James R Williamson

List of Publications by Year
in descending order

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183 papers	17,950 citations	18436 62 h-index	15683 125 g-index
191 all docs	191 docs citations	191 times ranked	14314 citing authors

#	Article	IF	Citations
1	Monovalent cation-induced structure of telomeric DNA: The G-quartet model. Cell, 1989, 59, 871-880.	13.5	1,198
2	Inhibition of telomerase by G-quartet DMA structures. Nature, 1991, 350, 718-720.	13.7	1,080
3	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. Nature Methods, 2017, 14, 793-796.	9.0	708
4	G-Quartet Structures in Telomeric DNA. Annual Review of Biophysics and Biomolecular Structure, 1994, 23, 703-730.	18.3	675
5	Conformation of the TAR RNA-arginine complex by NMR spectroscopy. Science, 1992, 257, 76-80.	6.0	607
6	alpha Helix-RNA Major Groove Recognition in an HIV-1 Rev Peptide-RRE RNA Complex. Science, 1996, 273, 1547-1551.	6.0	606
7	Overflow metabolism in Escherichia coli results from efficient proteome allocation. Nature, 2015, 528, 99-104.	13.7	566
8	A new system for naming ribosomal proteins. Current Opinion in Structural Biology, 2014, 24, 165-169.	2.6	481
9	Assembly of Bacterial Ribosomes. Annual Review of Biochemistry, 2011, 80, 501-526.	5.0	417
10	Induced fit in RNA-protein recognition. , 2000, 7, 834-837.		388
11	Kinetic intermediates in RNA folding. Science, 1994, 265, 918-924.	6.0	332
12	The catalytic diversity of RNAs. Nature Reviews Molecular Cell Biology, 2005, 6, 399-412.	16.1	307
13	Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria. Molecular Systems Biology, 2015, 11, 784.	3.2	291
14	Dual modes of RNA-silencing suppression by Flock House virus protein B2. Nature Structural and Molecular Biology, 2005, 12, 952-957.	3.6	289
15	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. Nucleic Acids Research, 1992, 20, 4515-4523.	6.5	288
16	Ligand-induced conformational changes observed in single RNA molecules. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 9077-9082.	3.3	253
17	Mg2+-dependent conformational change of RNA studied by fluorescence correlation and FRET on immobilized single molecules. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 4284-4289.	3.3	253
18	Reduction of translating ribosomes enables Escherichia coli to maintain elongation rates during slow growth. Nature Microbiology, 2017, 2, 16231.	5.9	251

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19	An assembly landscape for the 30S ribosomal subunit. Nature, 2005, 438, 628-632.	13.7	238
20	Exposing the kinetic traps in RNA folding. Current Opinion in Structural Biology, 1999, 9, 339-345.	2.6	222
21	Kinetic Intermediates Trapped by Native Interactions in RNA Folding. Science, 1998, 279, 1943-1946.	6.0	210
22	Role of RNA structure in arginine recognition of TAR RNA.. Proceedings of the National Academy of Sciences of the United States of America, 1993, 90, 3680-3684.	3.3	201
23	Structure of the S15,S6,S18-rRNA Complex: Assembly of the 30S Ribosome Central Domain. Science, 2000, 288, 107-112.	6.0	198
24	Beyond kinetic traps in RNA folding. Current Opinion in Structural Biology, 2001, 11, 309-314.	2.6	186
25	A global resource allocation strategy governs growth transition kinetics of Escherichia coli. Nature, 2017, 551, 119-123.	13.7	184
26	Visualizing Ribosome Biogenesis: Parallel Assembly Pathways for the 30 <i>S</i> Subunit. Science, 2010, 330, 673-677.	6.0	181
27	Modular Assembly of the Bacterial Large Ribosomal Subunit. Cell, 2016, 167, 1610-1622.e15.	13.5	163
28	Quantitative Analysis of Protein-RNA Interactions by Gel Mobility Shift. Methods in Molecular Biology, 2008, 488, 99-115.	0.4	157
29	The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenosine in tRNA. Nucleic Acids Research, 2009, 37, 2894-2909.	6.5	150
30	Enthalpy arrays. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 9517-9522.	3.3	147
31	Binding of an HIV Rev peptide to Rev responsive element RNA induces formation of purine-purine base pairs. Biochemistry, 1994, 33, 2741-2747.	1.2	144
32	Characterization of the overall and internal dynamics of short oligonucleotides by depolarized dynamic light scattering and NMR relaxation measurements. Biochemistry, 1990, 29, 799-811.	1.2	143
33	RNA Helical Packing in Solution: NMR Structure of a 30kDa GAAA Tetraloopâ€"Receptor Complex. Journal of Molecular Biology, 2005, 351, 371-382.	2.0	142
34	A universal trade-off between growth and lag in fluctuating environments. Nature, 2020, 584, 470-474.	13.7	139
35	[13] Preparation of isotopically enriched RNAs for heteronuclear NMR. Methods in Enzymology, 1995, 261, 300-322.	0.4	137
36	Solution structure of the HIV-2 TAR-argininamide complex 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1997, 267, 624-639.	2.0	137

