

Kevin M Weeks

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

153
papers

10,795
citations

53
h-index

102
g-index

161
ext. papers

12,735
ext. citations

11.8
avg, IF

6.69
L-index

#	Paper	IF	Citations
153	Subsite Ligand Recognition and Cooperativity in the TPP Riboswitch: Implications for Fragment-Linking in RNA Ligand Discovery.. <i>ACS Chemical Biology</i> , 2022 ,	4.9	3
152	Direct detection of RNA modifications and structure using single-molecule nanopore sequencing.. <i>Cell Genomics</i> , 2022 , 2, 100097-100097		9
151	Distinct MUNC lncRNA structural domains regulate transcription of different promyogenic factors.. <i>Cell Reports</i> , 2022 , 38, 110361	10.6	1
150	Discovery of a large-scale, cell-state-responsive allosteric switch in the 7SK RNA using DANCE-MaP.. <i>Molecular Cell</i> , 2022 ,	17.6	3
149	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	11.5	1
148	Identifying proximal RNA interactions from cDNA-encoded crosslinks with ShapeJumper.. <i>PLoS Computational Biology</i> , 2021 , 17, e1009632	5	0
147	SHAPE Directed Discovery of New Functions in Large RNAs. <i>Accounts of Chemical Research</i> , 2021 , 54, 2502-2517	24.3	11
146	Direct Mapping of Higher-Order RNA Interactions by SHAPE-JuMP. <i>Biochemistry</i> , 2021 , 60, 1971-1982	3.2	3
145	Double-stranded RNA drives SARS-CoV-2 nucleocapsid protein to undergo phase separation at specific temperatures 2021 ,		2
144	Analysis of RNA-protein networks with RNP-MaP defines functional hubs on RNA. <i>Nature Biotechnology</i> , 2021 , 39, 347-356	44.5	13
143	Piercing the fog of the RNA structure-ome. <i>Science</i> , 2021 , 373, 964-965	33.3	2
142	Visualization of lncRNA and mRNA Structure Models Within the Integrative Genomics Viewer. <i>Methods in Molecular Biology</i> , 2021 , 2254, 15-25	1.4	2
141	Genomic RNA Elements Drive Phase Separation of the SARS-CoV-2 Nucleocapsid. <i>Molecular Cell</i> , 2020 , 80, 1078-1091.e6	17.6	98
140	Targeting the Oncogenic Long Non-coding RNA SLNCR1 by Blocking Its Sequence-Specific Binding to the Androgen Receptor. <i>Cell Reports</i> , 2020 , 30, 541-554.e5	10.6	20
139	Specific viral RNA drives the SARS CoV-2 nucleocapsid to phase separate 2020 ,		28
138	Time-Resolved, Single-Molecule, Correlated Chemical Probing of RNA. <i>Journal of the American Chemical Society</i> , 2020 , 142, 18735-18740	16.4	5
137	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	8.7	10

136	Effects of Refolding on Large-Scale RNA Structure. <i>Biochemistry</i> , 2019 , 58, 3069-3077	3.2	5
135	Guidelines for SHAPE Reagent Choice and Detection Strategy for RNA Structure Probing Studies. <i>Biochemistry</i> , 2019 , 58, 2655-2664	3.2	45
134	SHAPE Probing Reveals Human rRNAs Are Largely Unfolded in Solution. <i>Biochemistry</i> , 2019 , 58, 3377-3385	3.2	5
133	Physical and Functional Analysis of Viral RNA Genomes by SHAPE. <i>Annual Review of Virology</i> , 2019 , 6, 93-117	14.6	25
132	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	11.5	45
131	mRNA structure determines specificity of a polyQ-driven phase separation. <i>Science</i> , 2018 , 360, 922-927	33.3	284
130	In-cell RNA structure probing with SHAPE-MaP. <i>Nature Protocols</i> , 2018 , 13, 1181-1195	18.8	49
129	Pervasive Regulatory Functions of mRNA Structure Revealed by High-Resolution SHAPE Probing. <i>Cell</i> , 2018 , 173, 181-195.e18	56.2	139
128	Messenger RNA Structure Regulates Translation Initiation: A Mechanism Exploited from Bacteria to Humans. <i>Biochemistry</i> , 2018 , 57, 3537-3539	3.2	22
127	Accurate detection of chemical modifications in RNA by mutational profiling (MaP) with ShapeMapper 2. <i>Rna</i> , 2018 , 24, 143-148	5.8	74
126	The roles of five conserved lentiviral RNA structures in HIV-1 replication. <i>Virology</i> , 2018 , 514, 1-8	3.6	6
125	High-Throughput Explorations of RNA Structural Modularity. <i>Biochemistry</i> , 2018 , 57, 6129-6131	3.2	
124	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	11.5	50
123	Functional classification of long non-coding RNAs by k-mer content. <i>Nature Genetics</i> , 2018 , 50, 1474-1483	36.3	86
122	Principles for targeting RNA with drug-like small molecules. <i>Nature Reviews Drug Discovery</i> , 2018 , 17, 547-558	64.1	246
121	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017 , 23, 655-672	5.8	118
120	Visualization of RNA structure models within the Integrative Genomics Viewer. <i>Rna</i> , 2017 , 23, 1012-1018	5.8	17
119	Packaged and Free Satellite Tobacco Mosaic Virus (STMV) RNA Genomes Adopt Distinct Conformational States. <i>Biochemistry</i> , 2017 , 56, 2175-2183	3.2	16

