Douglas H Turner

List of Publications by Year
in descending order

156 papers	15,733 citations	58 h-index	120 g-index
		23567	18130
201 all docs	201 docs citations	201 times ranked	8984 citing authors

#	Article	IF	Citations
1	Nuclear Magnetic Resonance Spectra and AMBER OL3 and ROC-RNA Simulations of UCUCGU Reveal Force Field Strengths and Weaknesses for Single-Stranded RNA. Journal of Chemical Theory and Computation, 2022, 18, 1241-1254.	5.3	11
2	Nuclear Magnetic Resonance reveals a two hairpin equilibrium near the 3'-splice site of Influenza A segment 7 mRNA that can be shifted by oligonucleotides. Rna, 2022, , rna.078951.121.	3.5	1
3	Nearest neighbor rules for RNA helix folding thermodynamics: improved end effects. Nucleic Acids Research, 2022, 50, 5251-5262.	14.5	12
4	Nuclear Magnetic Resonance of Single-Stranded RNAs and DNAs of CAAU and UCAAUC as Benchmarks for Molecular Dynamics Simulations. Journal of Chemical Theory and Computation, 2020, 16, 1968-1984.	5.3	22
5	Nuclear Magnetic Resonance Reveals That GU Base Pairs Flanking Internal Loops Can Adopt Diverse Structures. Biochemistry, 2019, 58, 1094-1108.	2.5	10
6	In vivo analysis of influenza A mRNA secondary structures identifies critical regulatory motifs. Nucleic Acids Research, 2019, 47, 7003-7017.	14.5	51
7	Accurate geometrical restraints for Watsonâ€“Crick base pairs. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2019, 75, 235-245.	1.1	14
8	Molecular dynamics correctly models the unusual major conformation of the GAGU RNA internal loop and with NMR reveals an unusual minor conformation. Rna, 2018, 24, 656-672.	3.5	9
9	Surprising Sequence Effects on GU Closure of Symmetric 2 Ã— 2 Nucleotide RNA Internal Loops. Biochemistry, 2018, 57, 2121-2131.	2.5	4
10	Conformational ensembles of RNA oligonucleotides from integrating NMR and molecular simulations. Science Advances, 2018, 4, eaar8521.	10.3	99
11	Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. Nucleic Acids Research, 2018, 46, 4883-4892.	14.5	22
12	Predicting the Kinetics of RNA Oligonucleotides Using Markov State Models. Journal of Chemical Theory and Computation, 2017, 13, 926-934.	5.3	26
13	Physicsâ€based allâ€atom modeling of <scp>RNA</scp> energetics and structure. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1422.	6.4	32
14	Nuclear Magnetic Resonance Structure of an 8 Ã— 8 Nucleotide RNA Internal Loop Flanked on Each Side by Three Watsonâ€“Crick Pairs and Comparison to Three-Dimensional Predictions. Biochemistry, 2017, 56, 3733-3744.	2.5	4
15	Self-Folding of Naked Segment 8 Genomic RNA of Influenza A Virus. PLoS ONE, 2016, 11, e0148281.	2.5	31
16	RNA Secondary Structure Determination by NMR. Methods in Molecular Biology, 2016, 1490, 177-186.	0.9	4
17	Antisense Oligonucleotides Targeting Influenza A Segment 8 Genomic RNA Inhibit Viral Replication. Nucleic Acid Therapeutics, 2016, 26, 277-285.	3.6	34
18	Crystal structure of a poly(rA) staggered zipper at acidic pH: evidence that adenine N1 protonation mediates parallel double helix formation. Nucleic Acids Research, 2016, 44, 8417-8424.	14.5	24

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19	Mutations Designed by Ensemble Defect to Misfold Conserved RNA Structures of Influenza A Segments 7 and 8 Affect Splicing and Attenuate Viral Replication in Cell Culture. PLoS ONE, 2016, 11, e0156906.	2.5	26
20	The Influenza A PB1-F2 and N40 Start Codons Are Contained within an RNA Pseudoknot. Biochemistry, 2015, 54, 3413-3415.	2.5	10
21	Structural Features of a 3â€² Splice Site in Influenza A. Biochemistry, 2015, 54, 3269-3285.	2.5	15
