

Sarah A Woodson

List of Publications by Year in descending order

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156
papers

9,420
citations

23500

58
h-index

46693

89
g-index

172
all docs

172
docs citations

172
times ranked

5030
citing authors

#	ARTICLE	IF	CITATIONS
1	Diversity of bacterial small RNAs drives competitive strategies for a mutual chaperone. <i>Nature Communications</i> , 2022, 13, 2449.	5.8	13
2	Stepwise sRNA targeting of structured bacterial mRNAs leads to abortive annealing. <i>Molecular Cell</i> , 2021, 81, 1988-1999.e4.	4.5	18
3	A roadmap for rRNA folding and assembly during transcription. <i>Trends in Biochemical Sciences</i> , 2021, 46, 889-901.	3.7	32
4	Stabilization of Hfq-mediated translational repression by the co-repressor Crc in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2021, 49, 7075-7087.	6.5	24
5	sRNA Toxicity and Perturbation of rRNA Processing in Spinocerebellar Ataxia Type 2. <i>Movement Disorders</i> , 2021, 36, 2519-2529.	2.2	11
6	RbfA and IF3 couple ribosome biogenesis and translation initiation to increase stress tolerance. <i>Nucleic Acids Research</i> , 2020, 48, 359-372.	6.5	26
7	Ribosomes clear the way for siRNA targeting. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 775-777.	3.6	2
8	Light-controlled twister ribozyme with single-molecule detection resolves RNA function in time and space. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 12080-12086.	3.3	15
9	Quantitative Analysis of RNA Chaperone Activity by Native Gel Electrophoresis and Fluorescence Spectroscopy. <i>Methods in Molecular Biology</i> , 2020, 2106, 19-39.	0.4	2
10	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , 2019, 47, 8301-8317.	6.5	34
11	A newborn RNA switches its fate. <i>Nature Chemical Biology</i> , 2019, 15, 1031-1032.	3.9	3
12	Monitoring co-transcriptional folding of riboswitches through helicase unwinding. <i>Methods in Enzymology</i> , 2019, 623, 209-227.	0.4	2
13	<i>Caulobacter crescentus</i> Hfq structure reveals a conserved mechanism of RNA annealing regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10978-10987.	3.3	20
14	Transcription Increases the Cooperativity of Ribonucleoprotein Assembly. <i>Cell</i> , 2019, 179, 1370-1381.e12.	13.5	56
15	Hfq chaperone brings speed dating to bacterial sRNA. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1475.	3.2	155
16	A metastable rRNA junction essential for bacterial 30S biogenesis. <i>Nucleic Acids Research</i> , 2018, 46, 5182-5194.	6.5	13
17	The <i>Pseudomonas aeruginosa</i> PrrF1 and PrrF2 Small Regulatory RNAs Promote 2-Alkyl-4-Quinolone Production through Redundant Regulation of the <i>antR</i> mRNA. <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	43
18	Effects of Preferential Counterion Interactions on the Specificity of RNA Folding. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 5726-5732.	2.1	1