118	Structure modeling of RNA using sparse NMR constraints. <i>Nucleic Acids Research</i> , 2017 , 45, 12638-12647	20.1	13
117	An RNA structure-mediated, posttranscriptional model of human E1-antitrypsin expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E10244-E10253	11.5	33
116	Direct identification of base-paired RNA nucleotides by correlated chemical probing. <i>Rna</i> , 2017 , 23, 6-13	5.8	20
115	SHAPE reveals transcript-wide interactions, complex structural domains, and protein interactions across the Xist lncRNA in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 10322-7	11.5	149
114	Direct Duplex Detection: An Emerging Tool in the RNA Structure Analysis Toolbox. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 734-736	10.3	20
113	The RNA Domain Vc1 Regulates Downstream Gene Expression in Response to Cyclic Diguanylate in <i>Vibrio cholerae</i> . <i>PLoS ONE</i> , 2016 , 11, e0148478	3.7	14
112	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. <i>PLoS Computational Biology</i> , 2015 , 11, e1004126	5	36
111	Structure-Based Alignment and Consensus Secondary Structures for Three HIV-Related RNA Genomes. <i>PLoS Computational Biology</i> , 2015 , 11, e1004230	5	28
110	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, 3692-7	11.5	89
109	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, 1643-69	18.8	182
108	Challenge of mimicking the influences of the cellular environment on RNA structure by PEG-induced macromolecular crowding. <i>Biochemistry</i> , 2015 , 54, 6447-53	3.2	42
107	RNA clubs. <i>Rna</i> , 2015 , 21, 760-1	5.8	
106	Detection of RNA-Protein Interactions in Living Cells with SHAPE. <i>Biochemistry</i> , 2015 , 54, 6867-75	3.2	109
105	Catalysts from synthetic genetic polymers. <i>Nature</i> , 2015 , 518, 427-30	50.4	187
104	IFNL3 mRNA structure is remodeled by a functional non-coding polymorphism associated with hepatitis C virus clearance. <i>Scientific Reports</i> , 2015 , 5, 16037	4.9	37
103	Multiple conformations are a conserved and regulatory feature of the RB1 5SUTR. <i>Rna</i> , 2015 , 21, 1274-85	5.8	45
102	Review toward all RNA structures, concisely. <i>Biopolymers</i> , 2015 , 103, 438-48	2.2	23
101	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, 2425-30	11.5	51

