# Douglas H Turner

List of Publications by Year
in descending order

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|---|---|---|---|
| 156 papers | 15,733 citations | 27035 58 h-index | 20625 120 g-index |
| 201 all docs | 201 docs citations | 201 times ranked | 10185 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. | 2.3 | 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. | 1.6 | 1 |
| 3 | Nearest neighbor rules for RNA helix folding thermodynamics: improved end effects. Nucleic Acids Research, 2022, 50, 5251-5262. | 6.5 | 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. | 2.3 | 22 |
| 5 | Nuclear Magnetic Resonance Reveals That GU Base Pairs Flanking Internal Loops Can Adopt Diverse Structures. Biochemistry, 2019, 58, 1094-1108. | 1.2 | 10 |
| 6 | In vivo analysis of influenza A mRNA secondary structures identifies critical regulatory motifs. Nucleic Acids Research, 2019, 47, 7003-7017. | 6.5 | 51 |
| 7 | Accurate geometrical restraints for Watsonâ€“Crick base pairs. Acta Crystallographica Section B: Structural Science, Crystal Engineering and Materials, 2019, 75, 235-245. | 0.5 | 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. | 1.6 | 9 |
| 9 | Surprising Sequence Effects on GU Closure of Symmetric 2 Ã— 2 Nucleotide RNA Internal Loops. Biochemistry, 2018, 57, 2121-2131. | 1.2 | 4 |
| 10 | Conformational ensembles of RNA oligonucleotides from integrating NMR and molecular simulations. Science Advances, 2018, 4, eaar8521. | 4.7 | 99 |
| 11 | Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. Nucleic Acids Research, 2018, 46, 4883-4892. | 6.5 | 22 |
| 12 | Predicting the Kinetics of RNA Oligonucleotides Using Markov State Models. Journal of Chemical Theory and Computation, 2017, 13, 926-934. | 2.3 | 26 |
| 13 | Physicsâ€based allâ€atom modeling of <scp>RNA</scp> energetics and structure. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1422. | 3.2 | 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. | 1.2 | 4 |
| 15 | Self-Folding of Naked Segment 8 Genomic RNA of Influenza A Virus. PLoS ONE, 2016, 11, e0148281. | 1.1 | 31 |
| 16 | RNA Secondary Structure Determination by NMR. Methods in Molecular Biology, 2016, 1490, 177-186. | 0.4 | 4 |
| 17 | Antisense Oligonucleotides Targeting Influenza A Segment 8 Genomic RNA Inhibit Viral Replication. Nucleic Acid Therapeutics, 2016, 26, 277-285. | 2.0 | 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. | 6.5 | 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. | 1.1 | 26 |
| 20 | The Influenza A PB1-F2 and N40 Start Codons Are Contained within an RNA Pseudoknot. Biochemistry, 2015, 54, 3413-3415. | 1.2 | 10 |
| 21 | Structural Features of a 3â€² Splice Site in Influenza A. Biochemistry, 2015, 54, 3269-3285. | 1.2 | 15 |
| 22 | Stacking in RNA: NMR of Four Tetramers Benchmark Molecular Dynamics. Journal of Chemical Theory and Computation, 2015, 11, 2729-2742. | 2.3 | 99 |
| 23 | Microarrays for identifying binding sites and probing structure of RNAs. Nucleic Acids Research, 2015, 43, 1-12. | 6.5 | 250 |
| 24 | Nuclear Magnetic Resonance-Assisted Prediction of Secondary Structure for RNA: Incorporation of Direction-Dependent Chemical Shift Constraints. Biochemistry, 2015, 54, 6769-6782. | 1.2 | 13 |
| 25 | Structure determination of noncanonical RNA motifs guided by 1H NMR chemical shifts. Nature Methods, 2014, 11, 413-416. | 9.0 | 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. | 0.6 | 13 |
| 27 | The contribution of pseudouridine to stabilities and structure of RNAs. Nucleic Acids Research, 2014, 42, 3492-3501. | 6.5 | 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. | 1.2 | 32 |
| 29 | Secondary Structure of a Conserved Domain in an Intron of Influenza A M1 mRNA. Biochemistry, 2014, 53, 5236-5248. | 1.2 | 24 |
| 30 | The Determination of RNA Folding Nearest Neighbor Parameters. Methods in Molecular Biology, 2014, 1097, 45-70. | 0.4 | 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. | 1.2 | 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. | 0.6 | 7 |
| 33 | Fundamental interactions in RNA: Questions answered and remaining. Biopolymers, 2013, 99, n/a-n/a. | 1.2 | 13 |
| 34 | Secondary Structure of a Conserved Domain in the Intron of Influenza A NS1 mRNA. PLoS ONE, 2013, 8, e70615. | 1.1 | 26 |
| 35 | The influenza A segment 7 mRNA 3â€² splice site pseudoknot/hairpin family. RNA Biology, 2012, 9, 1305-1310. | 1.5 | 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. | 2.3 | 65 |