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19	The Hfq chaperone helps the ribosome mature. <i>EMBO Journal</i> , 2018, 37, .	3.5	6
20	Mimicking Co-Transcriptional RNA Folding Using a Superhelicase. <i>Journal of the American Chemical Society</i> , 2018, 140, 10067-10070.	6.6	44
21	Proteins That Chaperone RNA Regulation. <i>Microbiology Spectrum</i> , 2018, 6, .	1.2	59
22	Time-Resolved Hydroxyl Radical Footprinting of RNA with X-Rays. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2018, 73, e52.	0.5	9
23	Metals induce transient folding and activation of the twister ribozyme. <i>Nature Chemical Biology</i> , 2017, 13, 1109-1114.	3.9	33
24	Probing RNA Folding Pathways by RNA Fingerprinting. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2017, 70, 11.4.1-11.4.19.	0.5	0
25	Evolution of protein-coupled RNA dynamics during hierarchical assembly of ribosomal complexes. <i>Nature Communications</i> , 2017, 8, 492.	5.8	30
26	Acidic C-terminal domains autoregulate the RNA chaperone Hfq. <i>ELife</i> , 2017, 6, .	2.8	53
27	Probing the structure of ribosome assembly intermediates in vivo using DMS and hydroxyl radical footprinting. <i>Methods</i> , 2016, 103, 49-56.	1.9	27
28	Arginine Patch Predicts the RNA Annealing Activity of Hfq from Gram-Negative and Gram-Positive Bacteria. <i>Journal of Molecular Biology</i> , 2016, 428, 2259-2264.	2.0	36
29	C-terminal domain of the RNA chaperone Hfq drives sRNA competition and release of target RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E6089-E6096.	3.3	92
30	Entropic stabilization of folded RNA in crowded solutions measured by SAXS. <i>Nucleic Acids Research</i> , 2016, 44, gkw597.	6.5	18
31	Light-Triggered RNA Annealing by an RNA Chaperone. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 7281-7284.	7.2	27
32	RNA folding retrospective: lessons from ribozymes big and small. <i>Rna</i> , 2015, 21, 502-503.	1.6	3
33	Molecular crowding overcomes the destabilizing effects of mutations in a bacterial ribozyme. <i>Nucleic Acids Research</i> , 2015, 43, 1170-1176.	6.5	23
34	Acidic Residues in the Hfq Chaperone Increase the Selectivity of sRNA Binding and Annealing. <i>Journal of Molecular Biology</i> , 2015, 427, 3491-3500.	2.0	28
35	Charge screening in RNA: an integral route for dynamical enhancements. <i>Soft Matter</i> , 2015, 11, 8741-8745.	1.2	4
36	Differential effects of ribosomal proteins and Mg ²⁺ ions on a conformational switch during 30S ribosome 5'-domain assembly. <i>Rna</i> , 2015, 21, 1859-1865.	1.6	16

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37	Preface. <i>Methods in Enzymology</i> , 2015, 558, xix-xxi.	0.4	0
38	Fluorescence Reporters for Hfq Oligomerization and RNA Annealing. <i>Methods in Molecular Biology</i> , 2015, 1259, 369-383.	0.4	4
39	Positional Effects of AAN Motifs in rpoS Regulation by sRNAs and Hfq. <i>Journal of Molecular Biology</i> , 2014, 426, 275-285.	2.0	43
40	Protein-guided RNA dynamics during early ribosome assembly. <i>Nature</i> , 2014, 506, 334-338.	13.7	133
41	Increased Ribozyme Activity in Crowded Solutions. <i>Journal of Biological Chemistry</i> , 2014, 289, 2972-2977.	1.6	50
42	An improved surface passivation method for single-molecule studies. <i>Nature Methods</i> , 2014, 11, 1233-1236.	9.0	120
43	Structural model of an mRNA in complex with the bacterial chaperone Hfq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17134-17139.	3.3	70
44	Introductory editorial: Biopolymers celebrates 50 years of nucleic acids research. <i>Biopolymers</i> , 2013, 99, n/a-n/a.	1.2	0
45	In Vivo X-Ray Footprinting of Pre-30S Ribosomes Reveals Chaperone-Dependent Remodeling of Late Assembly Intermediates. <i>Molecular Cell</i> , 2013, 52, 506-516.	4.5	96
46	Crowders Perturb the Entropy of RNA Energy Landscapes to Favor Folding. <i>Journal of the American Chemical Society</i> , 2013, 135, 10055-10063.	6.6	49
47	Conserved arginines on the rim of Hfq catalyze base pair formation and exchange. <i>Nucleic Acids Research</i> , 2013, 41, 7536-7546.	6.5	105
48	Specific contacts between protein S4 and ribosomal RNA are required at multiple stages of ribosome assembly. <i>Rna</i> , 2013, 19, 574-585.	1.6	21
49	Hfq proximity and orientation controls RNA annealing. <i>Nucleic Acids Research</i> , 2012, 40, 8690-8697.	6.5	46
50	Folding path of P5abc RNA involves direct coupling of secondary and tertiary structures. <i>Nucleic Acids Research</i> , 2012, 40, 8011-8020.	6.5	36
51	Antiproliferative small-molecule inhibitors of transcription factor LSF reveal oncogene addiction to LSF in hepatocellular carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4503-4508.	3.3	37
52	Assembly of the Five-Way Junction in the Ribosomal Small Subunit Using Hybrid MD-Go Simulations. <i>Journal of Physical Chemistry B</i> , 2012, 116, 6819-6831.	1.2	22
53	RNase Footprinting of Protein Binding Sites on an mRNA Target of Small RNAs. <i>Methods in Molecular Biology</i> , 2012, 905, 213-224.	0.4	20
54	Hexamer to Monomer Equilibrium of E. coli Hfq in Solution and Its Impact on RNA Annealing. <i>Journal of Molecular Biology</i> , 2012, 417, 406-412.	2.0	33