100	RNA tertiary structure analysis by 2S-hydroxyl molecular interference. <i>Biochemistry</i> , 2014 , 53, 6825-33	3.2	12
99	Single-molecule correlated chemical probing of RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 13858-63	11.5	95
98	An immature retroviral RNA genome resembles a kinetically trapped intermediate state. <i>Journal of Virology</i> , 2014 , 88, 6061-8	6.6	9
97	Ribosome RNA assembly intermediates visualized in living cells. <i>Biochemistry</i> , 2014 , 53, 3237-47	3.2	34
96	RNA motif discovery by SHAPE and mutational profiling (SHAPE-MaP). <i>Nature Methods</i> , 2014 , 11, 959-65	21.6	333
95	Structure and dynamics of the HIV-1 frameshift element RNA. <i>Biochemistry</i> , 2014 , 53, 4282-91	3.2	27
94	Validating fragment-based drug discovery for biological RNAs: lead fragments bind and remodel the TPP riboswitch specifically. <i>Chemistry and Biology</i> , 2014 , 21, 591-5		55
93	RNA secondary structure modeling at consistent high accuracy using differential SHAPE. <i>Rna</i> , 2014 , 20, 846-54	5.8	67
92	SHAPE analysis of small RNAs and riboswitches. <i>Methods in Enzymology</i> , 2014 , 549, 165-87	1.7	11
91	The cellular environment stabilizes adenine riboswitch RNA structure. <i>Biochemistry</i> , 2013 , 52, 8777-85	3.2	86
90	The genetic code as expressed through relationships between mRNA structure and protein function. <i>FEBS Letters</i> , 2013 , 587, 1180-1188	3.8	44
89	Principles for understanding the accuracy of SHAPE-directed RNA structure modeling. <i>Biochemistry</i> , 2013 , 52, 588-95	3.2	35
88	QuShape: rapid, accurate, and best-practices quantification of nucleic acid probing information, resolved by capillary electrophoresis. <i>Rna</i> , 2013 , 19, 63-73	5.8	147
87	A guanosine-centric mechanism for RNA chaperone function. <i>Science</i> , 2013 , 340, 190-5	33.3	42
86	Long-range architecture in a viral RNA genome. <i>Biochemistry</i> , 2013 , 52, 3182-90	3.2	29
85	Role of context in RNA structure: flanking sequences reconfigure CAG motif folding in huntingtin exon 1 transcripts. <i>Biochemistry</i> , 2013 , 52, 8219-25	3.2	25
84	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	7.6	65
83	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, 5498-503	11.5	210

82	Fingerprinting noncanonical and tertiary RNA structures by differential SHAPE reactivity. <i>Journal of the American Chemical Society</i> , 2012 , 134, 13160-3	16.4	60
81	The mechanisms of RNA SHAPE chemistry. <i>Journal of the American Chemical Society</i> , 2012 , 134, 6617-24	16.4	116
80	Three-dimensional RNA structure refinement by hydroxyl radical probing. <i>Nature Methods</i> , 2012 , 9, 603-8	11.6	64
79	RNA-Puzzles: a CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012 , 18, 610-25	5.8	181
78	SHAPE-directed discovery of potent shRNA inhibitors of HIV-1. <i>Molecular Therapy</i> , 2012 , 20, 820-8	11.7	31
77	Exploring RNA structural codes with SHAPE chemistry. <i>Accounts of Chemical Research</i> , 2011 , 44, 1280-91	24.3	112
76	RNA structure probing dash seq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 10933-4	11.5	8
75	Femtomole SHAPE reveals regulatory structures in the authentic XMRV RNA genome. <i>Journal of the American Chemical Society</i> , 2011 , 133, 20326-34	16.4	12
74	Selective 2Hydroxyl 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, 1683-94	18.8	23
73	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011 , 17, 1204-12	5.8	27
72	The Mrs1 splicing factor binds the bI3 group I intron at each of two tetraloop-receptor motifs. <i>PLoS ONE</i> , 2010 , 5, e8983	3.7	12
71	RNA structures facilitate recombination-mediated gene swapping in HIV-1. <i>Journal of Virology</i> , 2010 , 84, 12675-82	6.6	45
70	Secondary structure of the mature ex virio Moloney murine leukemia virus genomic RNA dimerization domain. <i>Journal of Virology</i> , 2010 , 84, 898-906	6.6	25
69	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, 19248-53	11.5	56
68	Robust and generic RNA modeling using inferred constraints: a structure for the hepatitis C virus IRES pseudoknot domain. <i>Biochemistry</i> , 2010 , 49, 4931-3	3.2	26
67	Selective 2Hydroxyl acylation analyzed by protection from exoribonuclease. <i>Journal of the American Chemical Society</i> , 2010 , 132, 9940-3	16.4	34
66	Nonhierarchical ribonucleoprotein assembly suggests a strain-propagation model for protein-facilitated RNA folding. <i>Biochemistry</i> , 2010 , 49, 5418-25	3.2	22
65	SHAPE-directed RNA secondary structure prediction. <i>Methods</i> , 2010 , 52, 150-8	4.6	201

