

# James R Williamson

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/6593371/james-r-williamson-publications-by-year.pdf>

**Version:** 2024-04-23

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

172  
papers

14,945  
citations

59  
h-index

119  
g-index

191  
ext. papers

16,650  
ext. citations

12.7  
avg, IF

6.61  
L-index

#	Paper	IF	Citations
172	The Histone H1-Like Protein AlgP Facilitates Even Spacing of Polyphosphate Granules in <i>Pseudomonas aeruginosa</i> .. <i>MBio</i> , <b>2022</b> , e0246321	7.8	0
171	Pytheas: a software package for the automated analysis of RNA sequences and modifications via tandem mass spectrometry.. <i>Nature Communications</i> , <b>2022</b> , 13, 2424	17.4	1
170	Global coordination of metabolic pathways in <i>Escherichia coli</i> by active and passive regulation. <i>Molecular Systems Biology</i> , <b>2021</b> , 17, e10064	12.2	5
169	Discrimination between Functional and Non-functional Cellular Gag Complexes involved in HIV-1 Assembly. <i>Journal of Molecular Biology</i> , <b>2021</b> , 433, 166842	6.5	4
168	An alternative resource allocation strategy in the chemolithoautotrophic archaeon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	6
167	SrmB Rescues Trapped Ribosome Assembly Intermediates. <i>Journal of Molecular Biology</i> , <b>2020</b> , 432, 978-990	6.5	6
166	A universal trade-off between growth and lag in fluctuating environments. <i>Nature</i> , <b>2020</b> , 584, 470-474	50.4	40
165	Novel Intersubunit Interaction Critical for HIV-1 Core Assembly Defines a Potentially Targetable Inhibitor Binding Pocket. <i>MBio</i> , <b>2019</b> , 10,	7.8	11
164	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, 8301-8317	20.1	20
163	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. <i>Cell</i> , <b>2019</b> , 179, 1357-1369.e16	16.2	31
162	Slowdown of Translational Elongation in under Hyperosmotic Stress. <i>MBio</i> , <b>2018</b> , 9,	7.8	34
161	A Survey of DDX21 Activity During Rev/RRE Complex Formation. <i>Journal of Molecular Biology</i> , <b>2018</b> , 430, 537-553	6.5	12
160	Translation attenuation by minocycline enhances longevity and proteostasis in old post-stress-responsive organisms. <i>ELife</i> , <b>2018</b> , 7,	8.9	30
159	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. <i>Nature Communications</i> , <b>2018</b> , 9, 5087	17.4	23
158	A DEAD-Box Helicase Mediates an RNA Structural Transition in the HIV-1 Rev Response Element. <i>Journal of Molecular Biology</i> , <b>2017</b> , 429, 697-714	6.5	9
157	Structure and dynamics of bacterial ribosome biogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2017</b> , 372,	5.8	52
156	A DEAD-box protein acts through RNA to promote HIV-1 Rev-RRE assembly. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, 4632-4641	20.1	9