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| 37 | Novel Conformation of an RNA Structural Switch. Biochemistry, 2012, 51, 9257-9259. | 1.2 | 16 |
| 38 | Testing the Nearest Neighbor Model for Canonical RNA Base Pairs: Revision of GU Parameters. Biochemistry, 2012, 51, 3508-3522. | 1.2 | 80 |
| 39 | Influenza A Virus Coding Regions Exhibit Host-Specific Global Ordered RNA Structure. PLoS ONE, 2012, 7, e35989. | 1.1 | 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. | 1.3 | 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. | 1.1 | 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. | 1.2 | 95 |
| 43 | The R2 retrotransposon RNA families. RNA Biology, 2011, 8, 714-718. | 1.5 | 9 |
| 44 | Identification of potential conserved RNA secondary structure throughout influenza A coding regions. Rna, 2011, 17, 991-1011. | 1.6 | 85 |
| 45 | Biophysical Analysis of Influenza A Virus RNA Promoter at Physiological Temperatures. Journal of Biological Chemistry, 2011, 286, 22965-22970. | 1.6 | 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. | 1.6 | 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. | 2.3 | 155 |
| 48 | Folding and Finding RNA Secondary Structure. Cold Spring Harbor Perspectives in Biology, 2010, 2, a003665-a003665. | 2.3 | 136 |
| 49 | NNDB: the nearest neighbor parameter database for predicting stability of nucleic acid secondary structure. Nucleic Acids Research, 2010, 38, D280-D282. | 6.5 | 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. | 2.3 | 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. | 1.2 | 10 |
| 52 | Fluorescence Competition Assay Measurements of Free Energy Changes for RNA Pseudoknots. Biochemistry, 2010, 49, 623-634. | 1.2 | 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. | 1.2 | 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. | 2.3 | 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. | 1.2 | 21 |
| 57 | Optical Melting Measurements of Nucleic Acid Thermodynamics. Methods in Enzymology, 2009, 468, 371-387. | 0.4 | 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. | 1.2 | 43 |
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| 60 | A CA<sup>+</sup> Pair Adjacent to a Sheared GA or AA Pair Stabilizes Size-Symmetric RNA Internal Loops. Biochemistry, 2009, 48, 5738-5752. | 1.2 | 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. | 6.6 | 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. | 1.2 | 25 |
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| 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. | 6.5 | 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. | 1.2 | 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. | 1.2 | 17 |
| 67 | NMR Reveals the Absence of Hydrogen Bonding in Adjacent UU and AG Mismatches in an Isolated Internal Loop from Ribosomal RNA<sup>,</sup>. Biochemistry, 2007, 46, 12665-12678. | 1.2 | 21 |
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| 69 | Facilitating RNA Structure Prediction with Microarraysâ€. Biochemistry, 2006, 45, 581-593. | 1.2 | 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. | 1.2 | 28 |
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| 73 | Prediction of RNA secondary structure by free energy minimization. Current Opinion in Structural Biology, 2006, 16, 270-278. | 2.6 | 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. | 6.5 | 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. | 1.4 | 16 |
| 76 | RNA Challenges for Computational Chemistsâ€. Biochemistry, 2005, 44, 13225-13234. | 1.2 | 47 |
| 77 | Solution Structure of an RNA Internal Loop with Three Consecutive Sheared GA Pairsâ€,â€¡. Biochemistry, 2005, 44, 2845-2856. | 1.2 | 36 |
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| 80 | Hoechst 33258 Selectively Inhibits Group I Intron Self-Splicing by Affecting RNA Folding. ChemBioChem, 2004, 5, 1647-1652. | 1.3 | 8 |
| 81 | Factors Affecting Thermodynamic Stabilities of RNA 3 Ã— 3 Internal Loops. Biochemistry, 2004, 43, 12865-12876. | 1.2 | 33 |
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| 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. | 1.2 | 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. | 1.2 | 10 |
| 90 | Dynalign: an algorithm for finding the secondary structure common to two RNA sequences. Journal of Molecular Biology, 2002, 317, 191-203. | 2.0 | 340 |

