

Frédéric Hai-Trieu Allain

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3416133/publications.pdf>

Version: 2024-02-01

145
papers

12,046
citations

22153

59
h-index

30087

103
g-index

152
all docs

152
docs citations

152
times ranked

13154
citing authors

#	ARTICLE	IF	CITATIONS
1	The RNA recognition motif, a plastic RNA-binding platform to regulate post-transcriptional gene expression. <i>FEBS Journal</i> , 2005, 272, 2118-2131.	4.7	901
2	Gac/Rsm signal transduction pathway of γ -proteobacteria: from RNA recognition to regulation of social behaviour. <i>Molecular Microbiology</i> , 2008, 67, 241-253.	2.5	487
3	SRSF2 Mutations Contribute to Myelodysplasia by Mutant-Specific Effects on Exon Recognition. <i>Cancer Cell</i> , 2015, 27, 617-630.	16.8	449
4	Structure of PTB Bound to RNA: Specific Binding and Implications for Splicing Regulation. <i>Science</i> , 2005, 309, 2054-2057.	12.6	392
5	NMR investigation of RNA structure. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 1996, 29, 51-127.	7.5	332
6	Structure of the P1 Helix from Group I Self-splicing Introns. <i>Journal of Molecular Biology</i> , 1995, 250, 333-353.	4.2	298
7	Molecular basis of UG-rich RNA recognition by the human splicing factor TDP-43. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1443-1449.	8.2	293
8	SRSF1-Regulated Alternative Splicing in Breast Cancer. <i>Molecular Cell</i> , 2015, 60, 105-117.	9.7	290
9	Sequence-specific binding of single-stranded RNA: is there a code for recognition?. <i>Nucleic Acids Research</i> , 2006, 34, 4943-4959.	14.5	265
10	Specificity of ribonucleoprotein interaction determined by RNA folding during complex formation. <i>Nature</i> , 1996, 380, 646-650.	27.8	260
11	The YTH Domain Is a Novel RNA Binding Domain. <i>Journal of Biological Chemistry</i> , 2010, 285, 14701-14710.	3.4	226
12	Molecular basis of RNA recognition by the human alternative splicing factor Fox-1. <i>EMBO Journal</i> , 2006, 25, 163-173.	7.8	215
13	The Solution Structure of the ADAR2 dsRBM-RNA Complex Reveals a Sequence-Specific Readout of the Minor Groove. <i>Cell</i> , 2010, 143, 225-237.	28.9	212
14	Molecular basis of messenger RNA recognition by the specific bacterial repressing clamp RsmA/CsrA. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 807-813.	8.2	194
15	RNA recognition by double-stranded RNA binding domains: a matter of shape and sequence. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 1875-95.	5.4	189
16	Structural basis of the non-coding RNA RsmZ acting as a protein sponge. <i>Nature</i> , 2014, 509, 588-592.	27.8	189
17	Solution structure of the YTH domain in complex with N6-methyladenosine RNA: a reader of methylated RNA. <i>Nucleic Acids Research</i> , 2014, 42, 13911-13919.	14.5	187
18	RRM-RNA recognition: NMR or crystallography and new findings. <i>Current Opinion in Structural Biology</i> , 2013, 23, 100-108.	5.7	171