155	A global resource allocation strategy governs growth transition kinetics of Escherichia coli. <i>Nature</i> , <b>2017</b> , 551, 119-123	50.4	96
154	Differential Sensitivity of Target Genes to Translational Repression by miR-17~92. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006623	6	26
153	ArcA overexpression induces fermentation and results in enhanced growth rates of E. coli. <i>Scientific Reports</i> , <b>2017</b> , 7, 11866	4.9	17
152	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , <b>2017</b> , 14, 793-796	21.6	368
151	Reduction of translating ribosomes enables Escherichia coli to maintain elongation rates during slow growth. <i>Nature Microbiology</i> , <b>2016</b> , 2, 16231	26.6	142
150	YphC and YsxC GTPases assist the maturation of the central protuberance, GTPase associated region and functional core of the 50S ribosomal subunit. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 8442-55	20.1	23
149	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. <i>Protein Science</i> , <b>2016</b> , 25, 1545-50	6.3	7
148	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> , <b>2016</b> , 11, 1347-53	4.9	38
147	Binding properties of YjeQ (RsgA), RbfA, RimM and Era to assembly intermediates of the 30S subunit. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 9918-9932	20.1	26
146	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , <b>2016</b> , 167, 1610-1622.e15	56.2	97
145	UHM-ULM interactions in the RBM39-U2AF65 splicing-factor complex. <i>Acta Crystallographica Section D: Structural Biology</i> , <b>2016</b> , 72, 497-511	5.5	21
144	Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 784	12.2	191
143	Toward a Whole-Cell Model of Ribosome Biogenesis: Kinetic Modeling of SSU Assembly. <i>Biophysical Journal</i> , <b>2015</b> , 109, 1117-35	2.9	20
142	Measuring Food Intake and Nutrient Absorption in Caenorhabditis elegans. <i>Genetics</i> , <b>2015</b> , 200, 443-54	4	55
141	Overflow metabolism in Escherichia coli results from efficient proteome allocation. <i>Nature</i> , <b>2015</b> , 528, 99-104	50.4	351
140	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> , <b>2015</b> , 10, e0144409	3.7	9
139	Really exasperating viral protein from HIV. <i>ELife</i> , <b>2015</b> , 4,	8.9	3
138	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , <b>2014</b> , 24, 165-9	8.1	365

137	Quantitative analysis of rRNA modifications using stable isotope labeling and mass spectrometry. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 2058-69	16.4	71
136	Discovery of a small molecule that inhibits bacterial ribosome biogenesis. <i>ELife</i> , <b>2014</b> , 3, e03574	8.9	55
135	Functional interaction between ribosomal protein L6 and RbgA during ribosome assembly. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004694	6	20
134	Functional domains of the 50S subunit mature late in the assembly process. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 3419-35	20.1	47
133	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in E. coli. <i>ELife</i> , <b>2014</b> , 3,	8.9	42
132	Biochemical characterization of the Caenorhabditis elegans FBF.CPB-1 translational regulation complex identifies conserved protein interaction hotspots. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 725-37	6.5	11
131	Vectorized data acquisition and fast triple-correlation integrals for Fluorescence Triple Correlation Spectroscopy. <i>Computer Physics Communications</i> , <b>2013</b> , 184, 1322-1332	4.2	1
130	A protein-protein interaction platform involved in recruitment of GLD-3 to the FBF.fem-3 mRNA complex. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 738-54	6.5	10
129	Characterization of the ribosome biogenesis landscape in E. coli using quantitative mass spectrometry. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 767-79	6.5	87
128	The spectroscopic basis of fluorescence triple correlation spectroscopy. <i>Journal of Physical Chemistry B</i> , <b>2012</b> , 116, 1908-19	3.4	19
127	DDX1 is an RNA-dependent ATPase involved in HIV-1 Rev function and virus replication. <i>Journal of Molecular Biology</i> , <b>2012</b> , 415, 61-74	6.5	53
126	The structure of Aquifex aeolicus ribosomal protein S8 reveals a unique subdomain that contributes to an extremely tight association with 16S rRNA. <i>Journal of Molecular Biology</i> , <b>2012</b> , 415, 489-502	6.5	4
125	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> , <b>2012</b> , 415, 649-65	6.5	17
124	Cooperativity in RNA-protein interactions: global analysis of RNA binding specificity. <i>Cell Reports</i> , <b>2012</b> , 1, 570-81	10.6	86
123	Measuring the dynamics of E. coli ribosome biogenesis using pulse-labeling and quantitative mass spectrometry. <i>Molecular BioSystems</i> , <b>2012</b> , 8, 3325-34		37
122	Structural analysis of the quaking homodimerization interface. <i>Journal of Molecular Biology</i> , <b>2012</b> , 423, 766-81	6.5	24
121	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> , <b>2012</b> , 109, 13614-9	11.5	21
120	Identification of a conserved interface between PUF and CPEB proteins. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 18854-62	5.4	33

