

Philip C Bevilacqua

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.

163
papers

7,832
citations

49
h-index

82
g-index

173
ext. papers

8,976
ext. citations

8.6
avg, IF

6.36
L-index

#	Paper	IF	Citations
163	Experimental demonstration and pan-structurome prediction of climate-associated riboSNitches in Arabidopsis.. <i>Genome Biology</i> , 2022 , 23, 101	18.3	2
162	RNA Multimerization as an Organizing Force for Liquid-Liquid Phase Separation. <i>Rna</i> , 2021 ,	5.8	2
161	Inverse RNA Folding Workflow to Design and Test Ribozymes that Include Pseudoknots. <i>Methods in Molecular Biology</i> , 2021 , 2167, 113-143	1.4	
160	RNA sequence and structure control assembly and function of RNA condensates. <i>Rna</i> , 2021 , 27, 1589-1608	6.8	1
159	Investigation of the p of the Nucleophilic O2Tof the Hairpin Ribozyme. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 11869-11883	3.4	1
158	Functional Roles of Chelated Magnesium Ions in RNA Folding and Function. <i>Biochemistry</i> , 2021 , 60, 2374-2386	5.2	5
157	Amino Acid Specific Nonenzymatic Montmorillonite-Promoted RNA Polymerization. <i>ChemSystemsChem</i> , 2021 , 3, e2000060	3.1	1
156	Measuring the activity and structure of functional RNAs inside compartments formed by liquid-liquid phase separation. <i>Methods in Enzymology</i> , 2021 , 646, 307-327	1.7	1
155	Long Tracts of Guanines Drive Aggregation of RNA G-Quadruplexes in the Presence of Spermine. <i>Biochemistry</i> , 2021 , 60, 2715-2726	3.2	2
154	Structure-seq2 probing of RNA structure upon amino acid starvation reveals both known and novel RNA switches in. <i>Rna</i> , 2020 , 26, 1431-1447	5.8	7
153	Tissue-specific changes in the RNA structurome mediate salinity response in. <i>Rna</i> , 2020 , 26, 492-511	5.8	12
152	Prebiotically-relevant low polyion multivalency can improve functionality of membraneless compartments. <i>Nature Communications</i> , 2020 , 11, 5949	17.4	26
151	CsrA-Mediated Translational Activation of Expression in Escherichia coli. <i>MBio</i> , 2020 , 11,	7.8	8
150	Cellular Concentrations of Nucleotide Diphosphate-Chelated Magnesium Ions Accelerate Catalysis by RNA and DNA Enzymes. <i>Biochemistry</i> , 2019 , 58, 3971-3979	3.2	7
149	Probing RNA structure in vivo. <i>Current Opinion in Structural Biology</i> , 2019 , 59, 151-158	8.1	36
148	Template-directed RNA polymerization and enhanced ribozyme catalysis inside membraneless compartments formed by coacervates. <i>Nature Communications</i> , 2019 , 10, 490	17.4	115
147	Polyanion-Assisted Ribozyme Catalysis Inside Complex Coacervates. <i>ACS Chemical Biology</i> , 2019 , 14, 1243-1248	4.9	33