#	ARTICLE	IF	CITATIONS
19	Solution Structure of the N-terminal RNP Domain of U1A Protein: The Role of C-terminal Residues in Structure Stability and RNA Binding. <i>Journal of Molecular Biology</i> , 1996, 257, 398-411.	4.2	170
20	Solution structure of the HMG protein NHP6A and its interaction with DNA reveals the structural determinants for non-sequence-specific binding. <i>EMBO Journal</i> , 1999, 18, 2563-2579.	7.8	167
21	Binding to SMN2 pre-mRNA-protein complex elicits specificity for small molecule splicing modifiers. <i>Nature Communications</i> , 2017, 8, 1476.	12.8	155
22	RNA sequence- and shape-dependent recognition by proteins in the ribonucleoprotein particle. <i>EMBO Reports</i> , 2005, 6, 33-38.	4.5	154
23	The Solution Structure of FUS Bound to RNA Reveals a Bipartite Mode of RNA Recognition with Both Sequence and Shape Specificity. <i>Molecular Cell</i> , 2019, 73, 490-504.e6.	9.7	151
24	Molecular basis for temperature sensing by an RNA thermometer. <i>EMBO Journal</i> , 2006, 25, 2487-2497.	7.8	150
25	Molecular basis of RNA recognition and TAP binding by the SR proteins SRp20 and 9G8. <i>EMBO Journal</i> , 2006, 25, 5126-5137.	7.8	140
26	Structural basis of G-tract recognition and encaging by hnRNP F quasi-RRMs. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 853-861.	8.2	132
27	The Phosphoglucan Phosphatase Like Sex Four2 Dephosphorylates Starch at the C3-Position in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2011, 23, 4096-4111.	6.6	119
28	A <i>syn</i> - <i>anti</i> conformational difference allows SRSF2 to recognize guanines and cytosines equally well. <i>EMBO Journal</i> , 2012, 31, 162-174.	7.8	116
29	Solution structure of the loop B domain from the hairpin ribozyme. <i>Nature Structural Biology</i> , 1999, 6, 212-216.	9.7	113
30	The <i>S.cerevisiae</i> Architectural HMGB Protein NHP6A Complexed with DNA: DNA and Protein Conformational Changes upon Binding. <i>Journal of Molecular Biology</i> , 2002, 323, 263-284.	4.2	112
31	Structural basis of pre-let-7 miRNA recognition by the zinc knuckles of pluripotency factor Lin28. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 84-89.	8.2	111
32	Isolated pseudo-RNA-recognition motifs of SR proteins can regulate splicing using a noncanonical mode of RNA recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2802-11.	7.1	109
33	Divalent metal ion binding to a conserved wobble pair defining the upstream site of cleavage of group I self-splicing introns. <i>Nucleic Acids Research</i> , 1995, 23, 341-350.	14.5	105
34	Shape-specific recognition in the structure of the Vts1p SAM domain with RNA. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 160-167.	8.2	102
35	Structure and Specific RNA Binding of ADAR2 Double-Stranded RNA Binding Motifs. <i>Structure</i> , 2006, 14, 345-355.	3.3	101
36	Molecular basis of purine-rich RNA recognition by the human SR-like protein Tra2- β 1. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 443-450.	8.2	99