119	Enzymatic de novo pyrimidine nucleotide synthesis. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 297-304	16.4	53
118	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> , <b>2011</b> , 410, 959-71	6.5	41
117	Systematic chromosomal deletion of bacterial ribosomal protein genes. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 751-61	6.5	81
116	Assembly of bacterial ribosomes. <i>Annual Review of Biochemistry</i> , <b>2011</b> , 80, 501-26	29.1	325
115	Kinetic cooperativity in Escherichia coli 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> , <b>2010</b> , 107, 5417-22	11.5	40
114	Visualizing ribosome biogenesis: parallel assembly pathways for the 30S subunit. <i>Science</i> , <b>2010</b> , 330, 673-7	33.3	153
113	Quantitation of the ribosomal protein autoregulatory network using mass spectrometry. <i>Analytical Chemistry</i> , <b>2010</b> , 82, 5038-45	7.8	13
112	The effect of ribosome assembly cofactors on in vitro 30S subunit reconstitution. <i>Journal of Molecular Biology</i> , <b>2010</b> , 398, 1-7	6.5	55
111	Quantitative proteomic analysis of ribosome assembly and turnover in vivo. <i>Journal of Molecular Biology</i> , <b>2010</b> , 403, 331-45	6.5	37
110	Structure of the GLD-1 homodimerization domain: insights into STAR protein-mediated translational regulation. <i>Structure</i> , <b>2010</b> , 18, 377-89	5.2	23
109	High-affinity consensus binding of target RNAs by the STAR/GSG proteins GLD-1, STAR-2 and Quaking. <i>BMC Molecular Biology</i> , <b>2010</b> , 11, 48	4.5	12
108	Cellular Physiology of Bacterial Ribosome Assembly. <i>FASEB Journal</i> , <b>2010</b> , 24, 197.2	0.9	
107	A dominant negative mutant of the E. coli RNA helicase DbpA blocks assembly of the 50S ribosomal subunit. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 6503-14	20.1	50
106	The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenosine in tRNA. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 2894-909	20.1	118
105	RNA-protein binding kinetics in an automated microfluidic reactor. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, e142	0.1	20
104	Synergy of NMR, computation, and X-ray crystallography for structural biology. <i>Structure</i> , <b>2009</b> , 17, 499-507	5.07	48
103	A complex assembly landscape for the 30S ribosomal subunit. <i>Annual Review of Biophysics</i> , <b>2009</b> , 38, 197-215	21.1	79
102	Enzymatic synthesis and structural characterization of <sup>13</sup> C, <sup>15</sup> N-poly(ADP-ribose). <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 14571-8	16.4	26