22	Stacking in RNA: NMR of Four Tetramers Benchmark Molecular Dynamics. Journal of Chemical Theory and Computation, 2015, 11, 2729-2742.	5.3	99
23	Microarrays for identifying binding sites and probing structure of RNAs. Nucleic Acids Research, 2015, 43, 1-12.	14.5	250
24	Nuclear Magnetic Resonance-Assisted Prediction of Secondary Structure for RNA: Incorporation of Direction-Dependent Chemical Shift Constraints. Biochemistry, 2015, 54, 6769-6782.	2.5	13
25	Structure determination of noncanonical RNA motifs guided by 1H NMR chemical shifts. Nature Methods, 2014, 11, 413-416.	19.0	72
26	Identification of conserved RNA secondary structures at influenza B and C splice sites reveals similarities and differences between influenza A, B, and C. BMC Research Notes, 2014, 7, 22.	1.4	13
27	The contribution of pseudouridine to stabilities and structure of RNAs. Nucleic Acids Research, 2014, 42, 3492-3501.	14.5	177
28	Optimization of an AMBER Force Field for the Artificial Nucleic Acid, LNA, and Benchmarking with NMR of L(CAAU). Journal of Physical Chemistry B, 2014, 118, 1216-1228.	2.6	32
29	Secondary Structure of a Conserved Domain in an Intron of Influenza A M1 mRNA. Biochemistry, 2014, 53, 5236-5248.	2.5	24
30	The Determination of RNA Folding Nearest Neighbor Parameters. Methods in Molecular Biology, 2014, 1097, 45-70.	0.9	52
31	The Nuclear Magnetic Resonance of CCCC RNA Reveals a Right-Handed Helix, and Revised Parameters for AMBER Force Field Torsions Improve Structural Predictions from Molecular Dynamics. Biochemistry, 2013, 52, 996-1010.	2.5	78
32	Influenza B virus has global ordered RNA structure in (+) and (â^') strands but relatively less stable predicted RNA folding free energy than allowed by the encoded protein sequence. BMC Research Notes, 2013, 6, 330.	1.4	7
33	Fundamental interactions in RNA: Questions answered and remaining. Biopolymers, 2013, 99, n/a-n/a.	2.4	13
34	Secondary Structure of a Conserved Domain in the Intron of Influenza A NS1 mRNA. PLoS ONE, 2013, 8, e70615.	2.5	26
35	The influenza A segment 7 mRNA 3â€² splice site pseudoknot/hairpin family. RNA Biology, 2012, 9, 1305-1310.	3.1	25
36	Revision of AMBER Torsional Parameters for RNA Improves Free Energy Predictions for Tetramer Duplexes with GC and iGiC Base Pairs. Journal of Chemical Theory and Computation, 2012, 8, 172-181.	5.3	65

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37	Novel Conformation of an RNA Structural Switch. Biochemistry, 2012, 51, 9257-9259.	2.5	16
38	Testing the Nearest Neighbor Model for Canonical RNA Base Pairs: Revision of GU Parameters. Biochemistry, 2012, 51, 3508-3522.	2.5	80
39	Influenza A Virus Coding Regions Exhibit Host-Specific Global Ordered RNA Structure. PLoS ONE, 2012, 7, e35989.	2.5	30
40	Understanding the role of base stacking in nucleic acids. MD and QM analysis of tandem GA base pairs in RNA duplexes. Physical Chemistry Chemical Physics, 2012, 14, 12580.	2.8	24
41	The 3â€² Splice Site of Influenza A Segment 7 mRNA Can Exist in Two Conformations: A Pseudoknot and a Hairpin. PLoS ONE, 2012, 7, e38323.	2.5	39
42	Benchmarking AMBER Force Fields for RNA: Comparisons to NMR Spectra for Single-Stranded r(GACC) Are Improved by Revised Ï‡ Torsions. Journal of Physical Chemistry B, 2011, 115, 9261-9270.	2.6	95
43	The R2 retrotransposon RNA families. RNA Biology, 2011, 8, 714-718.	3.1	9
44	Identification of potential conserved RNA secondary structure throughout influenza A coding regions. Rna, 2011, 17, 991-1011.	3.5	85
45	Biophysical Analysis of Influenza A Virus RNA Promoter at Physiological Temperatures. Journal of Biological Chemistry, 2011, 286, 22965-22970.	3.4	19