146	An Ontology for Facilitating Discussion of Catalytic Strategies of RNA-Cleaving Enzymes. <i>ACS Chemical Biology</i> , 2019 , 14, 1068-1076	4.9	25
145	In Vivo Genome-Wide RNA Structure Probing with Structure-seq. <i>Methods in Molecular Biology</i> , 2019 , 1933, 305-341	1.4	5
144	Single-nucleotide control of tRNA folding cooperativity under near-cellular conditions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 23075-23082	11.5	6
143	Small Molecule Rescue and Glycosidic Conformational Analysis of the Twister Ribozyme. <i>Biochemistry</i> , 2019 , 58, 4857-4868	3.2	2
142	mRNA structural elements immediately upstream of the start codon dictate dependence upon eIF4A helicase activity. <i>Genome Biology</i> , 2019 , 20, 300	18.3	18
141	In vivo RNA structural probing of uracil and guanine base-pairing by 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide (EDC). <i>Rna</i> , 2019 , 25, 147-157	5.8	21
140	Design of highly active double-pseudoknotted ribozymes: a combined computational and experimental study. <i>Nucleic Acids Research</i> , 2019 , 47, 29-42	20.1	3
139	StructureFold2: Bringing chemical probing data into the computational fold of RNA structural analysis. <i>Methods</i> , 2018 , 143, 12-15	4.6	13
138	RNA structure: A LASER-focused view into cells. <i>Nature Chemical Biology</i> , 2018 , 14, 200-201	11.7	2
137	Complexity in pH-Dependent Ribozyme Kinetics: Dark pK Shifts and Wavy Rate-pH Profiles. <i>Biochemistry</i> , 2018 , 57, 483-488	3.2	18
136	Modeling RNA secondary structure folding ensembles using SHAPE mapping data. <i>Nucleic Acids Research</i> , 2018 , 46, 314-323	20.1	47
135	Physical Principles and Extant Biology Reveal Roles for RNA-Containing Membraneless Compartments in Origins of Life Chemistry. <i>Biochemistry</i> , 2018 , 57, 2509-2519	3.2	76
134	Glyoxals as in vivo RNA structural probes of guanine base-pairing. <i>Rna</i> , 2018 , 24, 114-124	5.8	20
133	Molecular Mechanism for Folding Cooperativity of Functional RNAs in Living Organisms. <i>Biochemistry</i> , 2018 , 57, 2994-3002	3.2	4
132	Cellular Small Molecules Contribute to Twister Ribozyme Catalysis. <i>Journal of the American Chemical Society</i> , 2018 , 140, 10578-10582	16.4	9
131	Cellular conditions of weakly chelated magnesium ions strongly promote RNA stability and catalysis. <i>Nature Communications</i> , 2018 , 9, 2149	17.4	30
130	Elucidation of Catalytic Strategies of Small Nucleolytic Ribozymes From Comparative Analysis of Active Sites. <i>ACS Catalysis</i> , 2018 , 8, 314-327	13.1	24
129	Genome-wide RNA structurome reprogramming by acute heat shock globally regulates mRNA abundance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 12170-12175	11.5	42

128	Technique Development for Probing RNA Structure In Vivo and Genome-Wide. <i>Cold Spring Harbor Perspectives in Biology</i> , 2018 , 10,	10.2	22
127	The GlcN6P cofactor plays multiple catalytic roles in the glmS ribozyme. <i>Nature Chemical Biology</i> , 2017 , 13, 439-445	11.7	37
126	Cooperative Interactions in the Hammerhead Ribozyme Drive pK Shifting of G12 and Its Stacked Base C17. <i>Biochemistry</i> , 2017 , 56, 2537-2548	3.2	23
125	Probing fast ribozyme reactions under biological conditions with rapid quench-flow kinetics. <i>Methods</i> , 2017 , 120, 125-134	4.6	2
124	Activation of the glmS Ribozyme Nucleophile via Overdetermined Hydrogen Bonding. <i>Biochemistry</i> , 2017 , 56, 4313-4317	3.2	13
123	Structure-seq2: sensitive and accurate genome-wide profiling of RNA structure in vivo. <i>Nucleic Acids Research</i> , 2017 , 45, e135	20.1	68
122	Cooperative RNA Folding under Cellular Conditions Arises From Both Tertiary Structure Stabilization and Secondary Structure Destabilization. <i>Biochemistry</i> , 2017 , 56, 3422-3433	3.2	23
121	Eliminating blurry bands in gels with a simple cost-effective repair to the gel cassette. <i>Rna</i> , 2016 , 22, 1929-1930	5.8	1
120	Genome-Wide Analysis of RNA Secondary Structure. <i>Annual Review of Genetics</i> , 2016 , 50, 235-266	14.5	146
119	Discriminating Self and Non-Self by RNA: Roles for RNA Structure, Misfolding, and Modification in Regulating the Innate Immune Sensor PKR. <i>Accounts of Chemical Research</i> , 2016 , 49, 1242-9	24.3	38
118	Steady-State and Time-Resolved Studies into the Origin of the Intrinsic Fluorescence of G-Quadruplexes. <i>Journal of Physical Chemistry B</i> , 2016 , 120, 5146-58	3.4	15
117	Molecular Dynamics Study of Twister Ribozyme: Role of Mg(2+) Ions and the Hydrogen-Bonding Network in the Active Site. <i>Biochemistry</i> , 2016 , 55, 3834-46	3.2	24
116	Bacterial Riboswitches and Ribozymes Potently Activate the Human Innate Immune Sensor PKR. <i>ACS Chemical Biology</i> , 2016 , 11, 1118-27	4.9	13
115	Polyamine/Nucleotide Coacervates Provide Strong Compartmentalization of Mg ²⁺ , Nucleotides, and RNA. <i>Langmuir</i> , 2016 , 32, 2041-9	4	84
114	Protein Structure Is Related to RNA Structural Reactivity In Vivo. <i>Journal of Molecular Biology</i> , 2016 , 428, 758-766	6.5	10
113	A High-Throughput Biological Calorimetry Core: Steps to Startup, Run, and Maintain a Multiuser Facility. <i>Methods in Enzymology</i> , 2016 , 567, 435-60	1.7	5
112	Bridging the gap between in vitro and in vivo RNA folding. <i>Quarterly Reviews of Biophysics</i> , 2016 , 49, e10	7	70
111	Assessing the Potential Effects of Active Site Mg Ions in the glmS Ribozyme-Cofactor Complex. <i>Journal of Physical Chemistry Letters</i> , 2016 , 7, 3984-3988	6.4	11