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| 91 | Thermodynamic Stabilities of Internal Loops with GU Closing Pairs in RNAâ€. Biochemistry, 2001, 40, 11509-11517. | 1.2 | 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. | 6.6 | 69 |
| 93 | Stability and Structure of RNA Duplexes Containing Isoguanosine and Isocytidine. Journal of the American Chemical Society, 2001, 123, 1267-1274. | 6.6 | 46 |
| 94 | C5-(1-Propynyl)-2â€˜-deoxy-Pyrimidines Enhance Mismatch Penalties of DNA:RNA Duplex Formationâ€. Biochemistry, 2001, 40, 12738-12745. | 1.2 | 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. | 1.2 | 24 |
| 96 | Thermodynamics of Three-Way Multibranch Loops in RNAâ€. Biochemistry, 2001, 40, 6971-6981. | 1.2 | 88 |
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| 99 | Thermodynamics of RNA Internal Loops with a Guanosine-Guanosine Pair Adjacent to Another Noncanonical Pair. Biochemistry, 2001, 40, 2478-2483. | 1.2 | 23 |
| 100 | Expanded CUG repeat RNAs form hairpins that activate the double-stranded RNA-dependent protein kinase PKR. Rna, 2000, 6, 79-87. | 1.6 | 225 |
| 101 | The Chemical Synthesis of Oligoribonucleotides with Selectively Placed 2â€²-O-Phosphates. Nucleosides, Nucleotides and Nucleic Acids, 2000, 19, 917-933. | 0.4 | 5 |
| 102 | Factors Affecting the Thermodynamic Stability of Small Asymmetric Internal Loops in RNAâ€. Biochemistry, 2000, 39, 9257-9274. | 1.2 | 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. | 1.2 | 22 |
| 104 | Contributions of Individual Nucleotides to Tertiary Binding of Substrate by aPneumocystis cariniiGroup I Intronâ€. Biochemistry, 2000, 39, 14269-14278. | 1.2 | 9 |
| 105 | NMR Structures of r(GCAGGCGUGC)2and Determinants of Stability for Single Guanosineâ^'Guanosine Base Pairsâ€,â€¡. Biochemistry, 2000, 39, 11748-11762. | 1.2 | 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. | 1.2 | 56 |
| 107 | Predicting oligonucleotide affinity to nucleic acid targets. Rna, 1999, 5, 1458-1469. | 1.6 | 228 |
| 108 | The energetics of small internal loops in RNA. Biopolymers, 1999, 52, 157-167. | 1.2 | 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. | 1.2 | 118 |
| 110 | Thermodynamics of Single Mismatches in RNA Duplexesâ€. Biochemistry, 1999, 38, 14214-14223. | 1.2 | 166 |
| 111 | Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. Journal of Molecular Biology, 1999, 288, 911-940. | 2.0 | 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. | 2.0 | 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. | 1.2 | 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. | 1.2 | 1,055 |
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| 117 | Solution Structure of (rGGCAGGCC)2by Two-Dimensional NMR and the Iterative Relaxation Matrix Approachâ€,â€¡. Biochemistry, 1997, 36, 4449-4460. | 1.2 | 82 |
| 118 | Thermodynamics of Nonsymmetric Tandem Mismatches Adjacent to GÂ·C Base Pairs in RNAâ€. Biochemistry, 1997, 36, 12486-12497. | 1.2 | 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. | 1.2 | 55 |
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| 121 | Measuring the thermodynamics of RNA secondary structure formation. , 1997, 44, 309-319. | | 100 |
| 122 | Measuring the thermodynamics of RNA secondary structure formation. , 1997, 44, 309. | | 2 |
| 123 | GÂ·A and UÂ·U Mismatches Can Stabilize RNA Internal Loops of Three Nucleotidesâ€. Biochemistry, 1996, 35, 16105-16109. | 1.2 | 35 |
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| 125 | Structural Features of a Six-Nucleotide RNA Hairpin Loop Found in Ribosomal RNAâ€. Biochemistry, 1996, 35, 6539-6548. | 1.2 | 66 |
| 126 | A Mechanistic Framework for the Second Step of Splicing Catalyzed by theTetrahymenaRibozymeâ€. Biochemistry, 1996, 35, 648-658. | 1.2 | 33 |

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| 134 | Sequence dependence of stability for coaxial stacking of RNA helixes with Watson-Crick base paired interfaces. Biochemistry, 1994, 33, 12715-12719. | 1.2 | 89 |
| 135 | Structure of (rGGCGAGCC)2 in solution from NMR and restrained molecular dynamics. Biochemistry, 1993, 32, 12612-12623. | 1.2 | 175 |
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| 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. | 1.2 | 129 |
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| 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. | 1.2 | 55 |
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