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37	Guanine quartets. Current Opinion in Structural Biology, 1993, 3, 357-362.	2.6	120
38	RNA target specificity of the STAR/GSG domain post-transcriptional regulatory protein GLD-1. Nature Structural and Molecular Biology, 2004, 11, 20-28.	3.6	115
39	A novel loop-loop recognition motif in the yeast ribosomal protein L30 autoregulatory RNA complex. Nature Structural Biology, 1999, 6, 1139-1147.	9.7	114
40	Cooperativity in macromolecular assembly. Nature Chemical Biology, 2008, 4, 458-465.	3.9	112
41	A CCHC metal-binding domain in Nanos is essential for translational regulation. EMBO Journal, 1997, 16, 834-843.	3.5	108
42	Fast folding mutants of the Tetrahymena group I ribozyme reveal a rugged folding energy landscape 1 1Edited by D. Draper. Journal of Molecular Biology, 1998, 281, 609-620.	2.0	106
43	Cooperativity in RNA-Protein Interactions: Global Analysis of RNA Binding Specificity. Cell Reports, 2012, 1, 570-581.	2.9	106
44	Characterization of the Ribosome Biogenesis Landscape in E. coli Using Quantitative Mass Spectrometry. Journal of Molecular Biology, 2013, 425, 767-779.	2.0	106
45	Structure and dynamics of bacterial ribosome biogenesis. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160181.	1.8	103
46	The kinetic folding pathway of the Tetrahymena ribozyme reveals possible similarities between RNA and protein folding. Nature Structural Biology, 1996, 3, 432-438.	9.7	102
47	Systematic Chromosomal Deletion of Bacterial Ribosomal Protein Genes. Journal of Molecular Biology, 2011, 413, 751-761.	2.0	100
48	Detection of N-Hmiddle dotmiddle dotmiddle dotN hydrogen bonding in RNA via scalar couplings in the absence of observable imino proton resonances. Nucleic Acids Research, 2000, 28, 1585-1593.	6.5	99
49	Quantitative Analysis of rRNA Modifications Using Stable Isotope Labeling and Mass Spectrometry. Journal of the American Chemical Society, 2014, 136, 2058-2069.	6.6	95
50	Multinuclear NMR studies of DNA hairpins. 1. Structure and dynamics of d(CGCGTTGTTCGCG). Biochemistry, 1989, 28, 2819-2831.	1.2	92
51	Preparation of Specifically Deuterated RNA for NMR Studies Using a Combination of Chemical and Enzymatic Synthesisâ€. Journal of the American Chemical Society, 1996, 118, 7929-7940.	6.6	89
52	A Complex Assembly Landscape for the 30S Ribosomal Subunit. Annual Review of Biophysics, 2009, 38, 197-215.	4.5	89
53	The PUMILIOâ˜’RNA Interaction:â€‰ A Single RNA-Binding Domain Monomer Recognizes a Bipartite Target Sequence. Biochemistry, 1999, 38, 596-604.	1.2	86
54	Protein and Mg2+-induced conformational changes in the S15 binding site of 16 s ribosomal RNA. Journal of Molecular Biology, 1998, 275, 453-464.	2.0	83