101	The ribosome at atomic resolution. <i>Cell</i> , <b>2009</b> , 139, 1041-3	56.2	5
100	Stable isotope pulse-chase monitored by quantitative mass spectrometry applied to E. coli 30S ribosome assembly kinetics. <i>Methods</i> , <b>2009</b> , 49, 136-41	4.6	5
99	Cooperativity in macromolecular assembly. <i>Nature Chemical Biology</i> , <b>2008</b> , 4, 458-65	11.7	93
98	Envelope: interactive software for modeling and fitting complex isotope distributions. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 446	3.6	9
97	Biophysical studies of bacterial ribosome assembly. <i>Current Opinion in Structural Biology</i> , <b>2008</b> , 18, 299-304	3.4	23
96	Crystal structure of Lsm3 octamer from <i>Saccharomyces cerevisiae</i> : implications for Lsm ring organisation and recruitment. <i>Journal of Molecular Biology</i> , <b>2008</b> , 377, 1357-71	6.5	23
95	Quantitative analysis of protein-RNA interactions by gel mobility shift. <i>Methods in Molecular Biology</i> , <b>2008</b> , 488, 99-115	1.4	129
94	Quantitative analysis of isotope distributions in proteomic mass spectrometry using least-squares Fourier transform convolution. <i>Analytical Chemistry</i> , <b>2008</b> , 80, 4906-17	7.8	41
93	Quantitative ESI-TOF analysis of macromolecular assembly kinetics. <i>Analytical Chemistry</i> , <b>2008</b> , 80, 9379-88	3.8	21
92	Pathway engineered enzymatic de novo purine nucleotide synthesis. <i>ACS Chemical Biology</i> , <b>2008</b> , 3, 499-511	5.1	68
91	NMR assignments of HIV-2 TAR RNA. <i>Biomolecular NMR Assignments</i> , <b>2008</b> , 2, 167-9	0.7	3
90	Protein structure and oligomerization are important for the formation of export-competent HIV-1 Rev-RRE complexes. <i>Protein Science</i> , <b>2008</b> , 17, 420-30	6.3	28
89	NMR structural characterization of the homodimerization domain of the translational repressor GLD-1. <i>FASEB Journal</i> , <b>2008</b> , 22, 783.1	0.9	
88	Monitoring assembly of ribonucleoprotein complexes by isothermal titration calorimetry. <i>Methods in Molecular Biology</i> , <b>2008</b> , 488, 117-27	1.4	9
87	Synthesis of 5-fluoropyrimidine nucleotides as sensitive NMR probes of RNA structure. <i>Journal of the American Chemical Society</i> , <b>2007</b> , 129, 14911-21	16.4	58
86	A higher degree of difficulty. <i>ACS Chemical Biology</i> , <b>2007</b> , 2, 197-9	4.9	
85	Balancing teaching and research in obtaining a faculty position at a predominantly undergraduate institution. <i>ACS Chemical Biology</i> , <b>2007</b> , 2, 521-4	4.9	0
84	Solution NMR studies of the maturation intermediates of a 13 MDa viral capsid. <i>Journal of the American Chemical Society</i> , <b>2007</b> , 129, 7867-76	16.4	14

83	Numerical Matrices Method for nonlinear system identification and description of dynamics of biochemical reaction networks. <i>Biophysical Journal</i> , <b>2007</b> , 92, 3459-73	2.9	22
82	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> , <b>2007</b> , 38, 41-6	3	18
81	The RNA Ontology Consortium: an open invitation to the RNA community. <i>Rna</i> , <b>2006</b> , 12, 533-41	5.8	49
80	Measurement of long-range <sup>1</sup> H- <sup>19</sup> F scalar coupling constants and their glycosidic torsion dependence in 5-fluoropyrimidine-substituted RNA. <i>Journal of the American Chemical Society</i> , <b>2006</b> , 128, 5851-8	16.4	58
79	New RNA labeling methods offer dramatic sensitivity enhancements in <sup>2</sup> H NMR relaxation spectra. <i>Journal of the American Chemical Society</i> , <b>2006</b> , 128, 9346-7	16.4	15
78	Shape-specific nucleotide binding of single-stranded RNA by the GLD-1 STAR domain. <i>Journal of Molecular Biology</i> , <b>2005</b> , 346, 91-104	6.5	9
77	RNA helical packing in solution: NMR structure of a 30 kDa GAAA tetraloop-receptor complex. <i>Journal of Molecular Biology</i> , <b>2005</b> , 351, 371-82	6.5	128
76	The binding interface between <i>Bacillus stearothermophilus</i> ribosomal protein S15 and its 5S rRNA translational operator mRNA. <i>Journal of Molecular Biology</i> , <b>2005</b> , 351, 280-90	6.5	19
75	Assembly of the 30S ribosomal subunit. <i>Quarterly Reviews of Biophysics</i> , <b>2005</b> , 38, 397-403	7	18
74	Dual modes of RNA-silencing suppression by Flock House virus protein B2. <i>Nature Structural and Molecular Biology</i> , <b>2005</b> , 12, 952-7	17.6	249
73	The catalytic diversity of RNAs. <i>Nature Reviews Molecular Cell Biology</i> , <b>2005</b> , 6, 399-412	48.7	270
72	An assembly landscape for the 30S ribosomal subunit. <i>Nature</i> , <b>2005</b> , 438, 628-32	50.4	214
71	Specificity of the STAR/GSG domain protein Qk1: implications for the regulation of myelination. <i>Rna</i> , <b>2004</b> , 10, 1449-58	5.8	72
70	Enthalpy arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 9517-22	11.5	122
69	RNA target specificity of the STAR/GSG domain post-transcriptional regulatory protein GLD-1. <i>Nature Structural and Molecular Biology</i> , <b>2004</b> , 11, 20-8	17.6	100
68	Joint X-ray and NMR refinement of the yeast L30e-mRNA complex. <i>Structure</i> , <b>2004</b> , 12, 1165-76	5.2	56
67	A three-fluorophore FRET assay for high-throughput screening of small-molecule inhibitors of ribosome assembly. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 2707-15	20.1	46
66	Enzymatic synthesis and <sup>19</sup> F NMR studies of 2-fluoroadenine-substituted RNA. <i>Journal of the American Chemical Society</i> , <b>2004</b> , 126, 11776-7	16.4	48