110	Genome-wide profiling of in vivo RNA structure at single-nucleotide resolution using structure-seq. <i>Nature Protocols</i> , 2015 , 10, 1050-66	18.8	63
109	Inverse thio effects in the hepatitis delta virus ribozyme reveal that the reaction pathway is controlled by metal ion charge density. <i>Biochemistry</i> , 2015 , 54, 2160-75	3.2	40
108	StructureFold: genome-wide RNA secondary structure mapping and reconstruction in vivo. <i>Bioinformatics</i> , 2015 , 31, 2668-75	7.2	36
107	The RNA structurome: transcriptome-wide structure probing with next-generation sequencing. <i>Trends in Biochemical Sciences</i> , 2015 , 40, 221-32	10.3	109
106	A stable RNA G-quadruplex within the 5TUTR of Arabidopsis thaliana ATR mRNA inhibits translation. <i>Biochemical Journal</i> , 2015 , 467, 91-102	3.8	51
105	Amyloid Precursor Protein Translation Is Regulated by a 3TUTR Guanine Quadruplex. <i>PLoS ONE</i> , 2015 , 10, e0143160	3.7	28
104	Mechanistic Analysis of Activation of the Innate Immune Sensor PKR by Bacterial RNA. <i>Journal of Molecular Biology</i> , 2015 , 427, 3501-3515	6.5	8
103	The wonder of RNA: a personal reflection of the last 20 years. <i>Rna</i> , 2015 , 21, 515-6	5.8	
102	Role of the active site guanine in the glmS ribozyme self-cleavage mechanism: quantum mechanical/molecular mechanical free energy simulations. <i>Journal of the American Chemical Society</i> , 2015 , 137, 784-98	16.4	48
101	In vivo genome-wide profiling of RNA secondary structure reveals novel regulatory features. <i>Nature</i> , 2014 , 505, 696-700	50.4	521
100	Molecular crowders and cosolutes promote folding cooperativity of RNA under physiological ionic conditions. <i>Rna</i> , 2014 , 20, 331-47	5.8	47
99	Quantum mechanical/molecular mechanical free energy simulations of the self-cleavage reaction in the hepatitis delta virus ribozyme. <i>Journal of the American Chemical Society</i> , 2014 , 136, 1483-96	16.4	57
98	Bioreactor droplets from liposome-stabilized all-aqueous emulsions. <i>Nature Communications</i> , 2014 , 5, 4670	17.4	164
97	Experimental approaches for measuring pKa _T in RNA and DNA. <i>Methods in Enzymology</i> , 2014 , 549, 189-219		54
96	Thio effects and an unconventional metal ion rescue in the genomic hepatitis delta virus ribozyme. <i>Biochemistry</i> , 2013 , 52, 6499-514	3.2	49
95	pKa shifting in double-stranded RNA is highly dependent upon nearest neighbors and bulge positioning. <i>Biochemistry</i> , 2013 , 52, 7470-6	3.2	20
94	Determination of in vivo RNA structure in low-abundance transcripts. <i>Nature Communications</i> , 2013 , 4, 2971	17.4	93
93	Molecular crowding favors reactivity of a human ribozyme under physiological ionic conditions. <i>Biochemistry</i> , 2013 , 52, 8187-97	3.2	36