46	NMR structure of a 4 Ã— 4 nucleotide RNA internal loop from an R2 retrotransposon: Identification of a three purineâ€“purine sheared pair motif and comparison to MC-SYM predictions. Rna, 2011, 17, 1664-1677.	3.5	24
47	Reparameterization of RNA Ï‡ Torsion Parameters for the AMBER Force Field and Comparison to NMR Spectra for Cytidine and Uridine. Journal of Chemical Theory and Computation, 2010, 6, 1520-1531.	5.3	155
48	Folding and Finding RNA Secondary Structure. Cold Spring Harbor Perspectives in Biology, 2010, 2, a003665-a003665.	5.5	136
49	NNDB: the nearest neighbor parameter database for predicting stability of nucleic acid secondary structure. Nucleic Acids Research, 2010, 38, D280-D282.	14.5	444
50	An RNA Molecular Switch: Intrinsic Flexibility of 23S rRNA Helices 40 and 68 5â€²-UAA/5â€²-GAN Internal Loops Studied by Molecular Dynamics Methods. Journal of Chemical Theory and Computation, 2010, 6, 910-929.	5.3	46
51	Comparisons between Chemical Mapping and Binding to Isoenergetic Oligonucleotide Microarrays Reveal Unexpected Patterns of Binding to the Bacillus subtilis RNase P RNA Specificity Domain. Biochemistry, 2010, 49, 8155-8168.	2.5	10
52	Fluorescence Competition Assay Measurements of Free Energy Changes for RNA Pseudoknots. Biochemistry, 2010, 49, 623-634.	2.5	15
53	RNA Internal Loops with Tandem AG Pairs: The Structure of the 5â€²G<u>AG</u>U/3â€²U<u>GA</u>G Loop Can Be Dramatically Different from Others, Including 5â€²A<u>AG</u>U/3â€²U<u>GA</u>A. Biochemistry, 2010, 49, 5817-5827.	2.5	31
54	RNA pseudoknots: folding and finding. F1000 Biology Reports, 2010, 2, 8.	4.0	30

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55	Effects of Restrained Sampling Space and Nonplanar Amino Groups on Free-Energy Predictions for RNA with Imino and Sheared Tandem GA Base Pairs Flanked by GC, CG, iGiC or iCiG Base Pairs. Journal of Chemical Theory and Computation, 2009, 5, 2088-2100.	5.3	39
56	Chemical Synthesis of LNA-2-thiouridine and Its Influence on Stability and Selectivity of Oligonucleotide Binding to RNA. Biochemistry, 2009, 48, 10882-10893.	2.5	21
57	Optical Melting Measurements of Nucleic Acid Thermodynamics. Methods in Enzymology, 2009, 468, 371-387.	1.0	86
58	Contributions of Stacking, Preorganization, and Hydrogen Bonding to the Thermodynamic Stability of Duplexes between RNA and 2â€²-O-Methyl RNA with Locked Nucleic Acids. Biochemistry, 2009, 48, 4377-4387.	2.5	43
59	Secondary Structures for 5â€² Regions of R2 Retrotransposon RNAs Reveal a Novel Conserved Pseudoknot and Regions that Evolve under Different Constraints. Journal of Molecular Biology, 2009, 390, 428-442.	4.2	35
60	A CA⁺ Pair Adjacent to a Sheared GA or AA Pair Stabilizes Size-Symmetric RNA Internal Loops. Biochemistry, 2009, 48, 5738-5752.	2.5	26
61	NMR-Assisted Prediction of RNA Secondary Structure: Identification of a Probable Pseudoknot in the Coding Region of an R2 Retrotransposon. Journal of the American Chemical Society, 2008, 130, 10233-10239.	13.7	45
62	The Thermodynamics of 3â€˜-Terminal Pyrene and Guanosine for the Design of Isoenergetic 2â€˜-O-Methyl-RNA-LNA Chimeric Oligonucleotide Probes of RNA Structure. Biochemistry, 2008, 47, 1249-1258.	2.5	25
63	Isoenergetic penta- and hexanucleotide microarray probing and chemical mapping provide a secondary structure model for an RNA element orchestrating R2 retrotransposon protein function. Nucleic Acids Research, 2008, 36, 1770-1782.	14.5	37