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55	Cooperative Tertiary Interaction Network Guides RNA Folding. <i>Cell</i> , 2012, 149, 348-357.	13.5	88
56	RNA Folding in Crowded Solutions. <i>Biophysical Journal</i> , 2012, 102, 3a-4a.	0.2	0
57	Single Molecule Views of the Ribosome Assembly. <i>Biophysical Journal</i> , 2012, 102, 645a.	0.2	0
58	Rendering RNA in 3D. <i>Nature Methods</i> , 2012, 9, 552-553.	9.0	0
59	Major role for mRNA binding and restructuring in sRNA recruitment by Hfq. <i>Rna</i> , 2011, 17, 1544-1550.	1.6	68
60	The RNA Chaperone Hfq Makes a Transient Ternary Complex with RNA Strands to Facilitate RNA Annealing. <i>Biophysical Journal</i> , 2011, 100, 231a.	0.2	0
61	The Dynamics of Unfolded versus Folded tRNA: The Role of Electrostatic Interactions. <i>Journal of the American Chemical Society</i> , 2011, 133, 16406-16409.	6.6	25
62	RNA Folding Pathways and the Self-Assembly of Ribosomes. <i>Accounts of Chemical Research</i> , 2011, 44, 1312-1319.	7.6	74
63	Slow Formation of Stable Complexes during Coincubation of Minimal rRNA and Ribosomal Protein S4. <i>Journal of Molecular Biology</i> , 2011, 412, 453-465.	2.0	23
64	New era of molecular structure and dynamics from solution scattering experiments. <i>Biopolymers</i> , 2011, 95, 503-504.	1.2	2
65	Rapid binding and release of Hfq from ternary complexes during RNA annealing. <i>Nucleic Acids Research</i> , 2011, 39, 5193-5202.	6.5	67
66	Positive regulation by small RNAs and the role of Hfq. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 9602-9607.	3.3	253
67	Taming free energy landscapes with RNA chaperones. <i>RNA Biology</i> , 2010, 7, 677-686.	1.5	87
68	Molecular Crowding Stabilizes Folded RNA Structure by the Excluded Volume Effect. <i>Journal of the American Chemical Society</i> , 2010, 132, 8690-8696.	6.6	178
69	Multistage Collapse of a Bacterial Ribozyme Observed by Time-Resolved Small-Angle X-ray Scattering. <i>Journal of the American Chemical Society</i> , 2010, 132, 10148-10154.	6.6	50
70	Dynamics of Biological Macromolecules: Not a Simple Slaving by Hydration Water. <i>Biophysical Journal</i> , 2010, 98, 1321-1326.	0.2	103
71	Compact Intermediates in RNA Folding. <i>Annual Review of Biophysics</i> , 2010, 39, 61-77.	4.5	176
72	A minimized rRNA-binding site for ribosomal protein S4 and its implications for 30S assembly. <i>Nucleic Acids Research</i> , 2009, 37, 1886-1896.	6.5	26

