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	RLDOCK method for predicting RNA-small molecule binding modes. Methods, 2022, 197, 97-105.	3.8	7
2	<scp>RNA</scp>â€“ligand molecular docking: Advances and challenges. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2022, 12, e1571.	14.6	20
3	VfoldMCPX: predicting multistrand RNA complexes. Rna, 2022, 28, 596-608.	3.5	8
4	Landscape Zooming toward the Prediction of RNA Cotranscriptional Folding. Journal of Chemical Theory and Computation, 2022, 18, 2002-2015.	5.3	8
5	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
6	Vfold-Pipeline: a web server for RNA 3D structure prediction from sequences. Bioinformatics, 2022, 38, 4042-4043.	4.1	8
7	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
8	IsRNA1: De Novo Prediction and Blind Screening of RNA 3D Structures. Journal of Chemical Theory and Computation, 2021, 17, 1842-1857.	5.3	37
9	Deciphering nucleotide modification-induced structure and stability changes. RNA Biology, 2021, 18, 1920-1930.	3.1	12
10	Graph, pseudoknot, and SARS-CoV-2 genomic RNA: A biophysical synthesis. Biophysical Journal, 2021, 120, 980-982.	0.5	6
11	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
12	SHAPER: A Web Server for Fast and Accurate SHAPE Reactivity Prediction. Frontiers in Molecular Biosciences, 2021, 8, 721955.	3.5	5
13	RNA 3D Structure Prediction Using Coarse-Grained Models. Frontiers in Molecular Biosciences, 2021, 8, 720937.	3.5	30
14	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
15	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
16	Predicting RNA Scaffolds with a Hybrid Method of Vfold3D and VfoldLA. Methods in Molecular Biology, 2021, 2323, 1-11.	0.9	3
17	Modeling Noncanonical RNA Base Pairs by a Coarse-Grained IsRNA2 Model. Journal of Physical Chemistry B, 2021, 125, 11907-11915.	2.6	13
18	Cas9-specific immune responses compromise local and systemic AAV CRISPR therapy in multiple dystrophic canine models. Nature Communications, 2021, 12, 6769.	12.8	73

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19	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
20	Modeling Loop Composition and Ion Concentration Effects in RNA Hairpin Folding Stability. Biophysical Journal, 2020, 119, 1439-1455.	0.5	7
21	RLDOCK: A New Method for Predicting RNAâ€“Ligand Interactions. Journal of Chemical Theory and Computation, 2020, 16, 7173-7183.	5.3	30
22	Structural basis of prostate-specific membrane antigen recognition by the A9g RNA aptamer. Nucleic Acids Research, 2020, 48, 11130-11145.	14.5	15
23	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. Rna, 2020, 26, 982-995.	3.5	100
24	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
25	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
26	Predicting Monovalent Ion Correlation Effects in Nucleic Acids. ACS Omega, 2019, 4, 13435-13446.	3.5	6
27	Minimizing off-target effects in CRISPR-Cas9 genome editing. Cell Biology and Toxicology, 2019, 35, 399-401.	5.3	28
28	Site-Specific Binding of Non-Site-Specific Ions. Biophysical Journal, 2019, 116, 2237-2239.	0.5	5
29	AAV9 Edits Muscle Stem Cells in Normal and Dystrophic Adult Mice. Molecular Therapy, 2019, 27, 1568-1585.	8.2	54
30	Predicting RNA-Metal Ion Binding with Ion Dehydration Effects. Biophysical Journal, 2019, 116, 184-195.	0.5	15
31	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
32	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
33	Kinetic Mechanism of RNA Helix-Terminal Basepairingâ€”A Kinetic Minima Network Analysis. Biophysical Journal, 2019, 117, 1674-1683.	0.5	5
34	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
35	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
36	Quantitative Understanding of SHAPE Mechanism from RNA Structure and Dynamics Analysis. Journal of Physical Chemistry B, 2018, 122, 4771-4783.	2.6	20

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37	Hierarchical Assembly of RNA Three-Dimensional Structures Based on Loop Templates. Journal of Physical Chemistry B, 2018, 122, 5327-5335.	2.6	33
38	Hexahydrated Mg2+ Binding and Outer-Shell Dehydration on RNA Surface. Biophysical Journal, 2018, 114, 1274-1284.	0.5	16
39	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
40	AAV CRISPR editing rescues cardiac and muscle function for 18 months in dystrophic mice. JCI Insight, 2018, 3, .	5.0	79
41	Predicting Cotranscriptional Folding Kinetics For Riboswitch. Journal of Physical Chemistry B, 2018, 122, 7484-7496.	2.6	23
42	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
43	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158
44	MCTBI: a web server for predicting metal ion effects in RNA structures. Rna, 2017, 23, 1155-1165.	3.5	17
45	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
46	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
47	Predicting RNA Structure with Vfold. Methods in Molecular Biology, 2017, 1654, 3-15.	0.9	44
48	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
49	Predicting Ion Effects in an RNA Conformational Equilibrium. Journal of Physical Chemistry B, 2017, 121, 8026-8036.	2.6	4
50	Nanopore electric snapshots of an RNA tertiary folding pathway. Nature Communications, 2017, 8, 1458.	12.8	50
51	Theory Meets Experiment: Metal Ion Effects in HCV Genomic RNA Kissing Complex Formation. Frontiers in Molecular Biosciences, 2017, 4, 92.	3.5	3
52	A New Method to Predict Ion Effects in RNA Folding. Methods in Molecular Biology, 2017, 1632, 1-17.	0.9	2
53	VfoldCPX Server: Predicting RNA-RNA Complex Structure and Stability. PLoS ONE, 2016, 11, e0163454.	2.5	12
54	A Method to Predict the Structure and Stability of RNA/RNA Complexes. Methods in Molecular Biology, 2016, 1490, 63-72.	0.9	10

