

Kevin M Weeks

List of Publications by Year in descending order

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151
papers

14,135
citations

26610

56
h-index

24232

110
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161
all docs

161
docs citations

161
times ranked

8405
citing authors

#	ARTICLE	IF	CITATIONS
1	Architecture and secondary structure of an entire HIV-1 RNA genome. <i>Nature</i> , 2009, 460, 711-716.	13.7	719
2	RNA Structure Analysis at Single Nucleotide Resolution by Selective 2'-Hydroxyl Acylation and Primer Extension (SHAPE). <i>Journal of the American Chemical Society</i> , 2005, 127, 4223-4231.	6.6	690
3	Selective 2'-hydroxyl acylation analyzed by primer extension (SHAPE): quantitative RNA structure analysis at single nucleotide resolution. <i>Nature Protocols</i> , 2006, 1, 1610-1616.	5.5	681
4	Accurate SHAPE-directed RNA structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 97-102.	3.3	624
5	Principles for targeting RNA with drug-like small molecules. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 547-558.	21.5	489
6	RNA motif discovery by SHAPE and mutational profiling (SHAPE-MaP). <i>Nature Methods</i> , 2014, 11, 959-965.	9.0	487
7	mRNA structure determines specificity of a polyQ-driven phase separation. <i>Science</i> , 2018, 360, 922-927.	6.0	421
8	RNA recognition by Tat-derived peptides: Interaction in the major groove?. <i>Cell</i> , 1991, 66, 577-588.	13.5	371
9	High-Throughput SHAPE Analysis Reveals Structures in HIV-1 Genomic RNA Strongly Conserved across Distinct Biological States. <i>PLoS Biology</i> , 2008, 6, e96.	2.6	351
10	A Fast-Acting Reagent for Accurate Analysis of RNA Secondary and Tertiary Structure by SHAPE Chemistry. <i>Journal of the American Chemical Society</i> , 2007, 129, 4144-4145.	6.6	325
11	Accurate SHAPE-directed RNA secondary structure modeling, including pseudoknots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5498-5503.	3.3	286
12	Selective 2'-hydroxyl acylation analyzed by primer extension and mutational profiling (SHAPE-MaP) for direct, versatile and accurate RNA structure analysis. <i>Nature Protocols</i> , 2015, 10, 1643-1669.	5.5	286
13	Advances in RNA structure analysis by chemical probing. <i>Current Opinion in Structural Biology</i> , 2010, 20, 295-304.	2.6	255
14	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020, 80, 1078-1091.e6.	4.5	255
15	SHAPE-directed RNA secondary structure prediction. <i>Methods</i> , 2010, 52, 150-158.	1.9	248
16	RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	1.6	241
17	Catalysts from synthetic genetic polymers. <i>Nature</i> , 2015, 518, 427-430.	13.7	230
18	Pervasive Regulatory Functions of mRNA Structure Revealed by High-Resolution SHAPE Probing. <i>Cell</i> , 2018, 173, 181-195.e18.	13.5	216