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73	Effect of salt and RNA structure on annealing and strand displacement by Hfq. <i>Nucleic Acids Research</i> , 2009, 37, 6205-6213.	6.5	40
74	S16 throws a conformational switch during assembly of 30S 5â€² domain. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 438-445.	3.6	35
75	Structural Rearrangements Linked to Global Folding Pathways of the Azoarcus Group I Ribozyme. <i>Journal of Molecular Biology</i> , 2009, 386, 1167-1178.	2.0	37
76	Global Stabilization of rRNA Structure by Ribosomal Proteins S4, S17, and S20. <i>Journal of Molecular Biology</i> , 2009, 392, 666-677.	2.0	41
77	Metal Ion Dependence of Cooperative Collapse Transitions in RNA. <i>Journal of Molecular Biology</i> , 2009, 393, 753-764.	2.0	86
78	Dynamics of tRNA at Different Levels of Hydration. <i>Biophysical Journal</i> , 2009, 96, 2755-2762.	0.2	81
79	Analysis of RNA Folding by Native Polyacrylamide Gel Electrophoresis. <i>Methods in Enzymology</i> , 2009, 469, 189-208.	0.4	41
80	Structural Analysis of RNA in Living Cells by In Vivo Synchrotron X-Ray Footprinting. <i>Methods in Enzymology</i> , 2009, 468, 239-258.	0.4	32
81	Group I Ribozymes as a Paradigm for RNA Folding and Evolution. <i>Springer Series in Biophysics</i> , 2009, , 145-166.	0.4	0
82	RNA folding and ribosome assembly. <i>Current Opinion in Chemical Biology</i> , 2008, 12, 667-673.	2.8	94
83	Concurrent nucleation of 16S folding and induced fit in 30S ribosome assembly. <i>Nature</i> , 2008, 455, 1268-1272.	13.7	161
84	Interactions of recombinant HMGB proteins with branched RNA substrates. <i>Biochemical and Biophysical Research Communications</i> , 2008, 377, 262-267.	1.0	15
85	Tertiary Interactions Determine the Accuracy of RNA Folding. <i>Journal of the American Chemical Society</i> , 2008, 130, 1296-1303.	6.6	92
86	The <i>rpoS</i> mRNA leader recruits Hfq to facilitate annealing with DsrA sRNA. <i>Rna</i> , 2008, 14, 1907-1917.	1.6	190
87	Loop dependence of the stability and dynamics of nucleic acid hairpins. <i>Nucleic Acids Research</i> , 2007, 36, 1098-1112.	6.5	90
88	Communication Between RNA Folding Domains Revealed by Folding of Circularly Permuted Ribozymes. <i>Journal of Molecular Biology</i> , 2007, 373, 197-210.	2.0	12
89	Charge Density of Divalent Metal Cations Determines RNA Stability. <i>Journal of the American Chemical Society</i> , 2007, 129, 2676-2682.	6.6	169
90	Dynamic Transition in tRNA is Solvent Induced. <i>Journal of the American Chemical Society</i> , 2006, 128, 32-33.	6.6	105

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91	Counterion Charge Density Determines the Position and Plasticity of RNA Folding Transition States. <i>Journal of Molecular Biology</i> , 2006, 359, 446-454.	2.0	59
92	Hydroxyl radical footprinting in vivo: mapping macromolecular structures with synchrotron radiation. <i>Nucleic Acids Research</i> , 2006, 34, e64-e64.	6.5	69
93	Self-splicing of a group I intron reveals partitioning of native and misfolded RNA populations in yeast. <i>Rna</i> , 2006, 12, 2149-2159.	1.6	29
94	Metal ions and RNA folding: a highly charged topic with a dynamic future. <i>Current Opinion in Chemical Biology</i> , 2005, 9, 104-109.	2.8	337
95	Assembly line inspection. <i>Nature</i> , 2005, 438, 566-567.	13.7	3
96	Structure and assembly of group I introns. <i>Current Opinion in Structural Biology</i> , 2005, 15, 324-330.	2.6	93
97	Persistence Length Changes Dramatically as RNA Folds. <i>Physical Review Letters</i> , 2005, 95, 268303.	2.9	81
98	Molecular beacons as probes of RNA unfolding under native conditions. <i>Nucleic Acids Research</i> , 2005, 33, 5763-5770.	6.5	28
99	Protein-independent Folding Pathway of the 16S rRNA 5' Domain. <i>Journal of Molecular Biology</i> , 2005, 351, 508-519.	2.0	75
100	RNA Tertiary Interactions Mediate Native Collapse of a Bacterial Group I Ribozyme. <i>Journal of Molecular Biology</i> , 2005, 353, 1199-1209.	2.0	66
101	Intracellular folding of the Tetrahymena group I intron depends on exon sequence and promoter choice. <i>Rna</i> , 2004, 10, 1526-1532.	1.6	32
102	Compaction of a Bacterial Group I Ribozyme Coincides with the Assembly of Core Helices. <i>Biochemistry</i> , 2004, 43, 1746-1753.	1.2	58
103	Architecture and folding mechanism of the Azoarcus Group I Pre-tRNA. <i>Journal of Molecular Biology</i> , 2004, 339, 41-51.	2.0	56
104	Folding of the Tetrahymena Ribozyme by Polyamines: Importance of Counterion Valence and Size. <i>Journal of Molecular Biology</i> , 2004, 341, 27-36.	2.0	65
105	Cycling of the Sm-like Protein Hfq on the DsrA Small Regulatory RNA. <i>Journal of Molecular Biology</i> , 2004, 344, 1211-1223.	2.0	177
106	EXPERIMENTAL APPROACHES TO RNA FOLDING. , 2004, , .		1
107	Perturbed Folding Kinetics of Circularly Permuted RNAs with Altered Topology. <i>Journal of Molecular Biology</i> , 2003, 328, 385-394.	2.0	31
108	Structural Requirement for Mg ²⁺ Binding in the Group I Intron Core. <i>Journal of Molecular Biology</i> , 2003, 329, 229-238.	2.0	79

