure and stability changes. RNA Biology, 2021, 18, 1920-1930.	3.1	12
87	RNA Folding Transitions and Cooperativity. Journal of Physical Chemistry B, 2001, 105, 1618-1630.	2.6	11
88	A New Computational Approach for Mechanical Folding Kinetics of RNA Hairpins. Biophysical Journal, 2009, 96, 4024-4034.	0.5	11
89	Topological constraints of RNA pseudoknotted and loop-kissing motifs: applications to three-dimensional structure prediction. Nucleic Acids Research, 2020, 48, 6503-6512.	14.5	11
90	A Method to Predict the 3D Structure of an RNA Scaffold. Methods in Molecular Biology, 2015, 1316, 1-11.	0.9	11

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91	Statistical thermodynamics for chain molecules with simple RNA tertiary contacts. Journal of Chemical Physics, 2005, 122, 094909.	3.0	10
92	Folding Kinetics for the Conformational Switch between Alternative RNA Structures. Journal of Physical Chemistry B, 2010, 114, 13609-13615.	2.6	10
93	Coarse-Grained Prediction of RNA Loop Structures. PLoS ONE, 2012, 7, e48460.	2.5	10
94	A Method to Predict the Structure and Stability of RNA/RNA Complexes. Methods in Molecular Biology, 2016, 1490, 63-72.	0.9	10
95	Nuclear Magnetic Resonance Study of RNA Structures at the 3â€²-End of the Hepatitis C Virus Genome. Biochemistry, 2017, 56, 4972-4984.	2.5	10
96	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.	14.5	9
97	VfoldMCPX: predicting multistrand RNA complexes. Rna, 2022, 28, 596-608.	3.5	8
98	Landscape Zooming toward the Prediction of RNA Cotranscriptional Folding. Journal of Chemical Theory and Computation, 2022, 18, 2002-2015.	5.3	8
99	Vfold-Pipeline: a web server for RNA 3D structure prediction from sequences. Bioinformatics, 2022, 38, 4042-4043.	4.1	8
100	Predicting free energy landscapes for complexes of double-stranded chain molecules. Journal of Chemical Physics, 2001, 114, 4253-4266.	3.0	7
101	Exploring the electrostatic energy landscape for tetraloopâ€“receptor docking. Physical Chemistry Chemical Physics, 2014, 16, 6367-6375.	2.8	7
102	Modeling Loop Composition and Ion Concentration Effects in RNA Hairpin Folding Stability. Biophysical Journal, 2020, 119, 1439-1455.	0.5	7
103	RLDOCK method for predicting RNA-small molecule binding modes. Methods, 2022, 197, 97-105.	3.8	7
104	TBI Server: A Web Server for Predicting Ion Effects in RNA Folding. PLoS ONE, 2015, 10, e0119705.	2.5	7
105	Quantitative analysis of the ion-dependent folding stability of DNA triplexes. Physical Biology, 2011, 8, 066006.	1.8	6
106	A domain-based model for predicting large and complex pseudoknotted structures. RNA Biology, 2012, 9, 200-211.	3.1	6
107	Predicting Molecular Crowding Effects in Ionâ€“RNA Interactions. Journal of Physical Chemistry B, 2016, 120, 8837-8844.	2.6	6
108	Predicting Monovalent Ion Correlation Effects in Nucleic Acids. ACS Omega, 2019, 4, 13435-13446.	3.5	6

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109	Sieving RNA 3D Structures with SHAPE and Evaluating Mechanisms Driving Sequence-Dependent Reactivity Bias. Journal of Physical Chemistry B, 2021, 125, 1156-1166.	2.6	6
110	Graph, pseudoknot, and SARS-CoV-2 genomic RNA: A biophysical synthesis. Biophysical Journal, 2021, 120, 980-982.	0.5	6
111	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.	0.2	6
112	Site-Specific Binding of Non-Site-Specific Ions. Biophysical Journal, 2019, 116, 2237-2239.	0.5	5
113	Kinetic Mechanism of RNA Helix-Terminal Basepairingâ€"A Kinetic Minima Network Analysis. Biophysical Journal, 2019, 117, 1674-1683.	0.5	5
114	SHAPER: A Web Server for Fast and Accurate SHAPE Reactivity Prediction. Frontiers in Molecular Biosciences, 2021, 8, 721955.	3.5	5
115	The gRNA Vector Level Determines the Outcome of Systemic AAV CRISPR Therapy for Duchenne Muscular Dystrophy. Human Gene Therapy, 2022, 33, 518-528.	2.7	5
116	Predicting Ion Effects in an RNA Conformational Equilibrium. Journal of Physical Chemistry B, 2017, 121, 8026-8036.	2.6	4
117	Vfold2D-MC: A Physics-Based Hybrid Model for Predicting RNA Secondary Structure Folding. Journal of Physical Chemistry B, 2021, 125, 10108-10118.	2.6	4
118	Theory Meets Experiment: Metal Ion Effects in HCV Genomic RNA Kissing Complex Formation. Frontiers in Molecular Biosciences, 2017, 4, 92.	3.5	3
119	A Bayes-inspired theory for optimally building an efficient coarse-grained folding force field. Communications in Information and Systems, 2021, 21, 65-83.	0.5	3
120	Predicting RNA Scaffolds with a Hybrid Method of Vfold3D and VfoldLA. Methods in Molecular Biology, 2021, 2323, 1-11.	0.9	3
121	Statistical Mechanical Modeling of RNA Folding: From Free Energy Landscape to Tertiary Structural Prediction. Nucleic Acids and Molecular Biology, 2012, 27, 185-212.	0.2	2
122	A New Method to Predict Ion Effects in RNA Folding. Methods in Molecular Biology, 2017, 1632, 1-17.	0.9	2
123	Analytical modeling and deep learning approaches to estimating RNA SHAPE reactivity from 3D structure. Communications in Information and Systems, 2019, 19, 299-319.	0.5	2
124	Designing RNA folding cooperativity. , 1999, , 56-61.		0
125	3 Importance of Diffuse Metal Ion Binding to RNA. , 2015, , 101-124.		0
126	Preface. Methods in Enzymology, 2015, 553, xv-xvii.	1.0	0