65	RNA tertiary structure and cooperative assembly of a large ribonucleoprotein complex. <i>Journal of Molecular Biology</i> , <b>2004</b> , 344, 395-407	6.5	56
64	Combinatorial crystallization of an RNA-protein complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , <b>2003</b> , 59, 466-73		5
63	Application of NMR SHAPES screening to an RNA target. <i>Journal of the American Chemical Society</i> , <b>2003</b> , 125, 15724-5	16.4	47
62	Inherent protein structural flexibility at the RNA-binding interface of L30e. <i>Journal of Molecular Biology</i> , <b>2003</b> , 326, 999-1004	6.5	31
61	RNA-protein interactions promote asymmetric sorting of the ASH1 mRNA ribonucleoprotein complex. <i>Rna</i> , <b>2003</b> , 9, 1383-99	5.8	31
60	Structural mimicry in the phage phi21 N peptide-boxB RNA complex. <i>Rna</i> , <b>2003</b> , 9, 663-76	5.8	24
59	After the ribosome structures: how are the subunits assembled?. <i>Rna</i> , <b>2003</b> , 9, 165-7	5.8	49
58	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> , <b>2002</b> , 22, 65-81	3	14
57	Mg <sup>2+</sup> -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> , <b>2002</b> , 99, 4284-9	11.5	238
56	Improvement in the apparent mass resolution of oligonucleotides by using <sup>12</sup> C/ <sup>14</sup> N-enriched samples. <i>Analytical Chemistry</i> , <b>2002</b> , 74, 226-31	7.8	15
55	Base flexibility in HIV-2 TAR RNA mapped by solution ( <sup>15</sup> N), ( <sup>13</sup> C) NMR relaxation. <i>Journal of Molecular Biology</i> , <b>2002</b> , 317, 263-78	6.5	70
54	Beyond kinetic traps in RNA folding. <i>Current Opinion in Structural Biology</i> , <b>2001</b> , 11, 309-14	8.1	172
53	Concerted kinetic folding of a multidomain ribozyme with a disrupted loop-receptor interaction. <i>Journal of Molecular Biology</i> , <b>2001</b> , 305, 11-21	6.5	40
52	Central domain assembly: thermodynamics and kinetics of S6 and S18 binding to an S15-RNA complex. <i>Journal of Molecular Biology</i> , <b>2001</b> , 313, 35-48	6.5	51
51	Interaction of the <i>Bacillus stearothermophilus</i> ribosomal protein S15 with its 5Rtranslational operator mRNA. <i>Journal of Molecular Biology</i> , <b>2001</b> , 314, 413-22	6.5	26
50	Residual dipolar coupling TOCSY for direct through space correlations of base protons and phosphorus nuclei in RNA. <i>Journal of the American Chemical Society</i> , <b>2001</b> , 123, 3395-6	16.4	14
49	Kinetic oligonucleotide hybridization for monitoring kinetic folding of large RNAs. <i>Methods in Enzymology</i> , <b>2000</b> , 317, 330-53	1.7	13
48	Preparation of specifically <sup>2</sup> H- and <sup>13</sup> C-labeled ribonucleotides. <i>Methods in Enzymology</i> , <b>2000</b> , 317, 18-38.7		56