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55	Pathway Engineered Enzymatic <i>de Novo</i> Purine Nucleotide Synthesis. ACS Chemical Biology, 2008, 3, 499-511.	1.6	83
56	3D15Nâ˜13Câ˜13C Chemical Shift Correlation Spectroscopy in Rotating Solids. Journal of the American Chemical Society, 1997, 119, 8540-8546.	6.6	81
57	Specificity of the STAR/GSG domain protein Qk1: Implications for the regulation of myelination. Rna, 2004, 10, 1449-1458.	1.6	81
58	Chemical Probe for Glycosidic Conformation in Telomeric DNAs. Journal of the American Chemical Society, 1994, 116, 4479-4480.	6.6	80
59	An optimal Mg2+ concentration for kinetic folding of the Tetrahymena ribozyme. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 12471-12476.	3.3	80
60	Discovery of a small molecule that inhibits bacterial ribosome biogenesis. ELife, 2014, 3, e03574.	2.8	74
61	Measuring Food Intake and Nutrient Absorption in <i>Caenorhabditis elegans</i>. Genetics, 2015, 200, 443-454.	1.2	74
62	Synthesis of 5-Fluoropyrimidine Nucleotides as Sensitive NMR Probes of RNA Structure. Journal of the American Chemical Society, 2007, 129, 14911-14921.	6.6	73
63	Base flexibility in HIV-2 TAR RNA mapped by solution 15N, 13C NMR relaxation. Journal of Molecular Biology, 2002, 317, 263-278.	2.0	71
64	Interaction of theBacillus stearothermophilusRibosomal Protein S15 with 16 S rRNA: I. Defining the Minimal RNA Site. Journal of Molecular Biology, 1996, 261, 536-549.	2.0	70
65	The Effect of Ribosome Assembly Cofactors on In Vitro 30S Subunit Reconstitution. Journal of Molecular Biology, 2010, 398, 1-7.	2.0	69
66	A dominant negative mutant of the E. coli RNA helicase DbpA blocks assembly of the 50S ribosomal subunit. Nucleic Acids Research, 2009, 37, 6503-6514.	6.5	65
67	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in E. coli. ELife, 2014, 3, .	2.8	65
68	Measurement of Long-Range1Hâ˜19F Scalar Coupling Constants and Their Glycosidic Torsion Dependence in 5-Fluoropyrimidine-Substituted RNA. Journal of the American Chemical Society, 2006, 128, 5851-5858.	6.6	64
69	Functional domains of the 50S subunit mature late in the assembly process. Nucleic Acids Research, 2014, 42, 3419-3435.	6.5	64
70	Effects of polyvalent cations on the folding of an rRNA three-way junction and binding of ribosomal protein S15. Rna, 1998, 4, 984-997.	1.6	63
71	DDX1 Is an RNA-Dependent ATPase Involved in HIV-1 Rev Function and Virus Replication. Journal of Molecular Biology, 2012, 415, 61-74.	2.0	62
72	Enzymatic Synthesis and19F NMR Studies of 2-Fluoroadenine-Substituted RNA. Journal of the American Chemical Society, 2004, 126, 11776-11777.	6.6	61