#	ARTICLE	IF	CITATIONS
37	RNA looping by PTB: Evidence using FRET and NMR spectroscopy for a role in splicing repression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4105-4110.	7.1	96
38	EPR-aided approach for solution structure determination of large RNAs or protein-RNA complexes. <i>Nature Communications</i> , 2014, 5, 3669.	12.8	96
39	RNA-PROTACs: Degraders of RNA-Binding Proteins. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 3163-3169.	13.8	95
40	Structure determination and dynamics of protein-RNA complexes by NMR spectroscopy. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2011, 58, 1-61.	7.5	91
41	Structural basis of a small molecule targeting RNA for a specific splicing correction. <i>Nature Chemical Biology</i> , 2019, 15, 1191-1198.	8.0	89
42	Structure of the two most C-terminal RNA recognition motifs of PTB using segmental isotope labeling. <i>EMBO Journal</i> , 2006, 25, 150-162.	7.8	85
43	NMR structure of the three quasi RNA recognition motifs (qRRMs) of human hnRNP F and interaction studies with Bcl-x G-tract RNA: a novel mode of RNA recognition. <i>Nucleic Acids Research</i> , 2006, 34, 3634-3645.	14.5	85
44	Interplay between the catabolite repression control protein Crc, Hfq and RNA in Hfq-dependent translational regulation in <i>Pseudomonas aeruginosa</i> . <i>Nucleic Acids Research</i> , 2018, 46, 1470-1485.	14.5	85
45	The testis-specific human protein RBMY recognizes RNA through a novel mode of interaction. <i>EMBO Reports</i> , 2007, 8, 372-379.	4.5	84
46	How accurately and precisely can RNA structure be determined by NMR?. <i>Journal of Molecular Biology</i> , 1997, 267, 338-351.	4.2	82
47	U1 snRNA Directly Interacts with Polypyrimidine Tract-Binding Protein during Splicing Repression. <i>Molecular Cell</i> , 2011, 41, 579-588.	9.7	82
48	Structural basis for σ^{70} promoter element melting by environmentally induced sigma factors. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 269-276.	8.2	82
49	Recent advances in segmental isotope labeling of proteins: NMR applications to large proteins and glycoproteins. <i>Journal of Biomolecular NMR</i> , 2010, 46, 51-65.	2.8	81
50	A distinct structural region of the prokaryotic ubiquitin-like protein (Pup) is recognized by the N-terminal domain of the proteasomal ATPase Mpa. <i>FEBS Letters</i> , 2009, 583, 3151-3157.	2.8	80
51	Molecular basis for the wide range of affinity found in Csr/Rsm protein-RNA recognition. <i>Nucleic Acids Research</i> , 2014, 42, 5332-5346.	14.5	77
52	A fast, efficient and sequence-independent method for flexible multiple segmental isotope labeling of RNA using ribozyme and RNase H cleavage. <i>Nucleic Acids Research</i> , 2010, 38, e188-e188.	14.5	75
53	A fly trap mechanism provides sequence-specific RNA recognition by CPEB proteins. <i>Genes and Development</i> , 2014, 28, 1498-1514.	5.9	74
54	NMR Structure Determination of a Segmentally Labeled Glycoprotein Using in Vitro Glycosylation. <i>Journal of the American Chemical Society</i> , 2009, 131, 1274-1281.	13.7	72

#	ARTICLE	IF	CITATIONS
55	Structural basis for sulfation-dependent self-glycan recognition by the human immune-inhibitory receptor Siglec-8. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E4170-9.	7.1	72
56	Tandem hnRNP A1 RNA recognition motifs act in concert to repress the splicing of survival motor neuron exon 7. <i>ELife</i> , 2017, 6, .	6.0	72
57	A bimodular nuclear localization signal assembled via an extended double-stranded RNA-binding domain acts as an RNA-sensing signal for transportin 1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1852-61.	7.1	70
58	Specific inhibition of splicing factor activity by decoy RNA oligonucleotides. <i>Nature Communications</i> , 2019, 10, 1590.	12.8	70
59	Solution structure of the two N-terminal RNA-binding domains of nucleolin and NMR study of the interaction with its RNA target. <i>Journal of Molecular Biology</i> , 2000, 303, 227-241.	4.2	69
60	Molecular basis for AU-rich element recognition and dimerization by the HuR C-terminal RRM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 2935-2944.	7.1	69
61	Plasticity of the β^2 -Trefoil Protein Fold in the Recognition and Control of Invertebrate Predators and Parasites by a Fungal Defence System. <i>PLoS Pathogens</i> , 2012, 8, e1002706.	4.7	65
62	Stabilization of Branched Oligosaccharides: Lewis ^x Benefits from a Nonconventional C α -H \cdots O Hydrogen Bond. <i>Journal of the American Chemical Society</i> , 2013, 135, 13464-13472.	13.7	65
63	NMR and EPR reveal a compaction of the RNA-binding protein FUS upon droplet formation. <i>Nature Chemical Biology</i> , 2021, 17, 608-614.	8.0	63
64	Prokaryotic Ubiquitin-like Protein (Pup) Is Coupled to Substrates via the Side Chain of Its C-Terminal Glutamate. <i>Journal of the American Chemical Society</i> , 2010, 132, 5610-5612.	13.7	62
65	Structural and Mechanistic Insights into Poly(uridine) Tract Recognition by the hnRNP \hat{A} C RNA Recognition Motif. <i>Journal of the American Chemical Society</i> , 2014, 136, 14536-14544.	13.7	62
66	Solution structure of the two RNA recognition motifs of hnRNP A1 using segmental isotope labeling: how the relative orientation between RRM \hat{s} influences the nucleic acid binding topology. <i>Journal of Biomolecular NMR</i> , 2013, 55, 119-138.	2.8	61
67	Conformation of Polypyrimidine Tract Binding Protein in Solution. <i>Structure</i> , 2006, 14, 1021-1027.	3.3	60
68	Recognition of Pre-formed and Flexible Elements of an RNA Stem-Loop by Nucleolin. <i>Journal of Molecular Biology</i> , 2001, 309, 763-775.	4.2	58
69	Solving the Structure of PTB in Complex with Pyrimidine Tracts: An NMR Study of Protein \hat{A} RNA Complexes of Weak Affinities \hat{A} . <i>Journal of Molecular Biology</i> , 2007, 367, 174-186.	4.2	58
70	Improved Segmental Isotope Labeling Methods for the NMR Study of Multidomain or Large Proteins: Application to the RRM \hat{s} of Npl3p and hnRNP L. <i>Journal of Molecular Biology</i> , 2008, 375, 151-164.	4.2	57
71	Extra Cytoplasmic Function sigma factors, recent structural insights into promoter recognition and regulation. <i>Current Opinion in Structural Biology</i> , 2015, 30, 71-78.	5.7	52
72	Structural basis for sigma factor mimicry in the general stress response of Alphaproteobacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1405-14.	7.1	49