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55	Predicting Molecular Crowding Effects in Ionâ€“RNA Interactions. Journal of Physical Chemistry B, 2016, 120, 8837-8844.	2.6	6
56	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
57	Structural computational modeling of RNA aptamers. Methods, 2016, 103, 175-179.	3.8	18
58	In vitro RNA SELEX for the generation of chemically-optimized therapeutic RNA drugs. Methods, 2016, 103, 167-174.	3.8	26
59	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
60	Physics-based RNA structure prediction. Biophysics Reports, 2015, 1, 2-13.	0.8	21
61	3 Importance of Diffuse Metal Ion Binding to RNA. , 2015, , 101-124.		0
62	RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures. Rna, 2015, 21, 1066-1084.	3.5	161
63	Mimicking Ribosomal Unfolding of RNA Pseudoknot in a Protein Channel. Journal of the American Chemical Society, 2015, 137, 15742-15752.	13.7	45
64	Preface. Methods in Enzymology, 2015, 553, xv-xvii.	1.0	0
65	A Method to Predict the 3D Structure of an RNA Scaffold. Methods in Molecular Biology, 2015, 1316, 1-11.	0.9	11
66	TBI Server: A Web Server for Predicting Ion Effects in RNA Folding. PLoS ONE, 2015, 10, e0119705.	2.5	7
67	Many-body effect in ion binding to RNA. Journal of Chemical Physics, 2014, 141, 055101.	3.0	12
68	Predicting structure and stability for RNA complexes with intermolecular loopâ€“loop base-pairing. Rna, 2014, 20, 835-845.	3.5	20
69	Exploring the electrostatic energy landscape for tetraloopâ€“receptor docking. Physical Chemistry Chemical Physics, 2014, 16, 6367-6375.	2.8	7
70	Vfold: A Web Server for RNA Structure and Folding Thermodynamics Prediction. PLoS ONE, 2014, 9, e107504.	2.5	139
71	Designing a Polycationic Probe for Simultaneous Enrichment and Detection of MicroRNAs in a Nanopore. ACS Nano, 2013, 7, 3962-3969.	14.6	94
72	Quantifying Coulombic and Solvent Polarization-Mediated Forces Between DNA Helices. Journal of Physical Chemistry B, 2013, 117, 7221-7227.	2.6	14

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73	RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction. Rna, 2012, 18, 610-625.	3.5	241
74	Predicting kissing interactions in microRNAâ€“target complex and assessment of microRNA activity. Nucleic Acids Research, 2012, 40, 4681-4690.	14.5	31
75	A domain-based model for predicting large and complex pseudoknotted structures. RNA Biology, 2012, 9, 200-211.	3.1	6
76	Kinetic Mechanism of Conformational Switch between Bistable RNA Hairpins. Journal of the American Chemical Society, 2012, 134, 12499-12507.	13.7	25
77	Predicting Ionâ€“Nucleic Acid Interactions by Energy Landscape-Guided Sampling. Journal of Chemical Theory and Computation, 2012, 8, 2095-2102.	5.3	19
78	Ion-Mediated RNA Structural Collapse: Effect of Spatial Confinement. Biophysical Journal, 2012, 103, 827-836.	0.5	42
79	Coarse-Grained Prediction of RNA Loop Structures. PLoS ONE, 2012, 7, e48460.	2.5	10
80	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
81	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
82	Cotranscriptional folding kinetics of ribonucleic acid secondary structures. Journal of Chemical Physics, 2011, 135, 245101.	3.0	41
83	Physics-Based De Novo Prediction of RNA 3D Structures. Journal of Physical Chemistry B, 2011, 115, 4216-4226.	2.6	142
84	Salt Contribution to RNA Tertiary Structure Folding Stability. Biophysical Journal, 2011, 101, 176-187.	0.5	86
85	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
86	Structure and stability of RNA/RNA kissing complex: with application to HIV dimerization initiation signal. Rna, 2011, 17, 2130-2143.	3.5	38
87	Quantitative analysis of the ion-dependent folding stability of DNA triplexes. Physical Biology, 2011, 8, 066006.	1.8	6
88	Importance of Diffuse Metal Ion Binding to RNA. Metal Ions in Life Sciences, 2011, , 101-124.	1.0	37
89	Importance of diffuse metal ion binding to RNA. Metal Ions in Life Sciences, 2011, 9, 101-24.	2.8	17
90	Predicting loopâ€“helix tertiary structural contacts in RNA pseudoknots. Rna, 2010, 16, 538-552.	3.5	38

