

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	Quantitative mining of compositional heterogeneity in cryo-EM datasets of ribosome assembly intermediates. <i>Structure</i> , 2022, 30, 498-509.e4.	1.6	14
2	The Histone H1-Like Protein AlgP Facilitates Even Spacing of Polyphosphate Granules in <i>Pseudomonas aeruginosa</i> . <i>MBio</i> , 2022, 13, e0246321.	1.8	5
3	Pytheas: a software package for the automated analysis of RNA sequences and modifications via tandem mass spectrometry. <i>Nature Communications</i> , 2022, 13, 2424.	5.8	13
4	Growth rate-dependent coordination of catabolism and anabolism in the archaeon <i>Methanococcus maripaludis</i> under phosphate limitation. <i>ISME Journal</i> , 2022, 16, 2313-2319.	4.4	1
5	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. <i>Molecular Systems Biology</i> , 2021, 17, e10064.	3.2	33
6	Discrimination between Functional and Non-functional Cellular Gag Complexes involved in HIV-1 Assembly. <i>Journal of Molecular Biology</i> , 2021, 433, 166842.	2.0	8
7	An alternative resource allocation strategy in the chemolithoautotrophic archaeon <i>Methanococcus maripaludis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	24
8	SrmB Rescues Trapped Ribosome Assembly Intermediates. <i>Journal of Molecular Biology</i> , 2020, 432, 978-990.	2.0	21
9	A universal trade-off between growth and lag in fluctuating environments. <i>Nature</i> , 2020, 584, 470-474.	13.7	139
10	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , 2019, 47, 8301-8317.	6.5	34
11	Novel Intersubunit Interaction Critical for HIV-1 Core Assembly Defines a Potentially Targetable Inhibitor Binding Pocket. <i>MBio</i> , 2019, 10, .	1.8	13
12	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. <i>Cell</i> , 2019, 179, 1357-1369.e16.	13.5	61
13	Slowdown of Translational Elongation in <i>Escherichia coli</i> under Hyperosmotic Stress. <i>MBio</i> , 2018, 9, .	1.8	53
14	A Survey of DDX21 Activity During Rev/RRE Complex Formation. <i>Journal of Molecular Biology</i> , 2018, 430, 537-553.	2.0	23
15	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. <i>Nature Communications</i> , 2018, 9, 5087.	5.8	43
16	Translation attenuation by minocycline enhances longevity and proteostasis in old post-stress-responsive organisms. <i>ELife</i> , 2018, 7, .	2.8	43
17	A DEAD-Box Helicase Mediates an RNA Structural Transition in the HIV-1 Rev Response Element. <i>Journal of Molecular Biology</i> , 2017, 429, 697-714.	2.0	11
18	Structure and dynamics of bacterial ribosome biogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160181.	1.8	103

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19	A DEAD-box protein acts through RNA to promote HIV-1 Rev-RRE assembly. <i>Nucleic Acids Research</i> , 2017, 45, 4632-4641.	6.5	17
20	Reduction of translating ribosomes enables <i>Escherichia coli</i> to maintain elongation rates during slow growth. <i>Nature Microbiology</i> , 2017, 2, 16231.	5.9	251
21	A global resource allocation strategy governs growth transition kinetics of <i>Escherichia coli</i> . <i>Nature</i> , 2017, 551, 119-123.	13.7	184
22	ArcA overexpression induces fermentation and results in enhanced growth rates of <i>E. coli</i> . <i>Scientific Reports</i> , 2017, 7, 11866.	1.6	32
23	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , 2017, 14, 793-796.	9.0	708
24	Differential Sensitivity of Target Genes to Translational Repression by miR-17~92. <i>PLoS Genetics</i> , 2017, 13, e1006623.	1.5	31
25	Binding properties of YjeQ (RsgA), RbfA, RimM and Era to assembly intermediates of the 30S subunit. <i>Nucleic Acids Research</i> , 2016, 44, gkw613.	6.5	32
26	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , 2016, 167, 1610-1622.e15.	13.5	163
27	UHMâ€“ULM interactions in the RBM39â€“U2AF65 splicing-factor complex. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 497-511.	1.1	36