64	A chemical synthesis of LNA-2,6-diaminopurine riboside, and the influence of 2â€²-O-methyl-2,6-diaminopurine and LNA-2,6-diaminopurine ribosides on the thermodynamic properties of 2â€²-O-methyl RNA/RNA heteroduplexes. Nucleic Acids Research, 2007, 35, 4055-4063.	14.5	34
65	NMR Structures of (rGCUGAGGCU)2and (rGCGGAUGCU)2:Â Probing the Structural Features That Shape the Thermodynamic Stability of GA Pairsâ€,â€¡. Biochemistry, 2007, 46, 1511-1522.	2.5	33
66	Stacking Effects on Local Structure in RNA:Â Changes in the Structure of Tandem GA Pairs when Flanking GC Pairs Are Replaced by isoGâ^'isoC Pairsâ€. Journal of Physical Chemistry B, 2007, 111, 6718-6727.	2.6	17
67	NMR Reveals the Absence of Hydrogen Bonding in Adjacent UU and AG Mismatches in an Isolated Internal Loop from Ribosomal RNA[,]. Biochemistry, 2007, 46, 12665-12678.	2.5	21
68	An Alternating Sheared AA Pair and Elements of Stability for a Single Sheared Purine-Purine Pair Flanked by Sheared GA Pairs in RNA,. Biochemistry, 2006, 45, 6889-6903.	2.5	27
69	Facilitating RNA Structure Prediction with Microarraysâ€. Biochemistry, 2006, 45, 581-593.	2.5	42
70	The NMR Structure of an Internal Loop from 23S Ribosomal RNA Differs from Its Structure in Crystals of 50S Ribosomal Subunitsâ€,â€¡. Biochemistry, 2006, 45, 11776-11789.	2.5	28
71	Consecutive GA Pairs Stabilize Medium-Size RNA Internal Loopsâ€. Biochemistry, 2006, 45, 4025-4043.	2.5	27
72	Nearest neighbor parameters for Watson-Crick complementary heteroduplexes formed between 2'-O-methyl RNA and RNA oligonucleotides. Nucleic Acids Research, 2006, 34, 3609-3614.	14.5	36

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73	Prediction of RNA secondary structure by free energy minimization. Current Opinion in Structural Biology, 2006, 16, 270-278.	5.7	339
74	The influence of locked nucleic acid residues on the thermodynamic properties of 2'-O-methyl RNA/RNA heteroduplexes. Nucleic Acids Research, 2005, 33, 5082-5093.	14.5	104
75	Activity of Hoechst 33258 against Pneumocystis carinii f. sp. muris , Candida albicans , and Candida dubliniensis. Antimicrobial Agents and Chemotherapy, 2005, 49, 1326-1330.	3.2	16
76	RNA Challenges for Computational Chemistsâ€. Biochemistry, 2005, 44, 13225-13234.	2.5	47
77	Solution Structure of an RNA Internal Loop with Three Consecutive Sheared GA Pairsâ€,â€¡. Biochemistry, 2005, 44, 2845-2856.	2.5	36
78	Secondary structure models of the 3' untranslated regions of diverse R2 RNAs. Rna, 2004, 10, 978-987.	3.5	23
79	New approaches to targeting RNA with oligonucleotides: Inhibition of group I intron self-splicing. Biopolymers, 2004, 73, 151-161.	2.4	18
80	Hoechst 33258 Selectively Inhibits Group I Intron Self-Splicing by Affecting RNA Folding. ChemBioChem, 2004, 5, 1647-1652.	2.6	8
81	Factors Affecting Thermodynamic Stabilities of RNA 3 Ã— 3 Internal Loops. Biochemistry, 2004, 43, 12865-12876.	2.5	33
82	Structural Features and Thermodynamics of the J4/5 Loop from theCandida albicansandCandida dubliniensisGroup I Intronsâ€,â€¡. Biochemistry, 2004, 43, 15822-15837.	2.5	22
83	Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7287-7292.	7.1	1,332
84	Inhibition of Escherichia coli RNase P by oligonucleotide directed misfolding of RNA. Rna, 2003, 9, 1437-1445.	3.5	18
85	Uptake and antifungal activity of oligonucleotides in Candida albicans. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 1530-1534.	7.1	31
86	Oligonucleotide directed misfolding of RNA inhibits Candida albicans group I intron splicing. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 11091-11096.	7.1	59
87	Experimentally Derived Nearest-Neighbor Parameters for the Stability of RNA Three- and Four-Way Multibranch Loopsâ€. Biochemistry, 2002, 41, 869-880.	2.5	73