47	Induced fit in RNA-protein recognition. <i>Nature Structural Biology</i> , <b>2000</b> , 7, 834-7		355
46	A hierarchy of RNA subdomains in assembly of the central domain of the 30 S ribosomal subunit. <i>Rna</i> , <b>2000</b> , 6, 402-8	5.8	37
45	Detection of N-H...N hydrogen bonding in RNA via scalar couplings in the absence of observable imino proton resonances. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 1585-93	20.1	93
44	Structure of the S15,S6,S18-rRNA complex: assembly of the 30S ribosome central domain. <i>Science</i> , <b>2000</b> , 288, 107-13	33.3	176
43	Ligand-induced conformational changes observed in single RNA molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1999</b> , 96, 9077-82	11.5	232
42	An optimal Mg(2+) concentration for kinetic folding of the tetrahymena ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1999</b> , 96, 12471-6	11.5	75
41	A novel loop-loop recognition motif in the yeast ribosomal protein L30 autoregulatory RNA complex. <i>Nature Structural Biology</i> , <b>1999</b> , 6, 1139-47		99
40	Exposing the kinetic traps in RNA folding. <i>Current Opinion in Structural Biology</i> , <b>1999</b> , 9, 339-45	8.1	198
39	PACE analysis of RNA-peptide interactions. <i>Methods in Molecular Biology</i> , <b>1999</b> , 118, 129-41	1.4	10
38	The PUMILIO-RNA interaction: a single RNA-binding domain monomer recognizes a bipartite target sequence. <i>Biochemistry</i> , <b>1999</b> , 38, 596-604	3.2	78
37	Local folding coupled to RNA binding in the yeast ribosomal protein L30. <i>Journal of Molecular Biology</i> , <b>1999</b> , 292, 345-59	6.5	28
36	3D C(CC)H TOCSY experiment for assigning protons and carbons in uniformly <sup>13</sup> C- and selectively <sup>2</sup> H-labeled RNA. <i>Journal of Magnetic Resonance</i> , <b>1998</b> , 130, 97-101	3	17
35	Protein and Mg(2+)-induced conformational changes in the S15 binding site of 16 S ribosomal RNA. <i>Journal of Molecular Biology</i> , <b>1998</b> , 275, 453-64	6.5	78
34	Fast folding mutants of the Tetrahymena group I ribozyme reveal a rugged folding energy landscape. <i>Journal of Molecular Biology</i> , <b>1998</b> , 281, 609-20	6.5	103
33	Kinetic intermediates trapped by native interactions in RNA folding. <i>Science</i> , <b>1998</b> , 279, 1943-6	33.3	201
32	NMR evidence for a base triple in the HIV-2 TAR C-G.C+ mutant-argininamide complex. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 1991-5	20.1	26
31	Effects of polyvalent cations on the folding of an rRNA three-way junction and binding of ribosomal protein S15. <i>Rna</i> , <b>1998</b> , 4, 984-97	5.8	58
30	Preparation of Specifically Deuterated and <sup>13</sup> C-Labeled RNA for NMR Studies Using Enzymatic Synthesis. <i>Journal of the American Chemical Society</i> , <b>1997</b> , 119, 12100-12108	16.4	44