64	On the significance of an RNA tertiary structure prediction. <i>Rna</i> , 2010 , 16, 1340-9	5.8	82
63	Advances in RNA structure analysis by chemical probing. <i>Current Opinion in Structural Biology</i> , 2010 , 20, 295-304	8.1	210
62	Influence of nucleotide identity on ribose 2'Shydroxyl reactivity in RNA. <i>Rna</i> , 2009 , 15, 1314-21	5.8	70
61	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	11.5	493
60	C2'Sendo nucleotides as molecular timers suggested by the folding of an RNA domain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 15622-7	11.5	35
59	Architecture and secondary structure of an entire HIV-1 RNA genome. <i>Nature</i> , 2009 , 460, 711-6	50.4	607
58	Time-resolved RNA SHAPE chemistry: quantitative RNA structure analysis in one-second snapshots and at single-nucleotide resolution. <i>Nature Protocols</i> , 2009 , 4, 1413-21	18.8	87
57	High-throughput SHAPE and hydroxyl radical analysis of RNA structure and ribonucleoprotein assembly. <i>Methods in Enzymology</i> , 2009 , 468, 67-89	1.7	67
56	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, 2541-6	16.4	60
55	Quantitative analysis of RNA solvent accessibility by N-silylation of guanosine. <i>Biochemistry</i> , 2009 , 48, 2109-14	3.2	16
54	High-Throughput Analysis of RNA Structure by SHAPE Chemistry. <i>FASEB Journal</i> , 2009 , 23, 326.3	0.9	
53	Accurate SHAPE-directed RNA structure prediction. <i>FASEB Journal</i> , 2009 , 23, 843.2	0.9	
52	In vivo analysis of ribosome structure and dynamics. <i>FASEB Journal</i> , 2009 , 23, 847.2	0.9	
51	Strong correlation between SHAPE chemistry and the generalized NMR order parameter (S2) in RNA. <i>Journal of the American Chemical Society</i> , 2008 , 130, 12244-5	16.4	75
50	SHAPE analysis of long-range interactions reveals extensive and thermodynamically preferred misfolding in a fragile group I intron RNA. <i>Biochemistry</i> , 2008 , 47, 8504-13	3.2	34
49	Time-resolved RNA SHAPE chemistry. <i>Journal of the American Chemical Society</i> , 2008 , 130, 16178-80	16.4	66
48	Complex ligand-induced conformational changes in tRNA(Asp) revealed by single-nucleotide resolution SHAPE chemistry. <i>Biochemistry</i> , 2008 , 47, 3454-61	3.2	40
47	Slow conformational dynamics at C2'Sendo nucleotides in RNA. <i>Journal of the American Chemical Society</i> , 2008 , 130, 8884-5	16.4	41

46	Lack of secondary structure characterizes the 5Sends of mammalian mitochondrial mRNAs. <i>Rna</i> , 2008 , 14, 862-71	5.8	45
45	High-throughput SHAPE analysis reveals structures in HIV-1 genomic RNA strongly conserved across distinct biological states. <i>PLoS Biology</i> , 2008 , 6, e96	9.7	313
44	ShapeFinder: a software system for high-throughput quantitative analysis of nucleic acid reactivity information resolved by capillary electrophoresis. <i>Rna</i> , 2008 , 14, 1979-90	5.8	185
43	Anti-cooperative assembly of the SRP19 and SRP68/72 components of the signal recognition particle. <i>Biochemical Journal</i> , 2008 , 415, 429-37	3.8	7
42	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, 4144-5	16.4	270
41	A threefold RNA-protein interface in the signal recognition particle gates native complex assembly. <i>Journal of Molecular Biology</i> , 2007 , 369, 512-24	6.5	16
40	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, 37952-61	5.4	16
39	Structure of an RNA switch that enforces stringent retroviral genomic RNA dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 13640-5	11.5	36
38	Compartmentalization directs assembly of the signal recognition particle. <i>Biochemistry</i> , 2006 , 45, 14955-64	5.4	15
37	Architecture of a gamma retroviral genomic RNA dimer. <i>Biochemistry</i> , 2006 , 45, 12664-72	3.2	36
36	Two distinct binding modes of a protein cofactor with its target RNA. <i>Journal of Molecular Biology</i> , 2006 , 361, 771-84	6.5	50
35	Selective 2Shydroxyl acylation analyzed by primer extension (SHAPE): quantitative RNA structure analysis at single nucleotide resolution. <i>Nature Protocols</i> , 2006 , 1, 1610-6	18.8	563
34	Structure-independent and quantitative ligation of single-stranded DNA. <i>Analytical Biochemistry</i> , 2006 , 349, 242-6	3.1	21
33	RNA structure analysis at single nucleotide resolution by selective 2Shydroxyl acylation and primer extension (SHAPE). <i>Journal of the American Chemical Society</i> , 2005 , 127, 4223-31	16.4	573
32	RNA SHAPE chemistry reveals nonhierarchical interactions dominate equilibrium structural transitions in tRNA(Asp) transcripts. <i>Journal of the American Chemical Society</i> , 2005 , 127, 4659-67	16.4	133
31	Crystal structures, reactivity and inferred acylation transition states for 2Samine substituted RNA. <i>Journal of the American Chemical Society</i> , 2005 , 127, 13622-8	16.4	12
30	Facile conversion of aptamers into sensors using a 2Sribose-linked fluorophore. <i>Journal of the American Chemical Society</i> , 2005 , 127, 12766-7	16.4	64
29	Evolution from DNA to RNA recognition by the b13 LAGLIDADG maturase. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 779-87	17.6	21