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19	Major groove accessibility of RNA. <i>Science</i> , 1993, 261, 1574-1577.	6.0	209
20	ShapeFinder: A software system for high-throughput quantitative analysis of nucleic acid reactivity information resolved by capillary electrophoresis. <i>Rna</i> , 2008, 14, 1979-1990.	1.6	209
21	SHAPE reveals transcript-wide interactions, complex structural domains, and protein interactions across the <i>Xist</i> lncRNA in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10322-10327.	3.3	201
22	Functional classification of long non-coding RNAs by k-mer content. <i>Nature Genetics</i> , 2018, 50, 1474-1482.	9.4	198
23	QuShape: Rapid, accurate, and best-practices quantification of nucleic acid probing information, resolved by capillary electrophoresis. <i>Rna</i> , 2013, 19, 63-73.	1.6	191
24	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
25	RNA SHAPE Chemistry Reveals Nonhierarchical Interactions Dominate Equilibrium Structural Transitions in tRNA ^{Asp} Transcripts. <i>Journal of the American Chemical Society</i> , 2005, 127, 4659-4667.	6.6	154
26	The Mechanisms of RNA SHAPE Chemistry. <i>Journal of the American Chemical Society</i> , 2012, 134, 6617-6624.	6.6	149
27	Detection of RNA-Protein Interactions in Living Cells with SHAPE. <i>Biochemistry</i> , 2015, 54, 6867-6875.	1.2	148
28	Single-molecule correlated chemical probing of RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13858-13863.	3.3	140
29	Accurate detection of chemical modifications in RNA by mutational profiling (MaP) with ShapeMapper 2. <i>Rna</i> , 2018, 24, 143-148.	1.6	139
30	Exploring RNA Structural Codes with SHAPE Chemistry. <i>Accounts of Chemical Research</i> , 2011, 44, 1280-1291.	7.6	132
31	Protein-facilitated RNA folding. <i>Current Opinion in Structural Biology</i> , 1997, 7, 336-342.	2.6	121
32	Functionally conserved architecture of hepatitis C virus RNA genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3692-3697.	3.3	117
33	Protein facilitation of group I intron splicing by assembly of the catalytic core and the 5' splice site domain. <i>Cell</i> , 1995, 82, 221-230.	13.5	114
34	Time-resolved RNA SHAPE chemistry: quantitative RNA structure analysis in one-second snapshots and at single-nucleotide resolution. <i>Nature Protocols</i> , 2009, 4, 1413-1421.	5.5	106
35	The Cellular Environment Stabilizes Adenine Riboswitch RNA Structure. <i>Biochemistry</i> , 2013, 52, 8777-8785.	1.2	104
36	On the significance of an RNA tertiary structure prediction. <i>Rna</i> , 2010, 16, 1340-1349.	1.6	103

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37	A collapsed non-native RNA folding state. <i>Nature Structural Biology</i> , 2000, 7, 362-366.	9.7	100
38	Van't Hoff enthalpies without baselines. <i>Protein Science</i> , 2000, 9, 1416-1419.	3.1	98
39	Guidelines for SHAPE Reagent Choice and Detection Strategy for RNA Structure Probing Studies. <i>Biochemistry</i> , 2019, 58, 2655-2664.	1.2	91
40	Time-Resolved RNA SHAPE Chemistry. <i>Journal of the American Chemical Society</i> , 2008, 130, 16178-16180.	6.6	89
41	In-cell RNA structure probing with SHAPE-MaP. <i>Nature Protocols</i> , 2018, 13, 1181-1195.	5.5	88
42	RNA secondary structure modeling at consistent high accuracy using differential SHAPE. <i>Rna</i> , 2014, 20, 846-854.	1.6	85
43	Strong Correlation between SHAPE Chemistry and the Generalized NMR Order Parameter ($\langle i^2 \rangle$) in RNA. <i>Journal of the American Chemical Society</i> , 2008, 130, 12244-12245.	6.6	84
44	Comparison of SIV and HIV-1 Genomic RNA Structures Reveals Impact of Sequence Evolution on Conserved and Non-Conserved Structural Motifs. <i>PLoS Pathogens</i> , 2013, 9, e1003294.	2.1	83
45	Pervasive tertiary structure in the dengue virus RNA genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11513-11518.	3.3	81
46	Efficient protein-facilitated splicing of the yeast mitochondrial bI5 intron. <i>Biochemistry</i> , 1995, 34, 7728-7738.	1.2	80
47	Influence of nucleotide identity on ribose 2'-hydroxyl reactivity in RNA. <i>Rna</i> , 2009, 15, 1314-1321.	1.6	79
48	Validating Fragment-Based Drug Discovery for Biological RNAs: Lead Fragments Bind and Remodel the TPP Riboswitch Specifically. <i>Chemistry and Biology</i> , 2014, 21, 591-595.	6.2	79
49	Three-dimensional RNA structure refinement by hydroxyl radical probing. <i>Nature Methods</i> , 2012, 9, 603-608.	9.0	77
50	High-Throughput SHAPE and Hydroxyl Radical Analysis of RNA Structure and Ribonucleoprotein Assembly. <i>Methods in Enzymology</i> , 2009, 468, 67-89.	0.4	73
51	Fingerprinting Noncanonical and Tertiary RNA Structures by Differential SHAPE Reactivity. <i>Journal of the American Chemical Society</i> , 2012, 134, 13160-13163.	6.6	72
52	Facile Conversion of Aptamers into Sensors Using a 2'-Ribose-Linked Fluorophore. <i>Journal of the American Chemical Society</i> , 2005, 127, 12766-12767.	6.6	70
53	RNA base-pairing complexity in living cells visualized by correlated chemical probing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24574-24582.	3.3	69
54	Native-like RNA Tertiary Structures Using a Sequence-Encoded Cleavage Agent and Refinement by Discrete Molecular Dynamics. <i>Journal of the American Chemical Society</i> , 2009, 131, 2541-2546.	6.6	65