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73	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. Cell, 2019, 179, 1357-1369.e16.	13.5	61
74	RNA Tertiary Structure and Cooperative Assembly of a Large Ribonucleoprotein Complex. Journal of Molecular Biology, 2004, 344, 395-407.	2.0	60
75	NMR analysis of tRNA acceptor stem microhelices: discriminator base change affects tRNA conformation at the 3' end.. Proceedings of the National Academy of Sciences of the United States of America, 1994, 91, 11467-11471.	3.3	59
76	[2] Preparation of specifically 2H- and 13C-labeled ribonucleotides. Methods in Enzymology, 2000, 317, 18-38.	0.4	59
77	The RNA Ontology Consortium: An open invitation to the RNA community. Rna, 2006, 12, 533-541.	1.6	59
78	Enzymatic De Novo Pyrimidine Nucleotide Synthesis. Journal of the American Chemical Society, 2011, 133, 297-304.	6.6	59
79	Joint X-Ray and NMR Refinement of the Yeast L30e-mRNA Complex. Structure, 2004, 12, 1165-1176.	1.6	58
80	Central domain assembly: thermodynamics and kinetics of S6 and S18 binding to an S15-RNA complex 1 1Edited by D. Draper. Journal of Molecular Biology, 2001, 313, 35-48.	2.0	55
81	Interaction of theBacillus stearothermophilusRibosomal Protein S15 with 16 S rRNA: II. Specificity Determinants of RNA-Protein Recognition. Journal of Molecular Biology, 1996, 261, 550-567.	2.0	54
82	Measuring the dynamics of E. coli ribosome biogenesis using pulse-labeling and quantitative mass spectrometry. Molecular BioSystems, 2012, 8, 3325.	2.9	54
83	Synergy of NMR, Computation, and X-Ray Crystallography for Structural Biology. Structure, 2009, 17, 499-507.	1.6	53
84	Slowdown of Translational Elongation in <i>Escherichia coli</i> under Hyperosmotic Stress. MBio, 2018, 9, .	1.8	53
85	After the ribosome structures: How are the subunits assembled?. Rna, 2003, 9, 165-167.	1.6	52
86	Application of NMR SHAPES Screening to an RNA Target. Journal of the American Chemical Society, 2003, 125, 15724-15725.	6.6	51
87	A three-fluorophore FRET assay for high-throughput screening of small-molecule inhibitors of ribosome assembly. Nucleic Acids Research, 2004, 32, 2707-2715.	6.5	50
88	Preparation of Specifically Deuterated and13C-Labeled RNA for NMR Studies Using Enzymatic Synthesisâ€. Journal of the American Chemical Society, 1997, 119, 12100-12108.	6.6	49
89	Single-Molecule Studies Reveal that DEAD Box Protein DDX1 Promotes Oligomerization of HIV-1 Rev on the Rev Response Element. Journal of Molecular Biology, 2011, 410, 959-971.	2.0	48
90	Quantitative Analysis of Isotope Distributions In Proteomic Mass Spectrometry Using Least-Squares Fourier Transform Convolution. Analytical Chemistry, 2008, 80, 4906-4917.	3.2	45

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91	Kinetic cooperativity in <i>Escherichia coli</i> 30S ribosomal subunit reconstitution reveals additional complexity in the assembly landscape. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 5417-5422.	3.3	44
92	FRET Characterization of Complex Conformational Changes in a Large 16S Ribosomal RNA Fragment Site-Specifically Labeled Using Unnatural Base Pairs. ACS Chemical Biology, 2016, 11, 1347-1353.	1.6	44
93	Multinuclear NMR studies of DNA hairpins. 2. Sequence-dependent structural variations. Biochemistry, 1989, 28, 2831-2836.	1.2	43
94	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. Nature Communications, 2018, 9, 5087.	5.8	43
95	Translation attenuation by minocycline enhances longevity and proteostasis in old post-stress-responsive organisms. ELife, 2018, 7, .	2.8	43
96	Concerted kinetic folding of a multidomain ribozyme with a disrupted loop-receptor interaction. Journal of Molecular Biology, 2001, 305, 11-21.	2.0	42
97	YphC and YsxC GTPases assist the maturation of the central protuberance, GTPase associated region and functional core of the 50S ribosomal subunit. Nucleic Acids Research, 2016, 44, 8442-8455.	6.5	42
98	Quantitative Proteomic Analysis of Ribosome Assembly and Turnover In Vivo. Journal of Molecular Biology, 2010, 403, 331-345.	2.0	41
99	A hierarchy of RNA subdomains in assembly of the central domain of the 30 S ribosomal subunit. Rna, 2000, 6, 402-408.	1.6	40
100	Identification of a Conserved Interface between PUF and CPEB Proteins. Journal of Biological Chemistry, 2012, 287, 18854-18862.	1.6	40
101	UHMâ€“ULM interactions in the RBM39â€“U2AF65 splicing-factor complex. Acta Crystallographica Section D: Structural Biology, 2016, 72, 497-511.	1.1	36
102	RNA-protein interactions promote asymmetric sorting of the ASH1 mRNA ribonucleoprotein complex. Rna, 2003, 9, 1383-1399.	1.6	34
103	Role of Era in assembly and homeostasis of the ribosomal small subunit. Nucleic Acids Research, 2019, 47, 8301-8317.	6.5	34
104	Protein structure and oligomerization are important for the formation of exportâ€·competent HIVâ€·1 Revâ€“RRE complexes. Protein Science, 2008, 17, 420-430.	3.1	33
105	Enzymatic Synthesis and Structural Characterization of ¹³C, ¹⁵N-Poly(ADP-ribose). Journal of the American Chemical Society, 2009, 131, 14571-14578.	6.6	33
106	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. Molecular Systems Biology, 2021, 17, e10064.	3.2	33
107	Inherent Protein Structural Flexibility at the RNA-binding Interface of L30e. Journal of Molecular Biology, 2003, 326, 999-1004.	2.0	32
108	Binding properties of YjeQ (RsgA), RbfA, RimM and Era to assembly intermediates of the 30S subunit. Nucleic Acids Research, 2016, 44, gkw613.	6.5	32