#	ARTICLE	IF	CITATIONS
73	The high kinetic stability of a G-quadruplex limits hnRNP F qRRM3 binding to G-tract RNA. <i>Nucleic Acids Research</i> , 2013, 41, 2505-2516.	14.5	48
74	Characterization of the RNA recognition mode of hnRNP G extends its role in SMN2 splicing regulation. <i>Nucleic Acids Research</i> , 2014, 42, 6659-6672.	14.5	47
75	Aberrant interaction of FUS with the U1 snRNA provides a molecular mechanism of FUS induced amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2020, 11, 6341.	12.8	47
76	Isotope Labeling and Segmental Labeling of Larger RNAs for NMR Structural Studies. <i>Advances in Experimental Medicine and Biology</i> , 2012, 992, 121-144.	1.6	46
77	An extended dsRBD with a novel zinc-binding motif mediates nuclear retention of fission yeast Dicer. <i>EMBO Journal</i> , 2011, 30, 4223-4235.	7.8	45
78	Systematic mapping of protein-metabolite interactions in central metabolism of <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2019, 15, e9008.	7.2	45
79	Structural modeling of protein-RNA complexes using crosslinking of segmentally isotope-labeled RNA and MS/MS. <i>Nature Methods</i> , 2017, 14, 487-490.	19.0	44
80	Structural basis of siRNA recognition by TRBP double-stranded RNA binding domains. <i>EMBO Journal</i> , 2018, 37, .	7.8	43
81	High-Resolution Structural Analysis Shows How Tah1 Tethers Hsp90 to the R2TP Complex. <i>Structure</i> , 2013, 21, 1834-1847.	3.3	42
82	Automated and assisted RNA resonance assignment using NMR chemical shift statistics. <i>Nucleic Acids Research</i> , 2013, 41, e172-e172.	14.5	42
83	NMR structure of the apoB mRNA stem-loop and its interaction with the C to U editing APOBEC1 complementary factor. <i>Rna</i> , 2005, 11, 173-186.	3.5	39
84	Structure of SRSF1 RRM1 bound to RNA reveals an unexpected bimodal mode of interaction and explains its involvement in SMN1 exon7 splicing. <i>Nature Communications</i> , 2021, 12, 428.	12.8	37
85	Exon-independent recruitment of SRSF1 is mediated by U1 snRNP stem-loop 3. <i>EMBO Journal</i> , 2022, 41, e107640.	7.8	37
86	Short, synthetic and selectively ¹³ C-labeled RNA sequences for the NMR structure determination of protein-RNA complexes. <i>Nucleic Acids Research</i> , 2006, 34, e79-e79.	14.5	34
87	Novel three-dimensional ¹ H/ ¹³ C/ ³¹ P triple resonance experiments for sequential backbone correlations in nucleic acids. <i>Journal of Biomolecular NMR</i> , 1995, 5, 315-20.	2.8	33
88	A strong ¹³ C chemical shift signature provides the coordination mode of histidines in zinc-binding proteins. <i>Journal of Biomolecular NMR</i> , 2012, 53, 93-101.	2.8	32
89	A Secondary Structural Element in a Wide Range of Fucosylated Glycoepitopes. <i>Chemistry - A European Journal</i> , 2017, 23, 11598-11610.	3.3	32
90	Sedimentation Yields Long-Term Stable Protein Samples as Shown by Solid-State NMR. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 17.	3.5	32