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55	Fluorogenic Resolution of Ligand Binding by a Nucleic Acid Aptamer. <i>Journal of the American Chemical Society</i> , 2003, 125, 12370-12371.	6.6	64
56	Definition of a high-affinity Gag recognition structure mediating packaging of a retroviral RNA genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19248-19253.	3.3	64
57	In-cell SHAPE reveals that free 30S ribosome subunits are in the inactive state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2425-2430.	3.3	62
58	Multiple conformations are a conserved and regulatory feature of the <i>RB1</i> 5' UTR. <i>Rna</i> , 2015, 21, 1274-1285.	1.6	60
59	RNA-Tethered Phenyl Azide Photocrosslinking via a Short-Lived Indiscriminant Electrophile. <i>Journal of the American Chemical Society</i> , 2003, 125, 10850-10861.	6.6	57
60	Challenge of Mimicking the Influences of the Cellular Environment on RNA Structure by PEG-Induced Macromolecular Crowding. <i>Biochemistry</i> , 2015, 54, 6447-6453.	1.2	56
61	Direct detection of RNA modifications and structure using single-molecule nanopore sequencing. <i>Cell Genomics</i> , 2022, 2, 100097.	3.0	55
62	The genetic code as expressed through relationships between mRNA structure and protein function. <i>FEBS Letters</i> , 2013, 587, 1180-1188.	1.3	54
63	Two Distinct Binding Modes of a Protein Cofactor with its Target RNA. <i>Journal of Molecular Biology</i> , 2006, 361, 771-784.	2.0	53
64	Lack of secondary structure characterizes the 5' ends of mammalian mitochondrial mRNAs. <i>Rna</i> , 2008, 14, 862-871.	1.6	53
65	An RNA structure-mediated, posttranscriptional model of human α -1-antitrypsin expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10244-E10253.	3.3	52
66	RNA Structures Facilitate Recombination-Mediated Gene Swapping in HIV-1. <i>Journal of Virology</i> , 2010, 84, 12675-12682.	1.5	51
67	Analysis of RNA-protein networks with RNP-MaP defines functional hubs on RNA. <i>Nature Biotechnology</i> , 2021, 39, 347-356.	9.4	50
68	Protein-dependent transition states for ribonucleoprotein assembly. <i>Journal of Molecular Biology</i> , 2001, 309, 1087-1100.	2.0	49
69	Complex Ligand-Induced Conformational Changes in tRNA ^{Asp} Revealed by Single-Nucleotide Resolution SHAPE Chemistry. <i>Biochemistry</i> , 2008, 47, 3454-3461.	1.2	49
70	IFNL3 mRNA structure is remodeled by a functional non-coding polymorphism associated with hepatitis C virus clearance. <i>Scientific Reports</i> , 2015, 5, 16037.	1.6	49
71	Messenger RNA Structure Regulates Translation Initiation: A Mechanism Exploited from Bacteria to Humans. <i>Biochemistry</i> , 2018, 57, 3537-3539.	1.2	48
72	A Guanosine-Centric Mechanism for RNA Chaperone Function. <i>Science</i> , 2013, 340, 190-195.	6.0	47