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109	ArcA overexpression induces fermentation and results in enhanced growth rates of E. coli. Scientific Reports, 2017, 7, 11866.	1.6	32
110	Local folding coupled to RNA binding in the yeast ribosomal protein L30 1 1Edited by D. E. Draper. Journal of Molecular Biology, 1999, 292, 345-359.	2.0	31
111	Interaction of the Bacillus stearothermophilus ribosomal protein S15 with its 5â€²-translational operator mRNA 1 1Edited by I. Tinoco. Journal of Molecular Biology, 2001, 314, 413-422.	2.0	31
112	Differential Sensitivity of Target Genes to Translational Repression by miR-17~92. PLoS Genetics, 2017, 13, e1006623.	1.5	31
113	Biophysical studies of bacterial ribosome assembly. Current Opinion in Structural Biology, 2008, 18, 299-304.	2.6	29
114	Crystal Structure of Lsm3 Octamer from Saccharomyces cerevisiae: Implications for Lsm Ring Organisation and Recruitment. Journal of Molecular Biology, 2008, 377, 1357-1371.	2.0	29
115	NMR evidence for a base triple in the HIV-2 TAR C-G.C+ mutant- argininamide complex. Nucleic Acids Research, 1998, 26, 1991-1995.	6.5	28
116	Synthesis of a thymidine phospboramidite labelled with13C at C6: relaxation studies of the loop region in a13C labelled DNA hairpin. Nucleic Acids Research, 1988, 16, 1529-1540.	6.5	27
117	Rapid procedure for chemical sequencing of small oligonucleotides without ethanol precipitation. Nucleic Acids Research, 1990, 18, 379-379.	6.5	27
118	Structural mimicry in the phage phi21 N peptide-boxB RNA complex. Rna, 2003, 9, 663-676.	1.6	26
119	Numerical Matrices Method for Nonlinear System Identification and Description of Dynamics of Biochemical Reaction Networks. Biophysical Journal, 2007, 92, 3459-3473.	0.2	26
120	Structural Analysis of the Quaking Homodimerization Interface. Journal of Molecular Biology, 2012, 423, 766-781.	2.0	26
121	Toward a Whole-Cell Model of Ribosome Biogenesis: Kinetic Modeling of SSU Assembly. Biophysical Journal, 2015, 109, 1117-1135.	0.2	25
122	RNAâ€"protein binding kinetics in an automated microfluidic reactor. Nucleic Acids Research, 2009, 37, e142-e142.	6.5	24
123	An alternative resource allocation strategy in the chemolithoautotrophic archaeon <i>Methanococcus maripaludis</i>. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	24
124	The Binding Interface between Bacillus stearothermophilus Ribosomal Protein S15 and its 5â€²-Translational Operator mRNA. Journal of Molecular Biology, 2005, 351, 280-290.	2.0	23
125	My h-index Turns 40: My Midlife Crisis of Impact. ACS Chemical Biology, 2009, 4, 311-313.	1.6	23
126	Structure of the GLD-1 Homodimerization Domain: Insights into STAR Protein-Mediated Translational Regulation. Structure, 2010, 18, 377-389.	1.6	23