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91	Computing the conformational entropy for RNA folds. Journal of Chemical Physics, 2010, 132, 235104.	3.0	19
92	Salt-Dependent Folding Energy Landscape of RNA Three-Way Junction. Biophysical Journal, 2010, 98, 111-120.	0.5	18
93	Predicting Secondary Structural Folding Kinetics for Nucleic Acids. Biophysical Journal, 2010, 98, 1617-1625.	0.5	41
94	Predicting Ion Binding Properties for RNA Tertiary Structures. Biophysical Journal, 2010, 99, 1565-1576.	0.5	66
95	Folding Kinetics for the Conformational Switch between Alternative RNA Structures. Journal of Physical Chemistry B, 2010, 114, 13609-13615.	2.6	10
96	Predicting structures and stabilities for H-type pseudoknots with interhelix loops. Rna, 2009, 15, 696-706.	3.5	89
97	Predicting Electrostatic Forces in RNA Folding. Methods in Enzymology, 2009, 469, 465-487.	1.0	33
98	A New Computational Approach for Mechanical Folding Kinetics of RNA Hairpins. Biophysical Journal, 2009, 96, 4024-4034.	0.5	11
99	Electrostatic Free Energy Landscapes for DNA Helix Bending. Biophysical Journal, 2008, 94, 3137-3149.	0.5	39
100	Salt Dependence of Nucleic Acid Hairpin Stability. Biophysical Journal, 2008, 95, 738-752.	0.5	87
101	RNA Folding: Conformational Statistics, Folding Kinetics, and Ion Electrostatics. Annual Review of Biophysics, 2008, 37, 197-214.	10.0	272
102	Predicting ribosomal frameshifting efficiency. Physical Biology, 2008, 5, 016002.	1.8	24
103	Biphasic Folding Kinetics of RNA Pseudoknots and Telomerase RNA Activity. Journal of Molecular Biology, 2007, 367, 909-924.	4.2	37
104	RNA Helix Stability in Mixed Na+/Mg2+ Solution. Biophysical Journal, 2007, 92, 3615-3632.	0.5	94
105	Exploring the Complex Folding Kinetics of RNA Hairpins: I. General Folding Kinetics Analysis. Biophysical Journal, 2006, 90, 765-777.	0.5	61
106	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
107	Nucleic Acid Helix Stability: Effects of Salt Concentration, Cation Valence and Size, and Chain Length. Biophysical Journal, 2006, 90, 1175-1190.	0.5	284
108	Ion-Mediated Nucleic Acid Helix-Helix Interactions. Biophysical Journal, 2006, 91, 518-536.	0.5	84

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109	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
110	Predicting RNA pseudoknot folding thermodynamics. Nucleic Acids Research, 2006, 34, 2634-2652.	14.5	135
111	Electrostatic free energy landscapes for nucleic acid helix assembly. Nucleic Acids Research, 2006, 34, 6629-6639.	14.5	49
112	Folding thermodynamics of pseudoknotted chain conformations. Journal of Chemical Physics, 2006, 124, 154903.	3.0	17
113	Statistical thermodynamics for chain molecules with simple RNA tertiary contacts. Journal of Chemical Physics, 2005, 122, 094909.	3.0	10
114	Electrostatic correlations and fluctuations for ion binding to a finite length polyelectrolyte. Journal of Chemical Physics, 2005, 122, 044903.	3.0	138
115	Predicting RNA folding thermodynamics with a reduced chain representation model. Rna, 2005, 11, 1884-1897.	3.5	117
116	Analyzing the biopolymer folding rates and pathways using kinetic cluster method. Journal of Chemical Physics, 2003, 119, 8716-8729.	3.0	14
117	Master equation approach to finding the rate-limiting steps in biopolymer folding. Journal of Chemical Physics, 2003, 118, 3413-3420.	3.0	18
118	RNA hairpin-folding kinetics. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 1931-1936.	7.1	122
119	RNA Folding Transitions and Cooperativity. Journal of Physical Chemistry B, 2001, 105, 1618-1630.	2.6	11
120	Predicting free energy landscapes for complexes of double-stranded chain molecules. Journal of Chemical Physics, 2001, 114, 4253-4266.	3.0	7
121	A three-dimensional statistical mechanical model of folding double-stranded chain molecules. Journal of Chemical Physics, 2001, 114, 7669-7681.	3.0	20
122	RNA folding energy landscapes. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 646-651.	7.1	203
123	Designing RNA folding cooperativity. , 1999, , 56-61.		0
124	Theory for the conformational changes of double-stranded chain molecules. Journal of Chemical Physics, 1998, 109, 4602-4616.	3.0	40
125	Symmetries in proteins: A knot theory approach. Journal of Chemical Physics, 1996, 104, 5964-5973.	3.0	17
126	Statistical thermodynamics of doubleâ€stranded polymer molecules. Journal of Chemical Physics, 1995, 103, 5802-5813.	3.0	43