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73	Physical and Functional Analysis of Viral RNA Genomes by SHAPE. Annual Review of Virology, 2019, 6, 93-117.	3.0	47
74	Targeting the Oncogenic Long Non-coding RNA SLNCR1 by Blocking Its Sequence-Specific Binding to the Androgen Receptor. Cell Reports, 2020, 30, 541-554.e5.	2.9	47
75	Recruitment of intron-encoded and co-opted proteins in splicing of the b13 group I intron RNA. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 128-133.	3.3	46
76	Visualizing induced fit in early assembly of the human signal recognition particle. , 2001, 8, 515-520.		45
77	Slow Conformational Dynamics at C2' endo Nucleotides in RNA. Journal of the American Chemical Society, 2008, 130, 8884-8885.	6.6	45
78	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. PLoS Computational Biology, 2015, 11, e1004126.	1.5	45
79	Catalysis of amide synthesis by RNA phosphodiester and hydroxyl groups. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 14688-14693.	3.3	41
80	RNA flexibility in the dimerization domain of a gamma retrovirus. Nature Chemical Biology, 2005, 1, 104-111.	3.9	41
81	Principles for Understanding the Accuracy of SHAPE-Directed RNA Structure Modeling. Biochemistry, 2013, 52, 588-595.	1.2	41
82	The RNA Domain Vc1 Regulates Downstream Gene Expression in Response to Cyclic Diguanylate in Vibrio cholerae. PLoS ONE, 2016, 11, e0148478.	1.1	40
83	Discovery of a large-scale, cell-state-responsive allosteric switch in the 7SK RNA using DANCE-MaP. Molecular Cell, 2022, 82, 1708-1723.e10.	4.5	40
84	A collapsed state functions to self-chaperone RNA folding into a native ribonucleoprotein complex. , 2001, 8, 135-140.		39
85	Ribosome RNA Assembly Intermediates Visualized in Living Cells. Biochemistry, 2014, 53, 3237-3247.	1.2	39
86	Architecture of a Gamma Retroviral Genomic RNA Dimer. Biochemistry, 2006, 45, 12664-12672.	1.2	38
87	C2' endo nucleotides as molecular timers suggested by the folding of an RNA domain. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 15622-15627.	3.3	38
88	Structure of an RNA switch that enforces stringent retroviral genomic RNA dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 13640-13645.	3.3	37
89	Selective 2'-Hydroxyl Acylation Analyzed by Protection from Exoribonuclease. Journal of the American Chemical Society, 2010, 132, 9940-9943.	6.6	37
90	SHAPE-directed Discovery of Potent shRNA Inhibitors of HIV-1. Molecular Therapy, 2012, 20, 820-828.	3.7	37

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91	SHAPE Analysis of Long-Range Interactions Reveals Extensive and Thermodynamically Preferred Misfolding in a Fragile Group I Intron RNA. <i>Biochemistry</i> , 2008, 47, 8504-8513.	1.2	36
92	Structure-Based Alignment and Consensus Secondary Structures for Three HIV-Related RNA Genomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004230.	1.5	34
93	SHAPE Directed Discovery of New Functions in Large RNAs. <i>Accounts of Chemical Research</i> , 2021, 54, 2502-2517.	7.6	34
94	Mapping Local Nucleotide Flexibility by Selective Acylation of 2'-Amino Substituted RNA. <i>Journal of the American Chemical Society</i> , 2000, 122, 216-224.	6.6	33
95	Long-Range Architecture in a Viral RNA Genome. <i>Biochemistry</i> , 2013, 52, 3182-3190.	1.2	33
96	Robust and Generic RNA Modeling Using Inferred Constraints: A Structure for the Hepatitis C Virus IRES Pseudoknot Domain. <i>Biochemistry</i> , 2010, 49, 4931-4933.	1.2	31
97	Structure and Dynamics of the HIV-1 Frameshift Element RNA. <i>Biochemistry</i> , 2014, 53, 4282-4291.	1.2	31
98	Direct identification of base-paired RNA nucleotides by correlated chemical probing. <i>Rna</i> , 2017, 23, 6-13.	1.6	31
99	Role of Context in RNA Structure: Flanking Sequences Reconfigure CAG Motif Folding in <i>Huntingtin</i> Exon 1 Transcripts. <i>Biochemistry</i> , 2013, 52, 8219-8225.	1.2	30
100	Selective 2'-hydroxyl acylation analyzed by protection from exoribonuclease (RNase-detected SHAPE) for direct analysis of covalent adducts and of nucleotide flexibility in RNA. <i>Nature Protocols</i> , 2011, 6, 1683-1694.	5.5	28
101	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	1.6	28
102	Secondary Structure of the Mature <i>Ex Virio</i> Moloney Murine Leukemia Virus Genomic RNA Dimerization Domain. <i>Journal of Virology</i> , 2010, 84, 898-906.	1.5	27
103	Review toward all RNA structures, concisely. <i>Biopolymers</i> , 2015, 103, 438-448.	1.2	26
104	Direct Duplex Detection: An Emerging Tool in the RNA Structure Analysis Toolbox. <i>Trends in Biochemical Sciences</i> , 2016, 41, 734-736.	3.7	25
105	Packaged and Free Satellite Tobacco Mosaic Virus (STMV) RNA Genomes Adopt Distinct Conformational States. <i>Biochemistry</i> , 2017, 56, 2175-2183.	1.2	25
106	Differential Helix Stabilities and Sites Pre-organized for Tertiary Interactions Revealed by Monitoring Local Nucleotide Flexibility in the b15 Group I Intron RNA. <i>Biochemistry</i> , 2003, 42, 901-909.	1.2	24
107	Nonhierarchical Ribonucleoprotein Assembly Suggests a Strain-Propagation Model for Protein-Facilitated RNA Folding. <i>Biochemistry</i> , 2010, 49, 5418-5425.	1.2	24
108	Direct Mapping of Higher-Order RNA Interactions by SHAPE-JuMP. <i>Biochemistry</i> , 2021, 60, 1971-1982.	1.2	24