28	YphC and YsxG GTPases assist the maturation of the central protuberance, GTPase associated region and functional core of the 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2016, 44, 8442-8455.	6.5	42
29	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. <i>Protein Science</i> , 2016, 25, 1545-1550.	3.1	9
30	FRET Characterization of Complex Conformational Changes in a Large 16S Ribosomal RNA Fragment Site-Specifically Labeled Using Unnatural Base Pairs. <i>ACS Chemical Biology</i> , 2016, 11, 1347-1353.	1.6	44
31	Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria. <i>Molecular Systems Biology</i> , 2015, 11, 784.	3.2	291
32	Toward a Whole-Cell Model of Ribosome Biogenesis: Kinetic Modeling of SSU Assembly. <i>Biophysical Journal</i> , 2015, 109, 1117-1135.	0.2	25
33	Measuring Food Intake and Nutrient Absorption in <i>Caenorhabditis elegans</i> . <i>Genetics</i> , 2015, 200, 443-454.	1.2	74
34	Overflow metabolism in <i>Escherichia coli</i> results from efficient proteome allocation. <i>Nature</i> , 2015, 528, 99-104.	13.7	566
35	The Activation-Induced Assembly of an RNA/Protein Interactome Centered on the Splicing Factor U2AF2 Regulates Gene Expression in Human CD4 T Cells. <i>PLoS ONE</i> , 2015, 10, e0144409.	1.1	15
36	Really exasperating viral protein from HIV. <i>ELife</i> , 2015, 4, .	2.8	4

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37	Discovery of a small molecule that inhibits bacterial ribosome biogenesis. <i>ELife</i> , 2014, 3, e03574.	2.8	74
38	Functional Interaction between Ribosomal Protein L6 and RbgA during Ribosome Assembly. <i>PLoS Genetics</i> , 2014, 10, e1004694.	1.5	23
39	Functional domains of the 50S subunit mature late in the assembly process. <i>Nucleic Acids Research</i> , 2014, 42, 3419-3435.	6.5	64
40	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014, 24, 165-169.	2.6	481
41	Quantitative Analysis of rRNA Modifications Using Stable Isotope Labeling and Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2014, 136, 2058-2069.	6.6	95
42	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in <i>E. coli</i> . <i>ELife</i> , 2014, 3, .	2.8	65
43	Biochemical Characterization of the <i>Caenorhabditis elegans</i> FBF $\hat{\alpha}$...CPB-1 Translational Regulation Complex Identifies Conserved Protein Interaction Hotspots. <i>Journal of Molecular Biology</i> , 2013, 425, 725-737.	2.0	18
44	Vectorized data acquisition and fast triple-correlation integrals for Fluorescence Triple Correlation Spectroscopy. <i>Computer Physics Communications</i> , 2013, 184, 1322-1332.	3.0	1
45	Dynamics of the Ribosome Assembly Line in Living Cells. <i>Biophysical Journal</i> , 2013, 104, 355a.	0.2	0
46	A Protein $\hat{\alpha}$...Protein Interaction Platform Involved in Recruitment of GLD-3 to the FBF $\hat{\alpha}$...fem-3 mRNA Complex. <i>Journal of Molecular Biology</i> , 2013, 425, 738-754.	2.0	16
47	Characterization of the Ribosome Biogenesis Landscape in <i>E. coli</i> Using Quantitative Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2013, 425, 767-779.	2.0	106
48	Identification of a Conserved Interface between PUF and CPEB Proteins. <i>Journal of Biological Chemistry</i> , 2012, 287, 18854-18862.	1.6	40
49	Fluorescence Triple Correlation Spectroscopy Resolves Ten Intermediates Along Different Parallel Ribosome Assembly Pathways. <i>Biophysical Journal</i> , 2012, 102, 599a-600a.	0.2	0
50	The Spectroscopic Basis of Fluorescence Triple Correlation Spectroscopy. <i>Journal of Physical Chemistry B</i> , 2012, 116, 1908-1919.	1.2	20
51	DDX1 Is an RNA-Dependent ATPase Involved in HIV-1 Rev Function and Virus Replication. <i>Journal of Molecular Biology</i> , 2012, 415, 61-74.	2.0	62
52	The Structure of <i>Aquifex aeolicus</i> Ribosomal Protein S8 Reveals a Unique Subdomain that Contributes to an Extremely Tight Association with 16S rRNA. <i>Journal of Molecular Biology</i> , 2012, 415, 489-502.	2.0	4