88	Molecular Recognition by theCandida albicansGroup I Intron:Â Tertiary Interactions with an Imino GÂ·A Pair Facilitate Binding of the 5â€˜ Exon and Lower theKMfor Guanosineâ€. Biochemistry, 2002, 41, 8113-8119.	2.5	9
89	Molecular Recognition in Purine-Rich Internal Loops:Â Thermodynamic, Structural, and Dynamic Consequences of Purine for Adenine Substitutions in 5â€˜(rGGCAAGCCU)2â€,â€¡. Biochemistry, 2002, 41, 14978-14987.	2.5	10
90	Dynalign: an algorithm for finding the secondary structure common to two RNA sequences. Journal of Molecular Biology, 2002, 317, 191-203.	4.2	340

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91	Thermodynamic Stabilities of Internal Loops with GU Closing Pairs in RNAâ€. Biochemistry, 2001, 40, 11509-11517.	2.5	41
92	Long-Range Cooperativity in Molecular Recognition of RNA by Oligodeoxynucleotides with Multiple C5-(1-Propynyl) Pyrimidines. Journal of the American Chemical Society, 2001, 123, 4107-4118.	13.7	69
93	Stability and Structure of RNA Duplexes Containing Isoguanosine and Isocytidine. Journal of the American Chemical Society, 2001, 123, 1267-1274.	13.7	46
94	C5-(1-Propynyl)-2â€˜-deoxy-Pyrimidines Enhance Mismatch Penalties of DNA:RNA Duplex Formationâ€. Biochemistry, 2001, 40, 12738-12745.	2.5	23
95	Binding Enhancement by Tertiary Interactions and Suicide Inhibition of aCandida albicansGroup I Intron by Phosphoramidate and 2â€˜-O-Methyl Hexanucleotidesâ€. Biochemistry, 2001, 40, 6520-6526.	2.5	24
96	Thermodynamics of Three-Way Multibranch Loops in RNAâ€. Biochemistry, 2001, 40, 6971-6981.	2.5	88
97	Long-Range Cooperativity Due to C5-Propynylation of Oligopyrimidines Enhances Specific Recognition by Uridine of ribo-Adenosine over ribo-Guanosine. Journal of the American Chemical Society, 2001, 123, 9186-9187.	13.7	12
98	Recognition Elements for 5â€˜ Exon Substrate Binding to theCandida albicansGroup I Intronâ€. Biochemistry, 2001, 40, 6507-6519.	2.5	23
99	Thermodynamics of RNA Internal Loops with a Guanosine-Guanosine Pair Adjacent to Another Noncanonical Pair. Biochemistry, 2001, 40, 2478-2483.	2.5	23
100	Expanded CUG repeat RNAs form hairpins that activate the double-stranded RNA-dependent protein kinase PKR. Rna, 2000, 6, 79-87.	3.5	225
101	The Chemical Synthesis of Oligoribonucleotides with Selectively Placed 2â€²-O-Phosphates. Nucleosides, Nucleotides and Nucleic Acids, 2000, 19, 917-933.	1.1	5
102	Factors Affecting the Thermodynamic Stability of Small Asymmetric Internal Loops in RNAâ€. Biochemistry, 2000, 39, 9257-9274.	2.5	73
103	Targeting aPneumocystis cariniiGroup I Intron with Methylphosphonate Oligonucleotides:Â Backbone Charge Is Not Required for Binding or Reactivityâ€. Biochemistry, 2000, 39, 6991-7000.	2.5	22
104	Contributions of Individual Nucleotides to Tertiary Binding of Substrate by aPneumocystis cariniiGroup I Intronâ€. Biochemistry, 2000, 39, 14269-14278.	2.5	9
105	NMR Structures of r(GCAGGCGUGC)2and Determinants of Stability for Single Guanosineâ^'Guanosine Base Pairsâ€,â€¡. Biochemistry, 2000, 39, 11748-11762.	2.5	61
106	Nuclear Magnetic Resonance Spectroscopy and Molecular Modeling Reveal That Different Hydrogen Bonding Patterns Are Possible for GÂ·U Pairs:Â One Hydrogen Bond for Each GÂ·U Pair in r(GGCGUGCC)2and Two for Each GÂ·U Pair in r(GAGUGCUC)2â€,â€¡. Biochemistry, 2000, 39, 8970-8982.	2.5	56
107	Predicting oligonucleotide affinity to nucleic acid targets. Rna, 1999, 5, 1458-1469.	3.5	228
108	The energetics of small internal loops in RNA. Biopolymers, 1999, 52, 157-167.	2.4	31