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109	Structure-independent and quantitative ligation of single-stranded DNA. <i>Analytical Biochemistry</i> , 2006, 349, 242-246.	1.1	23
110	Visualization of RNA structure models within the Integrative Genomics Viewer. <i>Rna</i> , 2017, 23, 1012-1018.	1.6	23
111	Evolution from DNA to RNA recognition by the b13 LAGLIDADG maturase. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 779-787.	3.6	22
112	Structural Basis for the Self-Chaperoning Function of an RNA Collapsed State. <i>Biochemistry</i> , 2004, 43, 15179-15186.	1.2	21
113	SHAPE-enabled fragment-based ligand discovery for RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2122660119.	3.3	21
114	Quantitative Analysis of RNA Solvent Accessibility by N-Silylation of Guanosine. <i>Biochemistry</i> , 2009, 48, 2109-2114.	1.2	19
115	Kinetic and Thermodynamic Framework for Assembly of the Six-Component b13 Group I Intron Ribonucleoprotein Catalyst. <i>Biochemistry</i> , 2003, 42, 9980-9988.	1.2	18
116	Toward global RNA structure analysis. <i>Nature Biotechnology</i> , 2010, 28, 1178-1179.	9.4	18
117	Single-molecule correlated chemical probing reveals large-scale structural communication in the ribosome and the mechanism of the antibiotic spectinomycin in living cells. <i>PLoS Biology</i> , 2019, 17, e3000393.	2.6	18
118	Subsite Ligand Recognition and Cooperativity in the TPP Riboswitch: Implications for Fragment-Linking in RNA Ligand Discovery. <i>ACS Chemical Biology</i> , 2022, 17, 438-448.	1.6	18
119	The SL1-SL2 (Stem-Loop) Domain Is the Primary Determinant for Stability of the Gamma Retroviral Genomic RNA Dimer. <i>Journal of Biological Chemistry</i> , 2006, 281, 37952-37961.	1.6	17
120	A Threefold RNA-Protein Interface in the Signal Recognition Particle Gates Native Complex Assembly. <i>Journal of Molecular Biology</i> , 2007, 369, 512-524.	2.0	17
121	RNA Tertiary Structure Analysis by ² H-Hydroxyl Molecular Interference. <i>Biochemistry</i> , 2014, 53, 6825-6833.	1.2	17
122	Tris-borate is a poor counterion for RNA: a cautionary tale for RNA folding studies. <i>Nucleic Acids Research</i> , 2004, 32, e184-e184.	6.5	16
123	Compartmentalization Directs Assembly of the Signal Recognition Particle. <i>Biochemistry</i> , 2006, 45, 14955-14964.	1.2	16
124	The Mrs1 Splicing Factor Binds the b13 Group I Intron at Each of Two Tetraloop-Receptor Motifs. <i>PLoS ONE</i> , 2010, 5, e8983.	1.1	16
125	Structure modeling of RNA using sparse NMR constraints. <i>Nucleic Acids Research</i> , 2017, 45, 12638-12647.	6.5	15
126	Crystal Structures, Reactivity and Inferred Acylation Transition States for α -Amine Substituted RNA. <i>Journal of the American Chemical Society</i> , 2005, 127, 13622-13628.	6.6	14