92	Identification of the catalytic Mg ²⁺ ion in the hepatitis delta virus ribozyme. <i>Biochemistry</i> , 2013 , 52, 557-62	3.6	34
91	Decrease in RNA Folding Cooperativity by Deliberate Population of Intermediates in RNA G-Quadruplexes. <i>Angewandte Chemie</i> , 2013 , 125, 711-714	3.6	5
90	Decrease in RNA folding cooperativity by deliberate population of intermediates in RNA G-quadruplexes. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 683-6	16.4	23
89	A hybridization-based approach for quantitative and low-bias single-stranded DNA ligation. <i>Analytical Biochemistry</i> , 2013 , 435, 181-6	3.1	29
88	Effect of loop sequence and loop length on the intrinsic fluorescence of G-quadruplexes. <i>Biochemistry</i> , 2013 , 52, 3019-21	3.2	41
87	A simple fluorescence method for pK(a) determination in RNA and DNA reveals highly shifted pK(a)s. <i>Journal of the American Chemical Society</i> , 2013 , 135, 7390-3	16.4	47
86	Native tertiary structure and nucleoside modifications suppress tRNA ^{fMet} intrinsic ability to activate the innate immune sensor PKR. <i>PLoS ONE</i> , 2013 , 8, e57905	3.7	22
85	Prospecting for aptamers in the human genome. <i>Chemistry and Biology</i> , 2012 , 19, 1218-20		1
84	Specificity of the double-stranded RNA-binding domain from the RNA-activated protein kinase PKR for double-stranded RNA: insights from thermodynamics and small-angle X-ray scattering. <i>Biochemistry</i> , 2012 , 51, 9312-22	3.2	15
83	Toward a digital gene response: RNA G-quadruplexes with fewer quartets fold with higher cooperativity. <i>Journal of the American Chemical Society</i> , 2012 , 134, 812-5	16.4	43
82	RNA catalysis through compartmentalization. <i>Nature Chemistry</i> , 2012 , 4, 941-6	17.6	229
81	Mechanistic characterization of the 5'Triphosphate-dependent activation of PKR: lack of 5'Tend nucleobase specificity, evidence for a distinct triphosphate binding site, and a critical role for the dsRBD. <i>Rna</i> , 2012 , 18, 1862-74	5.8	14
80	Activation of PKR by RNA misfolding: HDV ribozyme dimers activate PKR. <i>Rna</i> , 2012 , 18, 2157-65	5.8	18
79	Mechanistic analysis of the hepatitis delta virus (HDV) ribozyme: methods for RNA preparation, structure mapping, solvent isotope effects, and co-transcriptional cleavage. <i>Methods in Molecular Biology</i> , 2012 , 848, 21-40	1.4	4
78	Charged nucleobases and their potential for RNA catalysis. <i>Accounts of Chemical Research</i> , 2011 , 44, 1270-3	16.4	67
77	Regulation of innate immunity through RNA structure and the protein kinase PKR. <i>Current Opinion in Structural Biology</i> , 2011 , 21, 119-27	8.1	102
76	Quantum Mechanical/Molecular Mechanical Study of the HDV Ribozyme: Impact of the Catalytic Metal Ion on the Mechanism. <i>Journal of Physical Chemistry Letters</i> , 2011 , 2, 2906-2911	6.4	17
75	Metal binding motif in the active site of the HDV ribozyme binds divalent and monovalent ions. <i>Biochemistry</i> , 2011 , 50, 2672-82	3.2	49