#	ARTICLE	IF	CITATIONS
91	Solution Structure and Activation Mechanism of Ubiquitin-Like Small Archaeal Modifier Proteins. <i>Journal of Molecular Biology</i> , 2011, 405, 1040-1055.	4.2	29
92	A procedure to validate and correct the ¹³ C chemical shift calibration of RNA datasets. <i>Journal of Biomolecular NMR</i> , 2012, 52, 179-190.	2.8	29
93	Evidence for cooperative tandem binding of hnRNP C RRM s in mRNA processing. <i>Rna</i> , 2015, 21, 1931-1942.	3.5	29
94	A novel RNA pentaloop fold involved in targeting ADAR2. <i>Rna</i> , 2005, 11, 592-597.	3.5	26
95	Modularity and determinants of a (bi-)polarization control system from free-living and obligate intracellular bacteria. <i>ELife</i> , 2016, 5, .	6.0	26
96	Determination of the NMR structure of the complex between U1A protein and its RNA polyadenylation inhibition element. <i>Journal of Biomolecular NMR</i> , 1998, 11, 59-84.	2.8	25
97	The Signature of the Five-Stranded vRRM Fold Defined by Functional, Structural and Computational Analysis of the hnRNP L Protein. <i>Journal of Molecular Biology</i> , 2015, 427, 3001-3022.	4.2	25
98	Amino Acid-Selective Segmental Isotope Labeling of Multidomain Proteins for Structural Biology. <i>ChemBioChem</i> , 2013, 14, 457-466.	2.6	24
99	Aromatic side-chain conformational switch on the surface of the RNA Recognition Motif enables RNA discrimination. <i>Nature Communications</i> , 2017, 8, 654.	12.8	23
100	Structural biology of RNA-binding proteins in the context of phase separation: What NMR and EPR can bring?. <i>Current Opinion in Structural Biology</i> , 2021, 70, 132-138.	5.7	23
101	A Small Helical Bundle Prepares Primer Synthesis by Binding Two Nucleotides that Enhance Sequence-Specific Recognition of the DNA Template. <i>Cell</i> , 2019, 176, 154-166.e13.	28.9	22
102	Increase in Backbone Mobility of the VTS1p-SAM Domain on Binding to SRE-RNA. <i>Journal of Molecular Biology</i> , 2010, 396, 732-746.	4.2	21
103	Resolving distance variations by single-molecule FRET and EPR spectroscopy using rotamer libraries. <i>Biophysical Journal</i> , 2021, 120, 4842-4858.	0.5	21
104	Novel Enzymatic Activity Derived from the Semliki Forest Virus Capsid Protein. <i>Journal of Molecular Biology</i> , 2008, 376, 721-735.	4.2	20
105	Cut and Paste RNA for Nuclear Magnetic Resonance, Paramagnetic Resonance Enhancement, and Electron Paramagnetic Resonance Structural Studies. <i>Methods in Enzymology</i> , 2015, 565, 537-562.	1.0	20
106	Systematic Identification of Protein-Metabolite Interactions in Complex Metabolite Mixtures by Ligand-Detected Nuclear Magnetic Resonance Spectroscopy. <i>Biochemistry</i> , 2016, 55, 2590-2600.	2.5	20
107	Control of the polyamine biosynthesis pathway by G2-quadruplexes. <i>ELife</i> , 2018, 7, .	6.0	20
108	Changes in Dynamics of SRE-RNA on Binding to the VTS1p-SAM Domain Studied by ¹³ C NMR Relaxation. <i>Journal of the American Chemical Society</i> , 2008, 130, 12007-12020.	13.7	18