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127	Quantitation of ten 30S ribosomal assembly intermediates using fluorescence triple correlation spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 13614-13619.	3.3	23
128	Functional Interaction between Ribosomal Protein L6 and RbgA during Ribosome Assembly. PLoS Genetics, 2014, 10, e1004694.	1.5	23
129	A Survey of DDX21 Activity During Rev/RRE Complex Formation. Journal of Molecular Biology, 2018, 430, 537-553.	2.0	23
130	Quantitative ESI-TOF Analysis of Macromolecular Assembly Kinetics. Analytical Chemistry, 2008, 80, 9379-9386.	3.2	22
131	The Structure of the NXF2/NXT1 Heterodimeric Complex Reveals the Combined Specificity and Versatility of the NTF2-Like Fold. Journal of Molecular Biology, 2012, 415, 649-665.	2.0	22
132	SrmB Rescues Trapped Ribosome Assembly Intermediates. Journal of Molecular Biology, 2020, 432, 978-990.	2.0	21
133	Assembly of the 30S ribosomal subunit. Quarterly Reviews of Biophysics, 2006, 38, 397-403.	2.4	20
134	The Spectroscopic Basis of Fluorescence Triple Correlation Spectroscopy. Journal of Physical Chemistry B, 2012, 116, 1908-1919.	1.2	20
135	3D C(CC)H TOCSY Experiment for Assigning Protons and Carbons in Uniformly13C- and Selectively2H-Labeled RNA. Journal of Magnetic Resonance, 1998, 130, 97-101.	1.2	18
136	Strong coupling effects during X-pulse CPMG experiments recorded on heteronuclear ABX spin systems: artifacts and a simple solution. Journal of Biomolecular NMR, 2007, 38, 41-46.	1.6	18
137	Biochemical Characterization of the Caenorhabditis elegans FBFâ‹…CPB-1 Translational Regulation Complex Identifies Conserved Protein Interaction Hotspots. Journal of Molecular Biology, 2013, 425, 725-737.	2.0	18
138	NMR Pulse Schemes for the Sequential Assignment of Arginine Side-Chain HÏµProtons. Journal of Magnetic Resonance Series B, 1996, 113, 272-276.	1.6	17
139	Improvement in the Apparent Mass Resolution of Oligonucleotides by Using12C/14N-Enriched Samples. Analytical Chemistry, 2002, 74, 226-231.	3.2	17
140	A DEAD-box protein acts through RNA to promote HIV-1 Rev-RRE assembly. Nucleic Acids Research, 2017, 45, 4632-4641.	6.5	17
141	Small subunit, big science. Nature, 2000, 407, 306-307.	13.7	16
142	Solution NMR Studies of the Maturation Intermediates of a 13ÂMDa Viral Capsid. Journal of the American Chemical Society, 2007, 129, 7867-7876.	6.6	16
143	A Proteinâ‹…Protein Interaction Platform Involved in Recruitment of GLD-3 to the FBFâ‹…fem-3 mRNA Complex. Journal of Molecular Biology, 2013, 425, 738-754.	2.0	16
144	Residual Dipolar Coupling TOCSY for Direct Through Space Correlations of Base Protons and Phosphorus Nuclei in RNA. Journal of the American Chemical Society, 2001, 123, 3395-3396.	6.6	15

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145	A novel PH-cT-COSY methodology for measuring JPH coupling constants in unlabeled nucleic acids. application to HIV-2 TAR RNA. Journal of Biomolecular NMR, 2002, 22, 65-81.	1.6	15
146	New RNA Labeling Methods Offer Dramatic Sensitivity Enhancements in2H NMR Relaxation Spectra. Journal of the American Chemical Society, 2006, 128, 9346-9347.	6.6	15
147	Quantitation of the Ribosomal Protein Autoregulatory Network Using Mass Spectrometry. Analytical Chemistry, 2010, 82, 5038-5045.	3.2	15
148	The Activation-Induced Assembly of an RNA/Protein Interactome Centered on the Splicing Factor U2AF2 Regulates Gene Expression in Human CD4 T Cells. PLoS ONE, 2015, 10, e0144409.	1.1	15
149	Quantitative mining of compositional heterogeneity in cryo-EM datasets of ribosome assembly intermediates. Structure, 2022, 30, 498-509.e4.	1.6	14
150	[21] Kinetic oligonucleotide hybridization for monitoring kinetic folding of large RNAs. Methods in Enzymology, 2000, 317, 330-353.	0.4	13
151	Novel Intersubunit Interaction Critical for HIV-1 Core Assembly Defines a Potentially Targetable Inhibitor Binding Pocket. MBio, 2019, 10, .	1.8	13
152	Pytheas: a software package for the automated analysis of RNA sequences and modifications via tandem mass spectrometry. Nature Communications, 2022, 13, 2424.	5.8	13
153	High-affinity consensus binding of target RNAs by the STAR/GSG proteins GLD-1, STAR-2 and Quaking. BMC Molecular Biology, 2010, 11, 48.	3.0	12
154	RNA origami. Nature Structural and Molecular Biology, 1994, 1, 270-272.	3.6	11
155	PACE Analysis of RNA-Peptide Interactions. , 1999, 118, 129-141.		11
156	A DEAD-Box Helicase Mediates an RNA Structural Transition in the HIV-1 Rev Response Element. Journal of Molecular Biology, 2017, 429, 697-714.	2.0	11
157	RNA Recognition by HIV-1 Tat and Rev. Seminars in Virology, 1997, 8, 186-193.	4.1	10
158	Shape-specific Nucleotide Binding of Single-stranded RNA by the GLD-1 STAR Domain. Journal of Molecular Biology, 2005, 346, 91-104.	2.0	10
159	Envelope: interactive software for modeling and fitting complex isotope distributions. BMC Bioinformatics, 2008, 9, 446.	1.2	9
160	The Ribosome at Atomic Resolution. Cell, 2009, 139, 1041-1043.	13.5	9
161	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. Protein Science, 2016, 25, 1545-1550.	3.1	9
162	Monitoring Assembly of Ribonucleoprotein Complexes by Isothermal Titration Calorimetry. Methods in Molecular Biology, 2008, 488, 117-127.	0.4	9