53	The Structure of the NXF2/NXT1 Heterodimeric Complex Reveals the Combined Specificity and Versatility of the NTF2-Like Fold. <i>Journal of Molecular Biology</i> , 2012, 415, 649-665.	2.0	22
54	Cooperativity in RNA-Protein Interactions: Global Analysis of RNA Binding Specificity. <i>Cell Reports</i> , 2012, 1, 570-581.	2.9	106

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55	Measuring the dynamics of <i>E. coli</i> ribosome biogenesis using pulse-labeling and quantitative mass spectrometry. <i>Molecular BioSystems</i> , 2012, 8, 3325.	2.9	54
56	Structural Analysis of the Quaking Homodimerization Interface. <i>Journal of Molecular Biology</i> , 2012, 423, 766-781.	2.0	26
57	Quantitation of ten 30S ribosomal assembly intermediates using fluorescence triple correlation spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13614-13619.	3.3	23
58	Digging deep into nucleic acid structure and nucleic acid protein recognition. <i>Current Opinion in Structural Biology</i> , 2012, 22, 249-250.	2.6	0
59	Enzymatic De Novo Pyrimidine Nucleotide Synthesis. <i>Journal of the American Chemical Society</i> , 2011, 133, 297-304.	6.6	59
60	Single-Molecule Studies Reveal that DEAD Box Protein DDX1 Promotes Oligomerization of HIV-1 Rev on the Rev Response Element. <i>Journal of Molecular Biology</i> , 2011, 410, 959-971.	2.0	48
61	Systematic Chromosomal Deletion of Bacterial Ribosomal Protein Genes. <i>Journal of Molecular Biology</i> , 2011, 413, 751-761.	2.0	100
62	Assembly of Bacterial Ribosomes. <i>Annual Review of Biochemistry</i> , 2011, 80, 501-526.	5.0	417
63	Nucleic acids continue to surprise. <i>Current Opinion in Structural Biology</i> , 2010, 20, 259-261.	2.6	0
64	Structure of the GLD-1 Homodimerization Domain: Insights into STAR Protein-Mediated Translational Regulation. <i>Structure</i> , 2010, 18, 377-389.	1.6	23
65	High-affinity consensus binding of target RNAs by the STAR/GSG proteins GLD-1, STAR-2 and Quaking. <i>BMC Molecular Biology</i> , 2010, 11, 48.	3.0	12
66	Kinetic cooperativity in <i>Escherichia coli</i> 30S ribosomal subunit reconstitution reveals additional complexity in the assembly landscape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 5417-5422.	3.3	44
67	Visualizing Ribosome Biogenesis: Parallel Assembly Pathways for the 30S Subunit. <i>Science</i> , 2010, 330, 673-677.	6.0	181
68	Quantitation of the Ribosomal Protein Autoregulatory Network Using Mass Spectrometry. <i>Analytical Chemistry</i> , 2010, 82, 5038-5045.	3.2	15
69	The Effect of Ribosome Assembly Cofactors on In Vitro 30S Subunit Reconstitution. <i>Journal of Molecular Biology</i> , 2010, 398, 1-7.	2.0	69
70	Quantitative Proteomic Analysis of Ribosome Assembly and Turnover In Vivo. <i>Journal of Molecular Biology</i> , 2010, 403, 331-345.	2.0	41
71	Cellular Physiology of Bacterial Ribosome Assembly. <i>FASEB Journal</i> , 2010, 24, 197.2.	0.2	1
72	A dominant negative mutant of the <i>E. coli</i> RNA helicase DbpA blocks assembly of the 50S ribosomal subunit. <i>Nucleic Acids Research</i> , 2009, 37, 6503-6514.	6.5	65

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73	The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenosine in tRNA. <i>Nucleic Acids Research</i> , 2009, 37, 2894-2909.	6.5	150
74	RNA-protein binding kinetics in an automated microfluidic reactor. <i>Nucleic Acids Research</i> , 2009, 37, e142-e142.	6.5	24
75	Synergy of NMR, Computation, and X-Ray Crystallography for Structural Biology. <i>Structure</i> , 2009, 17, 499-507.	1.6	53
76	A Complex Assembly Landscape for the 30S Ribosomal Subunit. <i>Annual Review of Biophysics</i> , 2009, 38, 197-215.	4.5	89
77	My h-index Turns 40: My Midlife Crisis of Impact. <i>ACS Chemical Biology</i> , 2009, 4, 311-313.	1.6	23
78	Enzymatic Synthesis and Structural Characterization of ¹³ C, ¹⁵ N-Poly(ADP-ribose). <i>Journal of the American Chemical Society</i> , 2009, 131, 14571-14578.	6.6	33