28	RNA flexibility in the dimerization domain of a gamma retrovirus. <i>Nature Chemical Biology</i> , 2005 , 1, 104-111	11.7	37
27	Tris-borate is a poor counterion for RNA: a cautionary tale for RNA folding studies. <i>Nucleic Acids Research</i> , 2004 , 32, e184	20.1	12
26	Structural basis for the self-chaperoning function of an RNA collapsed state. <i>Biochemistry</i> , 2004 , 43, 1513-1518	12.86	20
25	Mechanics of DNA flexibility visualized by selective 2Samine acylation at nucleotide bulges. <i>Journal of Molecular Biology</i> , 2004 , 337, 611-9	6.5	6
24	RNA-tethered phenyl azide photocrosslinking via a short-lived indiscriminant electrophile. <i>Journal of the American Chemical Society</i> , 2003 , 125, 10850-61	16.4	57
23	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, 901-9	3.2	22
22	Fluorogenic resolution of ligand binding by a nucleic acid aptamer. <i>Journal of the American Chemical Society</i> , 2003 , 125, 12370-1	16.4	62
21	Kinetic and thermodynamic framework for assembly of the six-component b13 group I intron ribonucleoprotein catalyst. <i>Biochemistry</i> , 2003 , 42, 9980-8	3.2	17
20	Small structural costs for evolution from RNA to RNP-based catalysis. <i>Journal of Molecular Biology</i> , 2003 , 331, 57-73	6.5	2
19	Catalysis of amide synthesis by RNA phosphodiester and hydroxyl groups. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 14688-93	11.5	39
18	Recruitment of intron-encoded and co-opted proteins in splicing of the b13 group I intron RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 128-33	11.5	45
17	Chemical interrogation of mismatches in DNA-DNA and DNA-RNA duplexes under nonstringent conditions by selective 2Samine acylation. <i>Biochemistry</i> , 2002 , 41, 6866-74	3.2	12
16	A collapsed state functions to self-chaperone RNA folding into a native ribonucleoprotein complex. <i>Nature Structural Biology</i> , 2001 , 8, 135-40		35
15	Visualizing induced fit in early assembly of the human signal recognition particle. <i>Nature Structural Biology</i> , 2001 , 8, 515-20		42
14	Protein-dependent transition states for ribonucleoprotein assembly. <i>Journal of Molecular Biology</i> , 2001 , 309, 1087-100	6.5	48
13	A collapsed non-native RNA folding state. <i>Nature Structural Biology</i> , 2000 , 7, 362-6		92
12	Tagging DNA mismatches by selective 2Samine acylation. <i>Chemistry and Biology</i> , 2000 , 7, 405-10		11
11	van Hoff enthalpies without baselines. <i>Protein Science</i> , 2000 , 9, 1416-9	6.3	91

10	Mapping Local Nucleotide Flexibility by Selective Acylation of 2'-Amino Substituted RNA. <i>Journal of the American Chemical Society</i> , 2000 , 122, 216-224	16.4	31
9	Protein-facilitated RNA folding. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 336-42	8.1	110
8	Efficient protein-facilitated splicing of the yeast mitochondrial b15 intron. <i>Biochemistry</i> , 1995 , 34, 7728-33	3.2	76
7	Protein facilitation of group I intron splicing by assembly of the catalytic core and the 5'Splice site domain. <i>Cell</i> , 1995 , 82, 221-30	56.2	108
6	Major groove accessibility of RNA. <i>Science</i> , 1993 , 261, 1574-7	33.3	193
5	RNA targeting by the HIV-1 Tat protein. <i>Journal of Computer - Aided Molecular Design</i> , 1993 , 1, 225-234		4
4	RNA recognition by Tat-derived peptides: interaction in the major groove?. <i>Cell</i> , 1991 , 66, 577-88	56.2	332
3	RNP-MaP: In-cell analysis of protein interaction networks defines functional hubs in RNA		2
2	Direct detection of RNA modifications and structure using single molecule nanopore sequencing		9
1	Identifying proximal RNA interactions from cDNA-encoded crosslinks with ShapeJumper		1