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163	Aptly named aptamers display their aptitude. Nature, 1996, 382, 112-113.	13.7	8
164	Discrimination between Functional and Non-functional Cellular Gag Complexes involved in HIV-1 Assembly. Journal of Molecular Biology, 2021, 433, 166842.	2.0	8
165	Combinatorial crystallization of an RNAâ€"protein complex. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 466-473.	2.5	7
166	Stable isotope pulse-chase monitored by quantitative mass spectrometry applied to E. coli 30S ribosome assembly kinetics. Methods, 2009, 49, 136-141.	1.9	6
167	A simple method for preparing pools of synthetic oligonucleotides with random point deletions. Nucleic Acids Research, 1995, 23, 3603-3604.	6.5	5
168	The Histone H1-Like Protein AlgP Facilitates Even Spacing of Polyphosphate Granules in Pseudomonas aeruginosa. MBio, 2022, 13, e0246321.	1.8	5
169	The Structure of Aquifex aeolicus Ribosomal Protein S8 Reveals a Unique Subdomain that Contributes to an Extremely Tight Association with 16S rRNA. Journal of Molecular Biology, 2012, 415, 489-502.	2.0	4
170	Really exasperating viral protein from HIV. ELife, 2015, 4, .	2.8	4
171	NMR assignments of HIV-2 TAR RNA. Biomolecular NMR Assignments, 2008, 2, 167-169.	0.4	3
172	Balancing Teaching and Research in Obtaining a Faculty Position at a Predominantly Undergraduate Institution. ACS Chemical Biology, 2007, 2, 521-524.	1.6	2
173	Vectorized data acquisition and fast triple-correlation integrals for Fluorescence Triple Correlation Spectroscopy. Computer Physics Communications, 2013, 184, 1322-1332.	3.0	1
174	Cellular Physiology of Bacterial Ribosome Assembly. FASEB Journal, 2010, 24, 197.2.	0.2	1
175	Growth rate-dependent coordination of catabolism and anabolism in the archaeon <i>Methanococcus maripaludis</i> under phosphate limitation. ISME Journal, 2022, 16, 2313-2319.	4.4	1
176	A Higher Degree of Difficulty. ACS Chemical Biology, 2007, 2, 197-199.	1.6	0
177	Nucleic acids continue to surprise. Current Opinion in Structural Biology, 2010, 20, 259-261.	2.6	0
178	Fluorescence Triple Correlation Spectroscopy Resolves Ten Intermediates Along Different Parallel Ribosome Assembly Pathways. Biophysical Journal, 2012, 102, 599a-600a.	0.2	0
179	Digging deep into nucleic acid structure and nucleic acid protein recognition. Current Opinion in Structural Biology, 2012, 22, 249-250.	2.6	0
180	Dynamics of the Ribosome Assembly Line in Living Cells. Biophysical Journal, 2013, 104, 355a.	0.2	0

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181	OBSERVING CONFORMATIONAL CHANGES OF INDIVIDUAL RNA MOLECULES USING CONFOCAL MICROSCOPY. , 2001, , .		0
182	RNA FOLDING IN RIBOSOME ASSEMBLY. , 2004, , .		0
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