79	The Ribosome at Atomic Resolution. <i>Cell</i> , 2009, 139, 1041-1043.	13.5	9
80	Stable isotope pulse-chase monitored by quantitative mass spectrometry applied to E. coli 30S ribosome assembly kinetics. <i>Methods</i> , 2009, 49, 136-141.	1.9	6
81	NMR assignments of HIV-2 TAR RNA. <i>Biomolecular NMR Assignments</i> , 2008, 2, 167-169.	0.4	3
82	Protein structure and oligomerization are important for the formation of export-competent HIV-1 Rev-RRE complexes. <i>Protein Science</i> , 2008, 17, 420-430.	3.1	33
83	Cooperativity in macromolecular assembly. <i>Nature Chemical Biology</i> , 2008, 4, 458-465.	3.9	112
84	Envelope: interactive software for modeling and fitting complex isotope distributions. <i>BMC Bioinformatics</i> , 2008, 9, 446.	1.2	9
85	Biophysical studies of bacterial ribosome assembly. <i>Current Opinion in Structural Biology</i> , 2008, 18, 299-304.	2.6	29
86	Crystal Structure of Lsm3 Octamer from <i>Saccharomyces cerevisiae</i> : Implications for Lsm Ring Organisation and Recruitment. <i>Journal of Molecular Biology</i> , 2008, 377, 1357-1371.	2.0	29
87	Quantitative Analysis of Protein-RNA Interactions by Gel Mobility Shift. <i>Methods in Molecular Biology</i> , 2008, 488, 99-115.	0.4	157
88	Quantitative Analysis of Isotope Distributions In Proteomic Mass Spectrometry Using Least-Squares Fourier Transform Convolution. <i>Analytical Chemistry</i> , 2008, 80, 4906-4917.	3.2	45
89	Quantitative ESI-TOF Analysis of Macromolecular Assembly Kinetics. <i>Analytical Chemistry</i> , 2008, 80, 9379-9386.	3.2	22
90	Pathway Engineered Enzymatic <i>de Novo</i> Purine Nucleotide Synthesis. <i>ACS Chemical Biology</i> , 2008, 3, 499-511.	1.6	83

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91	Monitoring Assembly of Ribonucleoprotein Complexes by Isothermal Titration Calorimetry. <i>Methods in Molecular Biology</i> , 2008, 488, 117-127.	0.4	9
92	NMR structural characterization of the homodimerization domain of the translational repressor GLD-1. <i>FASEB Journal</i> , 2008, 22, 783.1.	0.2	0
93	Synthesis of 5-Fluoropyrimidine Nucleotides as Sensitive NMR Probes of RNA Structure. <i>Journal of the American Chemical Society</i> , 2007, 129, 14911-14921.	6.6	73
94	A Higher Degree of Difficulty. <i>ACS Chemical Biology</i> , 2007, 2, 197-199.	1.6	0
95	Balancing Teaching and Research in Obtaining a Faculty Position at a Predominantly Undergraduate Institution. <i>ACS Chemical Biology</i> , 2007, 2, 521-524.	1.6	2
96	Solution NMR Studies of the Maturation Intermediates of a 13ÅMDa Viral Capsid. <i>Journal of the American Chemical Society</i> , 2007, 129, 7867-7876.	6.6	16
97	Numerical Matrices Method for Nonlinear System Identification and Description of Dynamics of Biochemical Reaction Networks. <i>Biophysical Journal</i> , 2007, 92, 3459-3473.	0.2	26
98	Strong coupling effects during X-pulse CPMG experiments recorded on heteronuclear ABX spin systems: artifacts and a simple solution. <i>Journal of Biomolecular NMR</i> , 2007, 38, 41-46.	1.6	18
99	Assembly of the 30S ribosomal subunit. <i>Quarterly Reviews of Biophysics</i> , 2006, 38, 397-403.	2.4	20
100	Measurement of Long-Range ^1H - ^{19}F Scalar Coupling Constants and Their Glycosidic Torsion Dependence in 5-Fluoropyrimidine-Substituted RNA. <i>Journal of the American Chemical Society</i> , 2006, 128, 5851-5858.	6.6	64
101	New RNA Labeling Methods Offer Dramatic Sensitivity Enhancements in ^2H NMR Relaxation Spectra. <i>Journal of the American Chemical Society</i> , 2006, 128, 9346-9347.	6.6	15
102	The RNA Ontology Consortium: An open invitation to the RNA community. <i>Rna</i> , 2006, 12, 533-541.	1.6	59
103	Dual modes of RNA-silencing suppression by Flock House virus protein B2. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 952-957.	3.6	289