74	Mechanistic strategies in the HDV ribozyme: chelated and diffuse metal ion interactions and active site protonation. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 8346-57	3.4	35
73	RNA helical imperfections regulate activation of the protein kinase PKR: effects of bulge position, size, and geometry. <i>Rna</i> , 2011 , 17, 957-66	5.8	17
72	Prevalence of syn nucleobases in the active sites of functional RNAs. <i>Rna</i> , 2011 , 17, 1775-87	5.8	36
71	Incorporation of pseudouridine into mRNA enhances translation by diminishing PKR activation. <i>Nucleic Acids Research</i> , 2010 , 38, 5884-92	20.1	222
70	RNA G-Quadruplexes in the model plant species <i>Arabidopsis thaliana</i> : prevalence and possible functional roles. <i>Nucleic Acids Research</i> , 2010 , 38, 8149-63	20.1	69
69	Role of unsatisfied hydrogen bond acceptors in RNA energetics and specificity. <i>Journal of the American Chemical Society</i> , 2010 , 132, 5342-4	16.4	30
68	Regulation of PKR by HCV IRES RNA: importance of domain II and NS5A. <i>Journal of Molecular Biology</i> , 2010 , 400, 393-412	6.5	46
67	Long-distance communication in the HDV ribozyme: insights from molecular dynamics and experiments. <i>Journal of Molecular Biology</i> , 2010 , 402, 278-91	6.5	25
66	The human HDV-like CPEB3 ribozyme is intrinsically fast-reacting. <i>Biochemistry</i> , 2010 , 49, 5321-30	3.2	35
65	Driving forces for nucleic acid pK(a) shifting in an A(+).C wobble: effects of helix position, temperature, and ionic strength. <i>Biochemistry</i> , 2010 , 49, 3225-36	3.2	36
64	A 1.9 Å crystal structure of the HDV ribozyme precleavage suggests both Lewis acid and general acid mechanisms contribute to phosphodiester cleavage. <i>Biochemistry</i> , 2010 , 49, 6508-18	3.2	112
63	Thinking inside the box: designing, implementing, and interpreting thermodynamic cycles to dissect cooperativity in RNA and DNA folding. <i>Methods in Enzymology</i> , 2009 , 455, 365-93	1.7	20
62	Analyzing RNA and DNA folding using temperature gradient gel electrophoresis (TGGE) with application to in vitro selections. <i>Methods in Enzymology</i> , 2009 , 468, 389-408	1.7	5
61	Raman crystallography of RNA. <i>Methods</i> , 2009 , 49, 101-11	4.6	24
60	RNA dimerization promotes PKR dimerization and activation. <i>Journal of Molecular Biology</i> , 2009 , 390, 319-38	6.5	58
59	Contribution of the closing base pair to exceptional stability in RNA tetraloops: roles for molecular mimicry and electrostatic factors. <i>Journal of the American Chemical Society</i> , 2009 , 131, 8474-84	16.4	34
58	Molecular basis of TRAP-5'UTR RNA interaction in the <i>Bacillus subtilis</i> trp operon transcription attenuation mechanism. <i>Rna</i> , 2009 , 15, 55-66	5.8	9
57	Nucleoside modifications modulate activation of the protein kinase PKR in an RNA structure-specific manner. <i>FASEB Journal</i> , 2009 , 23, 662.4	0.9	

56	Structures, kinetics, thermodynamics, and biological functions of RNA hairpins. <i>Annual Review of Physical Chemistry</i> , 2008 , 59, 79-103	15.7	87
55	Nucleoside modifications modulate activation of the protein kinase PKR in an RNA structure-specific manner. <i>Rna</i> , 2008 , 14, 1201-13	5.8	101
54	Detection of innersphere interactions between magnesium hydrate and the phosphate backbone of the HDV ribozyme using Raman crystallography. <i>Journal of the American Chemical Society</i> , 2008 , 130, 9670-2	16.4	45
53	Mechanistic characterization of the HDV genomic ribozyme: solvent isotope effects and proton inventories in the absence of divalent metal ions support C75 as the general acid. <i>Journal of the American Chemical Society</i> , 2008 , 130, 14504-20	16.4	43
52	A brilliant disguise for self RNA: 5Tend and internal modifications of primary transcripts suppress elements of innate immunity. <i>RNA Biology</i> , 2008 , 5, 140-4	4.8	60
51	Mechanistic characterization of the HDV genomic ribozyme: the cleavage site base pair plays a structural role in facilitating catalysis. <i>Rna</i> , 2008 , 14, 1746-60	5.8	16
50	The biophysics of RNA. <i>ACS Chemical Biology</i> , 2007 , 2, 440-4	4.9	6
49	Folding cooperativity in RNA and DNA is dependent on position in the helix. <i>Biochemistry</i> , 2007 , 46, 172-81	3.1	39
48	Mechanistic characterization of the HDV genomic ribozyme: a mutant of the C41 motif provides insight into the positioning and thermodynamic linkage of metal ions and protons. <i>Biochemistry</i> , 2007 , 46, 3001-12	3.2	43
47	Direct measurement of a pK(a) near neutrality for the catalytic cytosine in the genomic HDV ribozyme using Raman crystallography. <i>Journal of the American Chemical Society</i> , 2007 , 129, 13335-42	16.4	93
46	A simple molecular model for thermophilic adaptation of functional nucleic acids. <i>Biochemistry</i> , 2007 , 46, 4232-40	3.2	10
45	A conformationally restricted guanosine analog reveals the catalytic relevance of three structures of an RNA enzyme. <i>Chemistry and Biology</i> , 2007 , 14, 23-30		23
44	Insight into the functional versatility of RNA through model-making with applications to data fitting. <i>Quarterly Reviews of Biophysics</i> , 2007 , 40, 55-85	7	2
43	TRAP-5Tstem loop interaction increases the efficiency of transcription termination in the <i>Bacillus subtilis</i> trpEDCFBA operon leader region. <i>Rna</i> , 2007 , 13, 2020-33	5.8	14
42	Wild-type is the optimal sequence of the HDV ribozyme under cotranscriptional conditions. <i>Rna</i> , 2007 , 13, 2189-201	5.8	41
41	5Ttriphosphate-dependent activation of PKR by RNAs with short stem-loops. <i>Science</i> , 2007 , 318, 1455-8	33.3	182
40	Exploring the energy landscape of a small RNA hairpin. <i>Journal of the American Chemical Society</i> , 2006 , 128, 1523-30	16.4	113
39	Nucleobase catalysis in ribozyme mechanism. <i>Current Opinion in Chemical Biology</i> , 2006 , 10, 455-64	9.7	108

