

# Charles G Hoogstraten

## List of Publications by Year in descending order

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32  
papers

843  
citations

516710

16  
h-index

552781

26  
g-index

32  
all docs

32  
docs citations

32  
times ranked

645  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spectroscopic characterization of Mn <sup>2+</sup> and Cd <sup>2+</sup> coordination to phosphorothioates in the conserved A9 metal site of the hammerhead ribozyme. <i>Journal of Inorganic Biochemistry</i> , 2022, 230, 111754.	3.5	2
2	Charge-driven condensation of RNA and proteins suggests broad role of phase separation in cytoplasmic environments. <i>ELife</i> , 2021, 10, .	6.0	38
3	Dynamics-Function Analysis in Catalytic RNA Using NMR Spin Relaxation and Conformationally Restricted Nucleotides. <i>Methods in Molecular Biology</i> , 2021, 2167, 183-202.	0.9	0
4	The 27 kDa <i>Trypanosoma brucei</i> Pentatricopeptide Repeat Protein is a G-tract Specific RNA Binding Protein. <i>Scientific Reports</i> , 2018, 8, 16989.	3.3	4
5	Coupling between conformational dynamics and catalytic function at the active site of the lead-dependent ribozyme. <i>Rna</i> , 2018, 24, 1542-1554.	3.5	12
6	Thermodynamics and kinetics of RNA tertiary structure formation in the junctionless hairpin ribozyme. <i>Biophysical Chemistry</i> , 2017, 228, 62-68.	2.8	3
7	Intrinsic Base-Pair Rearrangement in the Hairpin Ribozyme Directs RNA Conformational Sampling and Tertiary Interface Formation. <i>Journal of Physical Chemistry B</i> , 2016, 120, 10885-10898.	2.6	3
8	Unraveling the Thermodynamics and Kinetics of RNA Assembly. <i>Methods in Enzymology</i> , 2014, 549, 407-432.	1.0	4
9	Intermolecular domain docking in the hairpin ribozyme. <i>RNA Biology</i> , 2013, 10, 425-435.	3.1	3
10	Lead and RNA. , 2013, , 1166-1173.		1
11	Metabolic labeling: Taking advantage of bacterial pathways to prepare spectroscopically useful isotope patterns in proteins and nucleic acids. <i>Concepts in Magnetic Resonance Part A: Bridging Education and Research</i> , 2008, 32A, 34-55.	0.5	33
12	Extensive Backbone Dynamics in the GCAA RNA Tetraloop Analyzed Using <sup>13</sup> C NMR Spin Relaxation and Specific Isotope Labeling. <i>Journal of the American Chemical Society</i> , 2008, 130, 16757-16769.	13.7	71
13	Conformationally restricted nucleotides as a probe of structure–function relationships in RNA. <i>Rna</i> , 2008, 14, 1632-1643.	3.5	22
14	Structure–function relationships in RNA and RNP enzymes: Recent advances. <i>Biopolymers</i> , 2007, 87, 317-328.	2.4	30
15	Coordination Environment of a Site-Bound Metal Ion in the Hammerhead Ribozyme Determined by <sup>15</sup> N and <sup>2</sup> H ESEEM Spectroscopy. <i>Journal of the American Chemical Society</i> , 2006, 128, 16764-16770.	13.7	58
16	Alternate-site isotopic labeling of ribonucleotides for NMR studies of ribose conformational dynamics in RNA. <i>Journal of Biomolecular NMR</i> , 2006, 35, 261-274.	2.8	46
17	Analysis of Ribose Ring Dynamics in RNA Molecules Using <sup>13</sup> C NMR. <i>FASEB Journal</i> , 2006, 20, A69.	0.5	0
18	Structural Analysis of Metal Ion Ligation to Nucleotides and Nucleic Acids Using Pulsed EPR Spectroscopy. <i>Journal of the American Chemical Society</i> , 2002, 124, 834-842.	13.7	57

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19	Water counting: Quantitating the hydration level of paramagnetic metal ions bound to nucleotides and nucleic acids. <i>Rna</i> , 2002, 8, 252-260.	3.5	27
20	<sup>31</sup> P NMR Probes of Chemical Dynamics: Paramagnetic Relaxation Enhancement of the <sup>1</sup> H and <sup>31</sup> P NMR Resonances of Methyl Phosphite and Methylethyl Phosphate Anions by Selected Metal Complexes. <i>Inorganic Chemistry</i> , 2001, 40, 6547-6554.	4.0	8
21	Active Site Dynamics in the Lead-Dependent Ribozyme. <i>Biochemistry</i> , 2000, 39, 9951-9958.	2.5	103
22	Mn <sup>2+</sup> -Nitrogen Interactions in RNA Probed by Electron Spin Echo Envelope Modulation Spectroscopy: Application to the Hammerhead Ribozyme. <i>Journal of the American Chemical Society</i> , 1999, 121, 9215-9218.	13.7	66
23	Improved distance analysis in RNA using network-editing techniques for overcoming errors due to spin diffusion. , 1998, 11, 85-95.		6
24	Measurement of Carbon-Phosphorus Coupling Constants in RNA Using Spin Echo Difference Constant-Time HCC-COSY. <i>Journal of Magnetic Resonance</i> , 1998, 133, 236-240.	2.1	17
25	Order, dynamics and metal-binding in the lead-dependent ribozyme 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1998, 284, 325-335.	4.2	67
26	NMR solution structure of the lead-dependent ribozyme: evidence for dynamics in RNA catalysis 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1998, 284, 337-350.	4.2	82
27	Effects of Experimentally Achievable Improvements in the Quality of NMR Distance Constraints on the Accuracy of Calculated Protein Structures. <i>Journal of Molecular Biology</i> , 1996, 258, 334-348.	4.2	13
28	Approaches to the Determination of More Accurate Cross-Relaxation Rates and the Effects of Improved Distance Constraints on Protein Solution Structures. , 1996, , 73-111.		0
29	Comparison of the accuracy of protein solution structures derived from conventional and network-edited NOESY data. <i>Protein Science</i> , 1995, 4, 2289-2299.	7.6	38
30	NOE Measurements in the Absence of Spin Diffusion: Application to Methylene Groups in Proteins and Effects on Local Structural Parameters. [Erratum to document cited in CA122:310070]. <i>Journal of the American Chemical Society</i> , 1995, 117, 8885-8885.	13.7	0
31	NOE Measurements in the Absence of Spin Diffusion: Application to Methylene Groups in Proteins and Effects on Local Structural Parameters. <i>Journal of the American Chemical Society</i> , 1995, 117, 5610-5611.	13.7	13
32	Topological Editing of Cross-Relaxation Networks. <i>Israel Journal of Chemistry</i> , 1992, 32, 245-256.	2.3	16