104	The catalytic diversity of RNAs. <i>Nature Reviews Molecular Cell Biology</i> , 2005, 6, 399-412.	16.1	307
105	An assembly landscape for the 30S ribosomal subunit. <i>Nature</i> , 2005, 438, 628-632.	13.7	238
106	Shape-specific Nucleotide Binding of Single-stranded RNA by the GLD-1 STAR Domain. <i>Journal of Molecular Biology</i> , 2005, 346, 91-104.	2.0	10
107	RNA Helical Packing in Solution: NMR Structure of a 30kDa GAAA Tetraloop Receptor Complex. <i>Journal of Molecular Biology</i> , 2005, 351, 371-382.	2.0	142
108	The Binding Interface between <i>Bacillus stearothermophilus</i> Ribosomal Protein S15 and its 5'-Translational Operator mRNA. <i>Journal of Molecular Biology</i> , 2005, 351, 280-290.	2.0	23

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109	Specificity of the STAR/GSG domain protein Qk1: Implications for the regulation of myelination. <i>Rna</i> , 2004, 10, 1449-1458.	1.6	81
110	Enthalpy arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 9517-9522.	3.3	147
111	RNA target specificity of the STAR/GSG domain post-transcriptional regulatory protein GLD-1. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 20-28.	3.6	115
112	Joint X-Ray and NMR Refinement of the Yeast L30e-mRNA Complex. <i>Structure</i> , 2004, 12, 1165-1176.	1.6	58
113	A three-fluorophore FRET assay for high-throughput screening of small-molecule inhibitors of ribosome assembly. <i>Nucleic Acids Research</i> , 2004, 32, 2707-2715.	6.5	50
114	Enzymatic Synthesis and 19F NMR Studies of 2-Fluoro-adenine-Substituted RNA. <i>Journal of the American Chemical Society</i> , 2004, 126, 11776-11777.	6.6	61
115	RNA Tertiary Structure and Cooperative Assembly of a Large Ribonucleoprotein Complex. <i>Journal of Molecular Biology</i> , 2004, 344, 395-407.	2.0	60
116	RNA FOLDING IN RIBOSOME ASSEMBLY. , 2004, , .		0
117	Combinatorial crystallization of an RNA-protein complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 466-473.	2.5	7
118	Application of NMR SHAPES Screening to an RNA Target. <i>Journal of the American Chemical Society</i> , 2003, 125, 15724-15725.	6.6	51
119	Inherent Protein Structural Flexibility at the RNA-binding Interface of L30e. <i>Journal of Molecular Biology</i> , 2003, 326, 999-1004.	2.0	32
120	RNA-protein interactions promote asymmetric sorting of the ASH1 mRNA ribonucleoprotein complex. <i>Rna</i> , 2003, 9, 1383-1399.	1.6	34
121	Structural mimicry in the phage phi21 N peptide-boxB RNA complex. <i>Rna</i> , 2003, 9, 663-676.	1.6	26
122	After the ribosome structures: How are the subunits assembled?. <i>Rna</i> , 2003, 9, 165-167.	1.6	52
123	Mg ²⁺ -dependent conformational change of RNA studied by fluorescence correlation and FRET on immobilized single molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 4284-4289.	3.3	253
124	Improvement in the Apparent Mass Resolution of Oligonucleotides by Using ¹² C/ ¹⁴ N-Enriched Samples. <i>Analytical Chemistry</i> , 2002, 74, 226-231.	3.2	17
125	Base flexibility in HIV-2 TAR RNA mapped by solution ¹⁵ N, ¹³ C NMR relaxation. <i>Journal of Molecular Biology</i> , 2002, 317, 263-278.	2.0	71
126	A novel PH-CT-COSY methodology for measuring JPH coupling constants in unlabeled nucleic acids. application to HIV-2 TAR RNA. <i>Journal of Biomolecular NMR</i> , 2002, 22, 65-81.	1.6	15

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127	Concerted kinetic folding of a multidomain ribozyme with a disrupted loop-receptor interaction. Journal of Molecular Biology, 2001, 305, 11-21.	2.0	42
128	Central domain assembly: thermodynamics and kinetics of S6 and S18 binding to an S15-RNA complex 1 Edited by D. Draper. Journal of Molecular Biology, 2001, 313, 35-48.	2.0	55
129	Interaction of the Bacillus stearothermophilus ribosomal protein S15 with its 5â€²-translational operator mRNA 1 Edited by I. Tinoco. Journal of Molecular Biology, 2001, 314, 413-422.	2.0	31
130	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