38	Linkage between proton binding and folding in RNA: a thermodynamic framework and its experimental application for investigating pKa shifting. <i>Rna</i> , 2005 , 11, 157-72	5.8	51
37	Activation of the protein kinase PKR by short double-stranded RNAs with single-stranded tails. <i>Rna</i> , 2004 , 10, 1934-45	5.8	71
36	The double-stranded-RNA-binding motif: interference and much more. <i>Nature Reviews Molecular Cell Biology</i> , 2004 , 5, 1013-23	48.7	197
35	Catalytic roles for proton transfer and protonation in ribozymes. <i>Biopolymers</i> , 2004 , 73, 90-109	2.2	131
34	Simple method for determining nucleobase pK(a) values by indirect labeling and demonstration of a pK(a) of neutrality in dsDNA. <i>Journal of the American Chemical Society</i> , 2004 , 126, 10200-1	16.4	25
33	Folding thermodynamics and kinetics of YNMG RNA hairpins: specific incorporation of 8-bromoguanosine leads to stabilization by enhancement of the folding rate. <i>Biochemistry</i> , 2004 , 43, 14004-14	3.2	73
32	Evidence that folding of an RNA tetraloop hairpin is less cooperative than its DNA counterpart. <i>Biochemistry</i> , 2004 , 43, 7992-8	3.2	36
31	Continuous monitoring of enzyme reactions on a microchip: application to catalytic RNA self-cleavage. <i>Analytical Chemistry</i> , 2004 , 76, 6921-7	7.8	4
30	Structural and energetic consequences of expanding a highly cooperative stable DNA hairpin loop. <i>Journal of the American Chemical Society</i> , 2004 , 126, 9570-7	16.4	24
29	Design of a highly reactive HDV ribozyme sequence uncovers facilitation of RNA folding by alternative pairings and physiological ionic strength. <i>Journal of Molecular Biology</i> , 2004 , 341, 695-712	6.5	45
28	Mechanistic considerations for general acid-base catalysis by RNA: revisiting the mechanism of the hairpin ribozyme. <i>Biochemistry</i> , 2003 , 42, 2259-65	3.2	173
27	Folding of a stable DNA motif involves a highly cooperative network of interactions. <i>Journal of the American Chemical Society</i> , 2003 , 125, 16285-93	16.4	63
26	Mechanistic characterization of the HDV genomic ribozyme: classifying the catalytic and structural metal ion sites within a multichannel reaction mechanism. <i>Biochemistry</i> , 2003 , 42, 2982-94	3.2	77
25	Restricting the conformational heterogeneity of RNA by specific incorporation of 8-bromoguanosine. <i>Journal of the American Chemical Society</i> , 2003 , 125, 2390-1	16.4	32
24	Thermodynamic coupling of the loop and stem in unusually stable DNA hairpins closed by CG base pairs. <i>Journal of the American Chemical Society</i> , 2003 , 125, 2032-3	16.4	35
23	A Mg ²⁺ -dependent RNA tertiary structure forms in the <i>Bacillus subtilis</i> trp operon leader transcript and appears to interfere with trpE translation control by inhibiting TRAP binding. <i>Journal of Molecular Biology</i> , 2003 , 332, 555-74	6.5	20
22	Role of RNA structure in transcription attenuation in <i>Bacillus subtilis</i> : the trpEDCFBA operon as a model system. <i>Methods in Enzymology</i> , 2003 , 371, 392-404	1.7	15
21	Phylogenetic conservation of RNA secondary and tertiary structure in the trpEDCFBA operon leader transcript in <i>Bacillus</i> . <i>Rna</i> , 2003 , 9, 1502-15	5.8	3