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127	SHAPE Analysis of Small RNAs and Riboswitches. <i>Methods in Enzymology</i> , 2014, 549, 165-187.	0.4	14
128	Chemical Interrogation of Mismatches in DNA~DNA and DNA~RNA Duplexes under Nonstringent Conditions by Selective 2~Amine Acylation. <i>Biochemistry</i> , 2002, 41, 6866-6874.	1.2	13
129	Distinct MUNC lncRNA structural domains regulate transcription of different promyogenic factors. <i>Cell Reports</i> , 2022, 38, 110361.	2.9	13
130	Tagging DNA mismatches by selective 2~amine acylation. <i>Chemistry and Biology</i> , 2000, 7, 405-410.	6.2	12
131	Femtomole SHAPE Reveals Regulatory Structures in the Authentic XMRV RNA Genome. <i>Journal of the American Chemical Society</i> , 2011, 133, 20326-20334.	6.6	12
132	An Immature Retroviral RNA Genome Resembles a Kinetically Trapped Intermediate State. <i>Journal of Virology</i> , 2014, 88, 6061-6068.	1.5	11
133	SHAPE Probing Reveals Human rRNAs Are Largely Unfolded in Solution. <i>Biochemistry</i> , 2019, 58, 3377-3385.	1.2	11
134	The roles of five conserved lentiviral RNA structures in HIV-1 replication. <i>Virology</i> , 2018, 514, 1-8.	1.1	10
135	Effects of Refolding on Large-Scale RNA Structure. <i>Biochemistry</i> , 2019, 58, 3069-3077.	1.2	10
136	Time-Resolved, Single-Molecule, Correlated Chemical Probing of RNA. <i>Journal of the American Chemical Society</i> , 2020, 142, 18735-18740.	6.6	10
137	RNA structure probing <i>dash seq</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10933-10934.	3.3	8
138	RNA~Ligand Interactions Quantified by Surface Plasmon Resonance with Reference Subtraction. <i>Biochemistry</i> , 2022, 61, 1625-1632.	1.2	8
139	Anti-cooperative assembly of the SRP19 and SRP68/72 components of the signal recognition particle. <i>Biochemical Journal</i> , 2008, 415, 429-437.	1.7	7
140	Mechanics of DNA Flexibility Visualized by Selective 2~Amine Acylation at Nucleotide Bulges. <i>Journal of Molecular Biology</i> , 2004, 337, 611-619.	2.0	6
141	Quantitative prediction of variant effects on alternative splicing in MAPT using endogenous pre-messenger RNA structure probing. <i>ELife</i> , 0, 11, .	2.8	6
142	RNA targeting by the HIV-1 Tat protein. <i>Journal of Computer - Aided Molecular Design</i> , 1993, 1, 225-234.	1.0	5
143	Piercing the fog of the RNA structure-ome. <i>Science</i> , 2021, 373, 964-965.	6.0	5
144	Identifying proximal RNA interactions from cDNA-encoded crosslinks with ShapeJumper. <i>PLoS Computational Biology</i> , 2021, 17, e1009632.	1.5	3

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145	Small Structural Costs for Evolution from RNA to RNP-based Catalysis. <i>Journal of Molecular Biology</i> , 2003, 331, 57-73.	2.0	2
146	Visualization of lncRNA and mRNA Structure Models Within the Integrative Genomics Viewer. <i>Methods in Molecular Biology</i> , 2021, 2254, 15-25.	0.4	2
147	RNA clubs. <i>Rna</i> , 2015, 21, 760-761.	1.6	0
148	High-Throughput Explorations of RNA Structural Modularity. <i>Biochemistry</i> , 2018, 57, 6129-6131.	1.2	0
149	High-Throughput Analysis of RNA Structure by SHAPE Chemistry. <i>FASEB Journal</i> , 2009, 23, 326.3.	0.2	0
150	Accurate SHAPE-directed RNA structure prediction. <i>FASEB Journal</i> , 2009, 23, 843.2.	0.2	0
151	In vivo analysis of ribosome structure and dynamics. <i>FASEB Journal</i> , 2009, 23, 847.2.	0.2	0