#	ARTICLE	IF	CITATIONS
109	Solution structure of the N-terminal dsRBD of Drosophila ADAR and interaction studies with RNA. <i>Biochimie</i> , 2012, 94, 1499-1509.	2.6	18
110	Selective Amino Acid Segmental Labeling of Multi-Domain Proteins. <i>Methods in Enzymology</i> , 2015, 565, 389-422.	1.0	18
111	Segmental isotope labelling and solid-state NMR of a 12 kDa motor protein: identification of structural variability. <i>Journal of Biomolecular NMR</i> , 2018, 71, 237-245.	2.8	18
112	Sequence-specific RNA recognition by an RGG motif connects U1 and U2 snRNP for spliceosome assembly. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	18
113	Molecular basis for disassembly of an importin:ribosomal protein complex by the escortin Tsr2. <i>Nature Communications</i> , 2018, 9, 3669.	12.8	17
114	Systems NMR: single-sample quantification of RNA, proteins and metabolites for biomolecular network analysis. <i>Nature Methods</i> , 2019, 16, 743-749.	19.0	17
115	A transient α -helix in the N-terminal RNA recognition motif of polypyrimidine tract binding protein senses RNA secondary structure. <i>Nucleic Acids Research</i> , 2020, 48, 4521-4537.	14.5	16
116	How a rotavirus hijacks the human protein synthesis machinery. <i>Nature Structural Biology</i> , 2002, 9, 158-160.	9.7	15
117	Recognition of N6-Methyladenosine by the YTHDC1 YTH Domain Studied by Molecular Dynamics and NMR Spectroscopy: The Role of Hydration. <i>Journal of Physical Chemistry B</i> , 2021, 125, 7691-7705.	2.6	15
118	Nucleotide-amino acid π -stacking interactions initiate photo cross-linking in RNA-protein complexes. <i>Nature Communications</i> , 2022, 13, 2719.	12.8	15
119	Role of the PFXFATG[G/Y] Motif in the Activation of SdrG, a Response Regulator Involved in the Alphaproteobacterial General Stress Response. <i>Structure</i> , 2016, 24, 1237-1247.	3.3	14
120	Comparative analyses of the thermodynamic RNA binding signatures of different types of RNA recognition motifs. <i>Nucleic Acids Research</i> , 2017, 45, 6037-6050.	14.5	14
121	Protein Side-Chain-DNA Contacts Probed by Fast Magic-Angle Spinning NMR. <i>Journal of Physical Chemistry B</i> , 2020, 124, 11089-11097.	2.6	13
122	RNA-PROTACs: Degradars of RNA-Binding Proteins. <i>Angewandte Chemie</i> , 2021, 133, 3200-3206.	2.0	12
123	An <i>in vitro</i> reconstituted U1 snRNP allows the study of the disordered regions of the particle and the interactions with proteins and ligands. <i>Nucleic Acids Research</i> , 2021, 49, e63-e63.	14.5	12
124	Characterization of Weak Protein Domain Structure by Spin-Label Distance Distributions. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 636599.	3.5	12
125	Inosine Substitutions in RNA Activate Latent G-Quadruplexes. <i>Journal of the American Chemical Society</i> , 2021, 143, 15120-15130.	13.7	12
126	Structural and functional implications of the QUA2 domain on RNA recognition by GLD-1. <i>Nucleic Acids Research</i> , 2014, 42, 8092-8105.	14.5	11

