Pascale Legault

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Methods for Measurement of Intermolecular NOEs by Multinuclear NMR Spectroscopy:Â Application to a Bacteriophage λ N-Peptide/boxBRNA Complex. Journal of the American Chemical Society, 1997, 119, 6711-6721.	13.7	583
2	Preparation of13C and15N labelled RNAs for heteronuclear multi-dimensional NMR studies. Nucleic Acids Research, 1992, 20, 4507-4513.	14.5	328
3	NMR Structure of the Bacteriophage λ N Peptide/boxB RNA Complex: Recognition of a GNRA Fold by an Arginine-Rich Motif. Cell, 1998, 93, 289-299.	28.9	257
4	Structure of the Tfb1/p53 Complex: Insights into the Interaction between the p62/Tfb1 Subunit of TFIIH and the Activation Domain of p53. Molecular Cell, 2006, 22, 731-740.	9.7	190
5	Unusual Dynamics and pKaShift at the Active Site of a Lead-Dependent Ribozyme‡. Journal of the American Chemical Society, 1997, 119, 6621-6628.	13.7	167
6	Solution Structure of Bovine Neutrophil .betaDefensin-12: The Peptide Fold of the .betaDefensins Is Identical to That of the Classical Defensins. Biochemistry, 1995, 34, 13663-13671.	2.5	158
7	Improved RNA Structure Determination by Detection of NOE Contacts to Exchange-Broadened Amino Protons. Journal of the American Chemical Society, 1995, 117, 11043-11048.	13.7	112
8	In situ Probing of Adenine Protonation in RNA by 13C NMR. Journal of the American Chemical Society, 1994, 116, 8390-8391.	13.7	93
9	Independent Ligand-Induced Folding of the RNA-Binding Domain and Two Functionally Distinct Antitermination Regions in the Phage λ N Protein. Molecular Cell, 1998, 1, 265-275.	9.7	87
10	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
11	Through-Bond Correlation of Adenine Protons in a 13C-Labeled Ribozyme. Journal of the American Chemical Society, 1994, 116, 2203-2204.	13.7	73
12	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
13	Structure of a (Cys ₃ His) zinc ribbon, a ubiquitous motif in archaeal and eucaryal transcription. Protein Science, 2000, 9, 1743-1752.	7.6	62
14	NMR structure of the active conformation of the Varkud satellite ribozyme cleavage site. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7003-7008.	7.1	61
15	Structural characterization of interactions between transactivation domain 1 of the p65 subunit of NF-κB and transcription regulatory factors. Nucleic Acids Research, 2017, 45, 5564-5576.	14.5	51
16	A Stable Mercury-Containing Complex of the Organomercurial Lyase MerB:  Catalysis, Product Release, and Direct Transfer to MerA. Biochemistry, 2004, 43, 8333-8345.	2.5	49
17	NMR Structure of the Complex between the Tfb1 Subunit of TFIIH and the Activation Domain of VP16: Structural Similarities between VP16 and p53. Journal of the American Chemical Society, 2008, 130, 10596-10604.	13.7	48
18	Improved measurement of13C,31P J coupling constants in isotopically labeled RNA. FEBS Letters, 1995, 362, 156-160.	2.8	47

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19	NMR Structure of the Amino-Terminal Domain from the Tfb1 Subunit of TFIIH and Characterization of Its Phosphoinositide and VP16 Binding Sitesâ€,‡. Biochemistry, 2005, 44, 7678-7686.	2.5	46
20	p53 and TFIIEα share a common binding site on the Tfb1/p62 subunit of TFIIH. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 106-111.	7.1	45
21	Riboswitch structure: an internal residue mimicking the purine ligand. Nucleic Acids Research, 2010, 38, 2057-2068.	14.5	45
22	Studies on the Mechanism of Inactivation of the HIV-1 Nucleocapsid Protein NCp7 with 2-Mercaptobenzamide Thioesters. Journal of Medicinal Chemistry, 2005, 48, 2847-2858.	6.4	44
23	Functional and structural characterization of a dense core secretory granule sorting domain from the PC1/3 protease. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7408-7413.	7.1	39
