Charles G Hoogstraten

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8783135/publications.pdf

Version: 2024-02-01

516710 552781 32 843 16 26 citations g-index h-index papers 32 32 32 645 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	Active Site Dynamics in the Lead-Dependent Ribozyme. Biochemistry, 2000, 39, 9951-9958.	2.5	103
2	NMR solution structure of the lead-dependent ribozyme: evidence for dynamics in RNA catalysis 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1998, 284, 337-350.	4.2	82
3	Extensive Backbone Dynamics in the GCAA RNA Tetraloop Analyzed Using ¹³ C NMR Spin Relaxation and Specific Isotope Labeling. Journal of the American Chemical Society, 2008, 130, 16757-16769.	13.7	71
4	Order, dynamics and metal-binding in the lead-dependent ribozyme 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1998, 284, 325-335.	4.2	67
5	Mn2+â^'Nitrogen Interactions in RNA Probed by Electron Spinâ^'Echo Envelope Modulation Spectroscopy:Â Application to the Hammerhead Ribozyme. Journal of the American Chemical Society, 1999, 121, 9215-9218.	13.7	66
6	Coordination Environment of a Site-Bound Metal Ion in the Hammerhead Ribozyme Determined by 15N and 2H ESEEM Spectroscopy. Journal of the American Chemical Society, 2006, 128, 16764-16770.	13.7	58
7	Structural Analysis of Metal Ion Ligation to Nucleotides and Nucleic Acids Using Pulsed EPR Spectroscopy. Journal of the American Chemical Society, 2002, 124, 834-842.	13.7	57
8	Alternate-site isotopic labeling of ribonucleotides for NMR studies of ribose conformational dynamics in RNA. Journal of Biomolecular NMR, 2006, 35, 261-274.	2.8	46
9	Comparison of the accuracy of protein solution structures derived from conventional and networkâ€edited NOESY data. Protein Science, 1995, 4, 2289-2299.	7.6	38
10	Charge-driven condensation of RNA and proteins suggests broad role of phase separation in cytoplasmic environments. ELife, 2021, 10, .	6.0	38
11	Metabolic labeling: Taking advantage of bacterial pathways to prepare spectroscopically useful isotope patterns in proteins and nucleic acids. Concepts in Magnetic Resonance Part A: Bridging Education and Research, 2008, 32A, 34-55.	0.5	33
12	Structure–function relationships in RNA and RNP enzymes: Recent advances. Biopolymers, 2007, 87, 317-328.	2.4	30
13	Water counting: Quantitating the hydration level of paramagnetic metal ions bound to nucleotides and nucleic acids. Rna, 2002, 8, 252-260.	3.5	27
14	Conformationally restricted nucleotides as a probe of structure–function relationships in RNA. Rna, 2008, 14, 1632-1643.	3.5	22
15	Measurement of Carbon–PhosphorusJCoupling Constants in RNA Using Spin–Echo Difference Constant-Time HCCH–COSY. Journal of Magnetic Resonance, 1998, 133, 236-240.	2.1	17
16	Topological Editing of Crossâ€Relaxation Networks. Israel Journal of Chemistry, 1992, 32, 245-256.	2.3	16
17	NOE Measurements in the Absence of Spin Diffusion: Application to Methylene Groups in Proteins and Effects on Local Structural Parameters. Journal of the American Chemical Society, 1995, 117, 5610-5611.	13.7	13
18	Effects of Experimentally Achievable Improvements in the Quality of NMR Distance Constraints on the Accuracy of Calculated Protein Structures. Journal of Molecular Biology, 1996, 258, 334-348.	4.2	13

#	Article	IF	CITATIONS
19	Coupling between conformational dynamics and catalytic function at the active site of the lead-dependent ribozyme. Rna, 2018, 24, 1542-1554.	3.5	12
20	31P NMR Probes of Chemical Dynamics:Â Paramagnetic Relaxation Enhancement of the1H and31P NMR Resonances of Methyl Phosphite and Methylethyl Phosphate Anions by Selected Metal Complexes. Inorganic Chemistry, 2001, 40, 6547-6554.	4.0	8
21	Improved distance analysis in RNA using network-editing techniques for overcoming errors due to spin diffusion., 1998, 11, 85-95.		6
22	Unraveling the Thermodynamics and Kinetics of RNA Assembly. Methods in Enzymology, 2014, 549, 407-432.	1.0	4
23	The 27 kDa Trypanosoma brucei Pentatricopeptide Repeat Protein is a G-tract Specific RNA Binding Protein. Scientific Reports, 2018, 8, 16989.	3.3	4
24	Intermolecular domain docking in the hairpin ribozyme. RNA Biology, 2013, 10, 425-435.	3.1	3
25	Intrinsic Base-Pair Rearrangement in the Hairpin Ribozyme Directs RNA Conformational Sampling and Tertiary Interface Formation. Journal of Physical Chemistry B, 2016, 120, 10885-10898.	2.6	3
26	Thermodynamics and kinetics of RNA tertiary structure formation in the junctionless hairpin ribozyme. Biophysical Chemistry, 2017, 228, 62-68.	2.8	3
27	Spectroscopic characterization of Mn2+ and Cd2+ coordination to phosphorothioates in the conserved A9 metal site of the hammerhead ribozyme. Journal of Inorganic Biochemistry, 2022, 230, 111754.	3.5	2
28	Lead and RNA. , 2013, , 1166-1173.		1
29	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]. Journal of the American Chemical Society, 1995, 117, 8885-8885.	13.7	0
30	Analysis of Ribose Ring Dynamics in RNA Molecules Using 13C NMR. FASEB Journal, 2006, 20, A69.	0.5	0
31	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
32	Dynamics-Function Analysis in Catalytic RNA Using NMR Spin Relaxation and Conformationally Restricted Nucleotides. Methods in Molecular Biology, 2021, 2167, 183-202.	0.9	O