20	Battle for the bulge: directing small molecules to DNA and RNA defects. <i>Chemistry and Biology</i> , 2002 , 9, 854-5		3
19	The folding pathway of the genomic hepatitis delta virus ribozyme is dominated by slow folding of the pseudoknots. <i>Journal of Molecular Biology</i> , 2002 , 317, 559-75	6.5	58
18	Isolation and characterization of a family of stable RNA tetraloops with the motif YNMG that participate in tertiary interactions. <i>Biochemistry</i> , 2002 , 41, 12062-75	3.2	73
17	A mechanistic framework for co-transcriptional folding of the HDV genomic ribozyme in the presence of downstream sequence. <i>Journal of Molecular Biology</i> , 2002 , 324, 1-16	6.5	45
16	Mechanistic characterization of the HDV genomic ribozyme: assessing the catalytic and structural contributions of divalent metal ions within a multichannel reaction mechanism. <i>Biochemistry</i> , 2001 , 40, 12022-38	3.2	132
15	Proton inventory of the genomic HDV ribozyme in Mg(2+)-containing solutions. <i>Journal of the American Chemical Society</i> , 2001 , 123, 11333-4	16.4	45
14	A role for upstream RNA structure in facilitating the catalytic fold of the genomic hepatitis delta virus ribozyme. <i>Journal of Molecular Biology</i> , 2000 , 301, 349-67	6.5	71
13	General acid-base catalysis in the mechanism of a hepatitis delta virus ribozyme. <i>Science</i> , 2000 , 287, 1493-7	3.3	364
12	Single-nucleotide resolution of RNA strands in the presence of their RNA complements. <i>BioTechniques</i> , 1999 , 27, 450-2, 454, 456	2.5	3
11	Isolation and characterization of thermodynamically stable and unstable RNA hairpins from a triloop combinatorial library. <i>Biochemistry</i> , 1999 , 38, 15369-79	3.2	44
10	Thermodynamic stability of the P4-P6 domain RNA tertiary structure measured by temperature gradient gel electrophoresis. <i>Biochemistry</i> , 1998 , 37, 11162-70	3.2	36
9	Thermodynamic analysis of an RNA combinatorial library contained in a short hairpin. <i>Biochemistry</i> , 1998 , 37, 15877-84	3.2	59
8	Minor-groove recognition of double-stranded RNA by the double-stranded RNA-binding domain from the RNA-activated protein kinase PKR. <i>Biochemistry</i> , 1996 , 35, 9983-94	3.2	209
7	Thermodynamic and activation parameters for binding of a pyrene-labeled substrate by the Tetrahymena ribozyme: docking is not diffusion-controlled and is driven by a favorable entropy change. <i>Biochemistry</i> , 1995 , 34, 14394-9	3.2	49
6	Fluorescence-detected stopped flow with a pyrene labeled substrate reveals that guanosine facilitates docking of the 5Tcleavage site into a high free energy binding mode in the Tetrahymena ribozyme. <i>Biochemistry</i> , 1994 , 33, 11340-8	3.2	45
5	5TAmio pyrene provides a sensitive, nonperturbing fluorescent probe of RNA secondary and tertiary structure formation. <i>Journal of the American Chemical Society</i> , 1993 , 115, 4985-4992	16.4	62
4	Comparison of binding of mixed ribose-deoxyribose analogues of CUCU to a ribozyme and to GGAGAA by equilibrium dialysis: evidence for ribozyme specific interactions with 2TOH groups. <i>Biochemistry</i> , 1991 , 30, 10632-40	3.2	120
3	Effects of substrate structure on the kinetics of circle opening reactions of the self-splicing intervening sequence from Tetrahymena thermophila: evidence for substrate and Mg2+ binding interactions. <i>Nucleic Acids Research</i> , 1989 , 17, 355-71	20.1	71

2	Prebiotically-relevant low polyion multivalency can improve functionality of membraneless compartments	2
1	Phase-specific RNA accumulation and duplex thermodynamics in multiphase coacervate models for membraneless organelles	1