24	NMR structure of a complex containing the TFIIF subunit RAP74 and the RNA polymerase II carboxyl-terminal domain phosphatase FCP1. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 5688-5693.	7.1	38
25	NMR Structure of Varkud Satellite Ribozyme Stemâ^'Loop V in the Presence of Magnesium lons and Localization of Metal-Binding Sites,. Biochemistry, 2006, 45, 10591-10605.	2.5	38
26	NMR Structural Studies Reveal a Novel Protein Fold for MerB, the Organomercurial Lyase Involved in the Bacterial Mercury Resistance System,. Biochemistry, 2004, 43, 8322-8332.	2.5	37
27	The ARiBo tag: a reliable tool for affinity purification of RNAs under native conditions. Nucleic Acids Research, 2011, 39, e18-e18.	14.5	32
28	Importance of the NCp7-like domain in the recognition of pre-let-7g by the pluripotency factor Lin28. Nucleic Acids Research, 2012, 40, 1767-1777.	14.5	32
29	A remarkably stable kissing-loop interaction defines substrate recognition by the <i>Neurospora</i> Varkud Satellite ribozyme. Rna, 2014, 20, 1451-1464.	3.5	32
30	Structural and functional evidence that Rad4 competes with Rad2 for binding to the Tfb1 subunit of TFIIH in NER. Nucleic Acids Research, 2013, 41, 2736-2745.	14.5	31
31	Nuclear Magnetic Resonance Structure of the Varkud Satellite Ribozyme Stemâ^'Loop V RNA and Magnesium-Ion Binding from Chemical-Shift Mappingâ€,‡. Biochemistry, 2005, 44, 4157-4170.	2.5	29
32	Affinity purification of T7 RNA transcripts with homogeneous ends using ARiBo and CRISPR tags. Rna, 2013, 19, 1003-1014.	3.5	28
33	Nuclear Magnetic Resonance Structure of the III–IV–V Three-Way Junction from the Varkud Satellite Ribozyme and Identification of Magnesium-Binding Sites Using Paramagnetic Relaxation Enhancement. Biochemistry, 2014, 53, 6264-6275.	2.5	27
34	NMR Localization of Divalent Cations at the Active Site of the <i>Neurospora</i> VS Ribozyme Provides Insights into RNA–Metal-Ion Interactions. Biochemistry, 2014, 53, 579-590.	2.5	26
35	VGluT2 Expression in Dopamine Neurons Contributes to Postlesional Striatal Reinnervation. Journal of Neuroscience, 2020, 40, 8262-8275.	3.6	26
36	Mutations at the guanosine-binding site of theTetrahymenaribozyme also affect site-specific hydrolysis. Nucleic Acids Research, 1992, 20, 6613-6619.	14.5	24

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37	Role of SLV in SLI substrate recognition by the <i>Neurospora</i> VS ribozyme. Rna, 2008, 14, 736-748.	3.5	24
38	Structural and functional characterization of interactions involving the Tfb1 subunit of TFIIH and the NER factor Rad2. Nucleic Acids Research, 2012, 40, 5739-5750.	14.5	24
39	Enhanced Binding of RNAP II CTD Phosphatase FCP1 to RAP74 Following CK2 Phosphorylationâ€. Biochemistry, 2005, 44, 2732-2745.	2.5	22
40	TDP-43 stabilizes <i>G3BP1</i> mRNA: relevance to amyotrophic lateral sclerosis/frontotemporal dementia. Brain, 2021, 144, 3461-3476.	7.6	22
41	Comparison of the Specificity of Interaction of Cellular and Viral Zinc-Binding Domains with 2-Mercaptobenzamide Thioesters. Journal of the American Chemical Society, 2006, 128, 11964-11976.	13.7	21
42	Structural Insights Into Substrate Recognition by the <i>Neurospora</i> Varkud Satellite Ribozyme: Importance of U-Turns at the Kissing-Loop Junction. Biochemistry, 2014, 53, 258-269.	2.5	21
43	Constitutive Regulatory Activity of an Evolutionarily Excluded Riboswitch Variant. Journal of Biological Chemistry, 2011, 286, 27406-27415.	3.4	20
44	NMR structure of the A730 loop of the Neurospora VS ribozyme: insights into the formation of the active site. Nucleic Acids Research, 2011, 39, 4427-4437.	14.5	20
45	Insights into <scp>RNA</scp> structure and dynamics from recent <scp>NMR</scp> and Xâ€ray studies of the <i>Neurospora</i> Varkud satellite ribozyme. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1421.	6.4	20