131	Beyond kinetic traps in RNA folding. Current Opinion in Structural Biology, 2001, 11, 309-314.	2.6	186
132	OBSERVING CONFORMATIONAL CHANGES OF INDIVIDUAL RNA MOLECULES USING CONFOCAL MICROSCOPY. , 2001, , .		0
133	[21] Kinetic oligonucleotide hybridization for monitoring kinetic folding of large RNAs. Methods in Enzymology, 2000, 317, 330-353.	0.4	13
134	[2] Preparation of specifically 2H- and 13C-labeled ribonucleotides. Methods in Enzymology, 2000, 317, 18-38.	0.4	59
135	Induced fit in RNA-protein recognition. , 2000, 7, 834-837.		388
136	Small subunit, big science. Nature, 2000, 407, 306-307.	13.7	16
137	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
138	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
139	Structure of the S15,S6,S18-rRNA Complex: Assembly of the 30S Ribosome Central Domain. Science, 2000, 288, 107-112.	6.0	198
140	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
141	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
142	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
143	Exposing the kinetic traps in RNA folding. Current Opinion in Structural Biology, 1999, 9, 339-345.	2.6	222
144	PACE Analysis of RNA-Peptide Interactions. , 1999, 118, 129-141.		11

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145	The PUMILIO ¹ RNA Interaction: A Single RNA-Binding Domain Monomer Recognizes a Bipartite Target Sequence. <i>Biochemistry</i> , 1999, 38, 596-604.	1.2	86
146	Local folding coupled to RNA binding in the yeast ribosomal protein L30 1 1 Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1999, 292, 345-359.	2.0	31
147	3D C(CC)H TOCSY Experiment for Assigning Protons and Carbons in Uniformly ¹³ C- and Selectively ² H-Labeled RNA. <i>Journal of Magnetic Resonance</i> , 1998, 130, 97-101.	1.2	18
148	Protein and Mg ²⁺ -induced conformational changes in the S15 binding site of 16 s ribosomal RNA. <i>Journal of Molecular Biology</i> , 1998, 275, 453-464.	2.0	83
149	Fast folding mutants of the Tetrahymena group I ribozyme reveal a rugged folding energy landscape 1 1 Edited by D. Draper. <i>Journal of Molecular Biology</i> , 1998, 281, 609-620.	2.0	106
150	Kinetic Intermediates Trapped by Native Interactions in RNA Folding. <i>Science</i> , 1998, 279, 1943-1946.	6.0	210
151	NMR evidence for a base triple in the HIV-2 TAR C-G.C+ mutant- argininamide complex. <i>Nucleic Acids Research</i> , 1998, 26, 1991-1995.	6.5	28
152	Effects of polyvalent cations on the folding of an rRNA three-way junction and binding of ribosomal protein S15. <i>Rna</i> , 1998, 4, 984-997.	1.6	63
153	Preparation of Specifically Deuterated and ¹³ C-Labeled RNA for NMR Studies Using Enzymatic Synthesis. <i>Journal of the American Chemical Society</i> , 1997, 119, 12100-12108.	6.6	49
154	³ D ¹⁵ N- ¹³ C ¹³ C Chemical Shift Correlation Spectroscopy in Rotating Solids. <i>Journal of the American Chemical Society</i> , 1997, 119, 8540-8546.	6.6	81
155	Solution structure of the HIV-2 TAR-argininamide complex 1 1 Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 1997, 267, 624-639.	2.0	137
156	RNA Recognition by HIV-1 Tat and Rev. <i>Seminars in Virology</i> , 1997, 8, 186-193.	4.1	10
157	A CCHC metal-binding domain in Nanos is essential for translational regulation. <i>EMBO Journal</i> , 1997, 16, 834-843.	3.5	108
158	Preparation of Specifically Deuterated RNA for NMR Studies Using a Combination of Chemical and Enzymatic Synthesis. <i>Journal of the American Chemical Society</i> , 1996, 118, 7929-7940.	6.6	89
159	Interaction of the <i>Bacillus stearothermophilus</i> Ribosomal Protein S15 with 16 S rRNA: I. Defining the Minimal RNA Site. <i>Journal of Molecular Biology</i> , 1996, 261, 536-549.	2.0	70
160	alpha Helix-RNA Major Groove Recognition in an HIV-1 Rev Peptide-RRE RNA Complex. <i>Science</i> , 1996, 273, 1547-1551.	6.0	606
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