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109	Thermodynamics of RNAâ^'RNA Duplexes with 2- or 4-Thiouridines:Â Implications for Antisense Design and Targeting a Group I Intronâ€. Biochemistry, 1999, 38, 16655-16662.	2.5	118
110	Thermodynamics of Single Mismatches in RNA Duplexesâ€. Biochemistry, 1999, 38, 14214-14223.	2.5	166
111	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. Journal of Molecular Biology, 1999, 288, 911-940.	4.2	3,486
112	Thermodynamics of unpaired terminal nucleotides on short RNA helixes correlates with stacking at helix termini in larger RNAs. Journal of Molecular Biology, 1999, 290, 967-982.	4.2	79
113	Antisense Binding Enhanced by Tertiary Interactions:â€‰ Binding of Phosphorothioate and N3â€˜â†'P5â€˜ Phosphoramidate Hexanucleotides to the Catalytic Core of a Group I Ribozyme from the Mammalian Pathogen Pneumocystis carinii. Biochemistry, 1998, 37, 9379-9385.	2.5	23
114	Thermodynamic Parameters for an Expanded Nearest-Neighbor Model for Formation of RNA Duplexes with Watsonâ^'Crick Base Pairsâ€. Biochemistry, 1998, 37, 14719-14735.	2.5	1,055
115	Effects of Mg2+ and the 2â€˜ OH of Guanosine on Steps Required for Substrate Binding and Reactivity with the Tetrahymena Ribozyme Reveal Several Local Folding Transitions. Biochemistry, 1997, 36, 11131-11139.	2.5	13
116	APneumocystis cariniiGroup I Intron Ribozyme That Does Not Require 2â€˜ OH Groups on Its 5â€˜ Exon Mimic for Binding to the Catalytic Coreâ€. Biochemistry, 1997, 36, 15303-15314.	2.5	41
117	Solution Structure of (rGGCAGGCC)2by Two-Dimensional NMR and the Iterative Relaxation Matrix Approachâ€,â€¡. Biochemistry, 1997, 36, 4449-4460.	2.5	82
118	Thermodynamics of Nonsymmetric Tandem Mismatches Adjacent to GÂ·C Base Pairs in RNAâ€. Biochemistry, 1997, 36, 12486-12497.	2.5	84
119	Investigation of the Structural Basis for Thermodynamic Stabilities of Tandem GU Wobble Pairs:Â NMR Structures of (rGGAGUUCC)2and (rGGAUGUCC)2â€,â€¡. Biochemistry, 1997, 36, 8030-8038.	2.5	55
120	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. ACS Symposium Series, 1997, , 246-257.	0.5	21
121	Measuring the thermodynamics of RNA secondary structure formation. , 1997, 44, 309-319.		100
122	Measuring the thermodynamics of RNA secondary structure formation. Biopolymers, 1997, 44, 309-319.	2.4	2
123	GÂ·A and UÂ·U Mismatches Can Stabilize RNA Internal Loops of Three Nucleotidesâ€. Biochemistry, 1996, 35, 16105-16109.	2.5	35
124	Thermodynamics of Coaxially Stacked Helixes with GA and CC Mismatches. Biochemistry, 1996, 35, 13753-13761.	2.5	52
125	Structural Features of a Six-Nucleotide RNA Hairpin Loop Found in Ribosomal RNAâ€. Biochemistry, 1996, 35, 6539-6548.	2.5	66
126	A Mechanistic Framework for the Second Step of Splicing Catalyzed by theTetrahymenaRibozymeâ€. Biochemistry, 1996, 35, 648-658.	2.5	33

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127	Investigation of the Structural Basis for Thermodynamic Stabilities of Tandem GU Mismatches:Â Solution Structure of (rGAGGUCUC)2by Two-Dimensional NMR and Simulated Annealingâ€‚â€¡. Biochemistry, 1996, 35, 14077-14089.	2.5	333
128	Solution Structure of (rGCGGACGC)2 by Two-Dimensional NMR and the Iterative Relaxation Matrix Approach. Biochemistry, 1996, 35, 9677-9689.	2.5	108
129	The time dependence of chemical modification reveals slow steps in the folding of a group I ribozyme. Biochemistry, 1995, 34, 6504-6512.	2.5	55
130	A Periodic Table of Tandem Mismatches in RNA. Biochemistry, 1995, 34, 3204-3211.	2.5	140