46	Solution Structure of the Carboxyl-Terminal Domain of RAP74 and NMR Characterization of the FCP1-Binding Sites of RAP74 and Human TFIIBâ€,‡. Biochemistry, 2003, 42, 1460-1469.	2.5	19
47	The NMR structure of the II–III–VI three-way junction from the <i>Neurospora</i> VS ribozyme reveals a critical tertiary interaction and provides new insights into the global ribozyme structure. Rna, 2015, 21, 1621-1632.	3.5	19
48	NMR Structure of a Complex Formed by the Carboxyl-Terminal Domain of Human RAP74 and a Phosphorylated Peptide from the Central Domain of the FCP1 Phosphatase. Biochemistry, 2009, 48, 1964-1974.	2.5	18
49	Interactions of the HIV-1 Tat and RAP74 Proteins with the RNA Polymerase II CTD Phosphatase FCP1â€. Biochemistry, 2005, 44, 2716-2731.	2.5	16
50	Stepwise assembly of multiple Lin28 proteins on the terminal loop of let-7 miRNA precursors. Nucleic Acids Research, 2014, 42, 4615-4628.	14.5	15
51	Biochemical characterization and osmolytes in papillary collecting ducts from pig and dog kidneys. Canadian Journal of Physiology and Pharmacology, 1988, 66, 1282-1290.	1.4	13
52	Structure-Based Design of a Potent Artificial Transactivation Domain Based on p53. Journal of the American Chemical Society, 2012, 134, 1715-1723.	13.7	12
53	Multivalent binding oligomers inhibit HIV Tat–TAR interaction critical for viral replication. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 6893-6897.	2.2	11
54	Helix-length compensation studies reveal the adaptability of the VS ribozyme architecture. Nucleic Acids Research, 2012, 40, 2284-2293.	14.5	11

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55	Affinity Purification of RNA Using an ARiBo Tag. Methods in Molecular Biology, 2013, 941, 137-155.	0.9	11
56	An integrative NMR-SAXS approach for structural determination of large RNAs defines the substrate-free state of a <i>trans</i> -cleaving <i>Neurospora</i> Varkud Satellite ribozyme. Nucleic Acids Research, 2021, 49, 11959-11973.	14.5	11
57	Structural Characterization of a Noncovalent Complex between Ubiquitin and the Transactivation Domain of the Erythroid-Specific Factor EKLF. Structure, 2013, 21, 2014-2024.	3.3	9
58	Rational engineering of the <i>Neurospora</i> VS ribozyme to allow substrate recognition via different kissing-loop interactions. Nucleic Acids Research, 2016, 44, 6924-6934.	14.5	9
59	ARiBo pull-down for riboproteomic studies based on label-free quantitative mass spectrometry. Rna, 2016, 22, 1760-1770.	3.5	6
60	A multi-axial RNA joint with a large range of motion promotes sampling of an active ribozyme conformation. Nucleic Acids Research, 2019, 47, 3739-3751.	14.5	6
61	Letter to the Editor:1H,15N, and13C Resonance Assignment of the 23ÂkDa Organomercurial Lyase MerB in its Free and Mercury-bound Forms. Journal of Biomolecular NMR, 2004, 29, 457-458.	2.8	5
62	Affinity Purification of In Vitro Transcribed RNA with Homogeneous Ends Using a 3′-ARiBo Tag. Methods in Enzymology, 2014, 549, 49-84.	1.0	5
63	Letter to the Editor: 1H, 15N, and 13C resonance assignment of the amino-terminal domain of the Tfb1 subunit of yeast TFIIH. Journal of Biomolecular NMR, 2005, 31, 173-174.	2.8	4
64	Preparation of λN-GST Fusion Protein for Affinity Immobilization of RNA. Methods in Molecular Biology, 2013, 941, 123-135.	0.9	4
65	High-yield production of human Dicer by transfection of human HEK293-EBNA1 cells grown in suspension. BMC Biotechnology, 2018, 18, 76.	3.3	3
66	Preparative Separation of Ribonucleoside Monophosphates by Ion-Pair Reverse-Phase HPLC. Methods in Molecular Biology, 2013, 941, 247-256.	0.9	2
67	In Vitro Selection of Varkud Satellite Ribozyme Variants that Cleave a Modified Stem-Loop Substrate. Methods in Molecular Biology, 2021, 2167, 61-77.	0.9	0