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109	Effect of transcription on folding of the Tetrahymena ribozyme. <i>Rna</i> , 2003, 9, 722-733.	1.6	96
110	Assembly of core helices and rapid tertiary folding of a small bacterial group I ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1574-1579.	3.3	136
111	Distribution of rRNA Introns in the Three-dimensional Structure of the Ribosome. <i>Journal of Molecular Biology</i> , 2002, 323, 35-52.	2.0	58
112	Role of counterion condensation in folding of the Tetrahymena ribozyme. I. Equilibrium stabilization by cations. <i>Journal of Molecular Biology</i> , 2001, 306, 1157-1166.	2.0	179
113	Role of counterion condensation in folding of the Tetrahymena ribozyme II. Counterion-dependence of folding kinetics. <i>Journal of Molecular Biology</i> , 2001, 309, 57-68.	2.0	114
114	EARLY EVENTS IN RNA FOLDING. <i>Annual Review of Physical Chemistry</i> , 2001, 52, 751-762.	4.8	195
115	Time-Resolved Hydroxyl Radical Footprinting of RNA with X-rays. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2001, 6, Unit 11.6.	0.5	3
116	[22] Time-resolved synchrotron X-ray footprinting and its application to RNA folding. <i>Methods in Enzymology</i> , 2000, 317, 353-368.	0.4	72
117	Compact but disordered states of RNA. , 2000, 7, 349-352.		38
118	Maximizing RNA folding rates: A balancing act. <i>Rna</i> , 2000, 6, 790-794.	1.6	46
119	Refolding of rRNA exons enhances dissociation of the Tetrahymena intron. <i>Rna</i> , 2000, 6, 1248-1256.	1.6	25
120	Fast folding of a ribozyme by stabilizing core interactions: evidence for multiple folding pathways in RNA 1 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2000, 296, 133-144.	2.0	100
121	Probing RNA Folding Pathways by RNA Fingerprinting. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2000, 2, Unit 11.4.	0.5	3
122	Folding Mechanism of the Tetrahymena Ribozyme P4 ^â P6 Domain. <i>Biochemistry</i> , 2000, 39, 10975-10985.	1.2	91
123	Multiple Folding Pathways for the P4 ^â P6 RNA Domain. <i>Biochemistry</i> , 2000, 39, 12465-12475.	1.2	91
124	Sequence specificity of in vivo reverse splicing of the Tetrahymena group I intron. <i>Rna</i> , 1999, 5, 1-13.	1.6	37
125	The RNA World, second edition, edited by Raymond F. Gesteland, Thomas R. Cech, and John F. Atkins. 1999. Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press. Hardcover, 709 pp. \$129.. <i>Rna</i> , 1999, 5, 1133-1134.	1.6	1
126	Magnesium-dependent folding of self-splicing RNA: Exploring the link between cooperativity, thermodynamics, and kinetics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999, 96, 6149-6154.	3.3	91