131	A model for the stabilities of RNA hairpins based on a study of the sequence dependence of stability for hairpins of six nucleotides. Biochemistry, 1994, 33, 14289-14296.	2.5	76
132	The Stability and Structure of Tandem GA Mismatches in RNA Depend on Closing Base Pairs. Biochemistry, 1994, 33, 11349-11354.	2.5	87
133	Replacement of the Conserved G.cntdot.U with a G-C Pair at the Cleavage Site of the Tetrahymena Ribozyme Decreases Binding, Reactivity, and Fidelity. Biochemistry, 1994, 33, 13856-13863.	2.5	66
134	Sequence dependence of stability for coaxial stacking of RNA helixes with Watson-Crick base paired interfaces. Biochemistry, 1994, 33, 12715-12719.	2.5	89
135	Structure of (rGGCGAGCC)2 in solution from NMR and restrained molecular dynamics. Biochemistry, 1993, 32, 12612-12623.	2.5	175
136	Nearest-neighbor parameters for G.cntdot.U mismatches: 5'GU3'/3'UG5' is destabilizing in the contexts CGUG/GUGC, UGUA/AUGU, and AGUU/UUGA but stabilizing in GGUC/CUGG. Biochemistry, 1991, 30, 11124-11132.	2.5	128
137	Comparison of binding of mixed ribose-deoxyribose analogs of CUCU to a ribozyme and to GGAGAA by equilibrium dialysis: evidence for ribozyme specific interactions with 2'-hydroxy groups. Biochemistry, 1991, 30, 10632-10640.	2.5	129
138	Stabilities of consecutive A.cntdot.C, C.cntdot.C, G.cntdot.G, U.cntdot.C, and U.cntdot.U mismatches in RNA internal loops: evidence for stable hydrogen-bonded U.cntdot.U and C.cntdot.C+ pairs. Biochemistry, 1991, 30, 8242-8251.	2.5	164
139	Thermodynamic study of internal loops in oligoribonucleotides: symmetric loops are more stable than asymmetric loops. Biochemistry, 1991, 30, 6428-6436.	2.5	98
140	Effects of GA mismatches on the structure and thermodynamics of RNA internal loops. Biochemistry, 1990, 29, 8813-8819.	2.5	117
141	Thermodynamic and spectroscopic study of bulge loops in oligoribonucleotides. Biochemistry, 1990, 29, 278-285.	2.5	161
142	Melting and chemical modification of a cyclized self-splicing group I intron: similarity of structures in 1 M sodium, in 10 mM magnesium and in the presence of substrate. Biochemistry, 1990, 29, 10147-10158.	2.5	55
143	Effects of substrate structure on the kinetics of circle opening reactions of the self-splicing intervening sequence fromTetrahymena thermophila: evidence for substrate and Mg2+binding Interactions. Nucleic Acids Research, 1989, 17, 355-371.	14.5	74
144	Laser temperature-jump, spectroscopic, and thermodynamic study of salt effects on duplex formation by dGCATGC. Biochemistry, 1989, 28, 4283-4291.	2.5	176

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146	Sequence dependence for the energetics of terminal mismatches in ribooligonucleotides. Biochemistry, 1987, 26, 4559-4562.	2.5	46
147	Polymer-supported RNA synthesis and its application to test the nearest-neighbor model for duplex stability. Biochemistry, 1986, 25, 7840-7846.	2.5	148
148	Stability of XGCGCp, GCGCYp, and XGCGCYp helixes: an empirical estimate of the energetics of hydrogen bonds in nucleic acids. Biochemistry, 1986, 25, 3214-3219.	2.5	134
149	Contributions of dangling end stacking and terminal base-pair formation to the stabilities of XGGCCp, XCCGGp, XGGCCYp, and XCCGGYp helixes. Biochemistry, 1985, 24, 4533-4539.	2.5	128
150	Thermodynamic Studies of RNA Stability. Journal of Biomolecular Structure and Dynamics, 1984, 1, 1229-1242.	3.5	52
151	Solvent effects on the dynamics of (dG-dC)3. Biopolymers, 1983, 22, 1107-1131.	2.4	92
152	Effects of 3' dangling end stacking on the stability of GGCC and CCGG double helixes. Biochemistry, 1983, 22, 6198-6206.	2.5	131
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