#	ARTICLE	IF	CITATIONS
127	Combining Mass Spectrometry (MS) and Nuclear Magnetic Resonance (NMR) Spectroscopy for Integrative Structural Biology of Protein-RNA Complexes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032359.	5.5	11
128	Structures to complement the archaeo-eukaryotic primases catalytic cycle description: What's next?. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 339-351.	4.1	10
129	A conserved motif in human BTC1 and BTC2 proteins mediates interaction with the poly(A) binding protein PABPC1 to stimulate mRNA deadenylation. <i>RNA Biology</i> , 2021, 18, 2450-2465.	3.1	10
130	Single Nucleotide Resolution RNA-Protein Cross-Linking Mass Spectrometry: A Simple Extension of the CLIR-MS Workflow. <i>Analytical Chemistry</i> , 2021, 93, 14626-14634.	6.5	10
131	Combining NMR Spectroscopy and Molecular Dynamic Simulations to Solve and Analyze the Structure of Protein-RNA Complexes. <i>Methods in Enzymology</i> , 2019, 614, 393-422.	1.0	9
132	Solution and crystal structures of a C-terminal fragment of the neuronal isoform of the polypyrimidine tract binding protein (nPTB). <i>PeerJ</i> , 2014, 2, e305.	2.0	9
133	NMR Spectroscopy: An Excellent Tool to Understand RNA and Carbohydrate Recognition by Proteins. <i>Chimia</i> , 2012, 66, 741.	0.6	8
134	Recent advances in understanding bacterial and archaeo-eukaryotic primases. <i>Current Opinion in Structural Biology</i> , 2019, 59, 159-167.	5.7	8
135	Use of ¹³ C, ¹⁵ N-Labeled DNA in a Non-Sequence-Specific Protein-DNA Complex Resolves Ambiguous Assignments of Intermolecular NOEs. <i>Journal of the American Chemical Society</i> , 1999, 121, 3547-3548.	13.7	7
136	Single-Stranded Nucleic Acid Recognition: Is There a Code after All?. <i>Structure</i> , 2013, 21, 4-6.	3.3	6
137	RNA modification does a regulatory two-step. <i>Nature</i> , 2015, 518, 492-493.	27.8	6
138	MINA-1 and WAGO-4 are part of regulatory network coordinating germ cell death and RNAi in <i>C. elegans</i> . <i>Cell Death and Differentiation</i> , 2019, 26, 2157-2178.	11.2	6
139	Letter to the Editor: Resonance assignments of the double-stranded RNA-binding of adenosine deaminase acting on RNA 2 (ADAR2). <i>Journal of Biomolecular NMR</i> , 2005, 31, 71-72.	2.8	5
140	Functional Siglec lectin domains from soluble expression in the cytoplasm of <i>Escherichia coli</i> . <i>Protein Expression and Purification</i> , 2015, 109, 14-22.	1.3	5
141	Resonance Assignments of the Two N-terminal RNA Recognition Motifs (RRM) of the Human Heterogeneous Nuclear Ribonucleoprotein F (HnRNP F). <i>Journal of Biomolecular NMR</i> , 2005, 33, 282-282.	2.8	3
142	An Integrated Cell-Free Assay to Study Translation Regulation by Small Bacterial Noncoding RNAs. <i>Methods in Molecular Biology</i> , 2018, 1737, 177-195.	0.9	3
143	A Step-by-Step Guide to Study Protein-RNA Interactions. <i>Chimia</i> , 2019, 73, 406.	0.6	2
144	Editorial overview: Nucleic acids and their protein complexes: Progress in nucleic acid structural biology: new technologies and discoveries. <i>Current Opinion in Structural Biology</i> , 2015, 30, vii-viii.	5.7	0

#	ARTICLE	IF	CITATIONS
145	Editorial overview: Protein–nucleic acid interactions – cryo-EM, what else?. <i>Current Opinion in Structural Biology</i> , 2019, 59, vi-viii.	5.7	0