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127	Facilitation of Group I Splicing in Vivo: Misfolding of the Tetrahymena IVS and the Role of Ribosomal RNA Exons. <i>Journal of Molecular Biology</i> , 1999, 292, 557-567.	2.0	39
128	The effect of long-range loop-loop interactions on folding of the Tetrahymena self-splicing RNA. <i>Journal of Molecular Biology</i> , 1999, 294, 955-965.	2.0	69
129	Structure and dynamics of ribosomal RNA. <i>Current Opinion in Structural Biology</i> , 1998, 8, 294-300.	2.6	17
130	Folding intermediates of a self-splicing RNA: mispairing of the catalytic core. <i>Journal of Molecular Biology</i> , 1998, 280, 597-609.	2.0	197
131	RNA Folding at Millisecond Intervals by Synchrotron Hydroxyl Radical Footprinting. <i>Science</i> , 1998, 279, 1940-1943.	6.0	378
132	[19] Following the folding of RNA with time-resolved synchrotron X-ray footprinting. <i>Methods in Enzymology</i> , 1998, 295, 379-402.	0.4	74
133	Destabilizing effect of an rRNA stem-loop on an attenuator hairpin in the 5' exon of the Tetrahymena pre-rRNA. <i>Rna</i> , 1998, 4, 901-914.	1.6	30
134	Integration of the Tetrahymena group I intron into bacterial rRNA by reverse splicing in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998, 95, 2134-2139.	3.3	63
135	Time-resolved synchrotron X-ray "footprinting", a new approach to the study of nucleic acid structure and function: application to protein-DNA interactions and RNA folding 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1997, 266, 144-159.	2.0	174
136	Folding of RNA involves parallel pathways. <i>Journal of Molecular Biology</i> , 1997, 273, 7-13.	2.0	192
137	Examining the conformational dynamics of macromolecules with time-resolved synchrotron X-ray "footprinting". <i>Structure</i> , 1997, 5, 865-869.	1.6	46
138	Analysis of Rate-Determining Conformational Changes during Self-Splicing of the Tetrahymena Intron. <i>Biochemistry</i> , 1996, 35, 13469-13477.	1.2	40
139	Macromolecular complexes: How RNA and protein get together. <i>Current Biology</i> , 1996, 6, 23-25.	1.8	4
140	Requirements for self-splicing of a group I intron from <i>Physarum polycephalum</i> . <i>Nucleic Acids Research</i> , 1994, 22, 4315-4320.	6.5	12
141	Fingerprinting the folding of a group I precursor RNA.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 9675-9679.	3.3	67
142	A highly sensitive probe for guanine N7 in folded structures of RNA: application to tRNA ^{Phe} and Tetrahymena group I intron. <i>Biochemistry</i> , 1993, 32, 7610-7616.	1.2	56
143	Self-splicing of the Tetrahymena pre-rRNA is decreased by misfolding during transcription. <i>Biochemistry</i> , 1993, 32, 14062-14067.	1.2	59
144	A primer extension assay for modification of guanine by Ni(II) complexes. <i>Nucleic Acids Research</i> , 1993, 21, 5524-5525.	6.5	39

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145	Exon sequence distant from the splice junction are required for efficient self-splicing of the Tetrahymena IVa. <i>Nucleic Acids Research</i> , 1992, 20, 4027-4032.	6.5	36
146	Alternative secondary structures in the 5' exon affect both forward and reverse self-splicing of the Tetrahymena intervening sequence RNA. <i>Biochemistry</i> , 1991, 30, 2042-2050.	1.2	89
147	Symposium 3: Non-enzymatic biocatalysts in nature and biotechnology. <i>Fresenius' Journal of Analytical Chemistry</i> , 1990, 337, 12-14.	1.5	0
148	Conformation of a bulge-containing oligomer from a hot-spot sequence by NMR and energy minimization. <i>Biopolymers</i> , 1989, 28, 1149-1177.	1.2	35
149	Reverse self-splicing of the Tetrahymena group I intron: Implication for the directionality of splicing and for intron transposition. <i>Cell</i> , 1989, 57, 335-345.	13.5	198
150	DNA sequence specificity of mitomycin cross-linking. <i>Biochemistry</i> , 1989, 28, 3901-3907.	1.2	92
151	Binding of 9-aminoacridine to bulged-base DNA oligomers from a frame-shift hot spot. <i>Biochemistry</i> , 1988, 27, 8904-8914.	1.2	53
152	Structural model for an oligonucleotide containing a bulged guanosine by NMR and energy minimization. <i>Biochemistry</i> , 1988, 27, 3130-3141.	1.2	100
153	Preferential location of bulged guanosine internal to a G.C tract by proton NMR. <i>Biochemistry</i> , 1988, 27, 436-445.	1.2	46
154	Proton nuclear magnetic resonance studies on bulge-containing DNA oligonucleotides from a mutational hot-spot sequence. <i>Biochemistry</i> , 1987, 26, 904-912.	1.2	72
155	Stereochemistry in trivalent nitrogen compounds. 39. Configurational biasing of tertiary amide ionophores by alkali metal chelation. <i>Journal of the American Chemical Society</i> , 1983, 105, 7252-7255.	6.6	7
156	Proteins That Chaperone RNA Regulation. , 0, , 383-397.		7