29	3D $^{15}\text{N}$ / $^{13}\text{C}$ / $^{13}\text{C}$ Chemical Shift Correlation Spectroscopy in Rotating Solids. <i>Journal of the American Chemical Society</i> , <b>1997</b> , 119, 8540-8546	16.4	76
28	Solution structure of the HIV-2 TAR-argininamide complex. <i>Journal of Molecular Biology</i> , <b>1997</b> , 267, 624-635	3.5	129
27	RNA Recognition by HIV-1 Tat and Rev. <i>Seminars in Virology</i> , <b>1997</b> , 8, 186-193		10
26	A CCHC metal-binding domain in Nanos is essential for translational regulation. <i>EMBO Journal</i> , <b>1997</b> , 16, 834-43	13	93
25	Preparation of Specifically Deuterated RNA for NMR Studies Using a Combination of Chemical and Enzymatic Synthesis. <i>Journal of the American Chemical Society</i> , <b>1996</b> , 118, 7929-7940	16.4	78
24	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> , <b>1996</b> , 261, 536-49	6.5	69
23	Alpha helix-RNA major groove recognition in an HIV-1 rev peptide-RRE RNA complex. <i>Science</i> , <b>1996</b> , 273, 1547-51	33.3	556
22	Interaction of the <i>Bacillus stearothermophilus</i> ribosomal protein S15 with 16 S rRNA: II. Specificity determinants of RNA-protein recognition. <i>Journal of Molecular Biology</i> , <b>1996</b> , 261, 550-67	6.5	52
21	NMR pulse schemes for the sequential assignment of arginine side-chain H epsilon protons. <i>Journal of Magnetic Resonance Series B</i> , <b>1996</b> , 113, 272-6		16
20	The kinetic folding pathway of the <i>Tetrahymena</i> ribozyme reveals possible similarities between RNA and protein folding. <i>Nature Structural Biology</i> , <b>1996</b> , 3, 432-8		93
19	A simple method for preparing pools of synthetic oligonucleotides with random point deletions. <i>Nucleic Acids Research</i> , <b>1995</b> , 23, 3603-4	20.1	4
18	Preparation of isotopically enriched RNAs for heteronuclear NMR. <i>Methods in Enzymology</i> , <b>1995</b> , 261, 300-22	1.7	129
17	G-quartet structures in telomeric DNA. <i>Annual Review of Biophysics and Biomolecular Structure</i> , <b>1994</b> , 23, 703-30		638
16	Chemical Probe for Glycosidic Conformation in Telomeric DNAs. <i>Journal of the American Chemical Society</i> , <b>1994</b> , 116, 4479-4480	16.4	72
15	Binding of an HIV Rev peptide to Rev responsive element RNA induces formation of purine-purine base pairs. <i>Biochemistry</i> , <b>1994</b> , 33, 2741-7	3.2	133
14	Kinetic intermediates in RNA folding. <i>Science</i> , <b>1994</b> , 265, 918-24	33.3	310
13	NMR analysis of tRNA acceptor stem microhelices: discriminator base change affects tRNA conformation at the 3' end. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1994</b> , 91, 11467-71	11.5	51
12	Guanine quartets. <i>Current Opinion in Structural Biology</i> , <b>1993</b> , 3, 357-362	8.1	115

11	Role of RNA structure in arginine recognition of TAR RNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1993</b> , 90, 3680-4	11.5	184
10	Conformation of the TAR RNA-arginine complex by NMR spectroscopy. <i>Science</i> , <b>1992</b> , 257, 76-80	33.3	557
9	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. <i>Nucleic Acids Research</i> , <b>1992</b> , 20, 4515-23	20.1	273
8	Inhibition of telomerase by G-quartet DNA structures. <i>Nature</i> , <b>1991</b> , 350, 718-20	50.4	1002
7	Rapid procedure for chemical sequencing of small oligonucleotides without ethanol precipitation. <i>Nucleic Acids Research</i> , <b>1990</b> , 18, 379	20.1	23
6	Characterization of the overall and internal dynamics of short oligonucleotides by depolarized dynamic light scattering and NMR relaxation measurements. <i>Biochemistry</i> , <b>1990</b> , 29, 799-811	3.2	133
5	Monovalent cation-induced structure of telomeric DNA: the G-quartet model. <i>Cell</i> , <b>1989</b> , 59, 871-80	56.2	1080
4	Multinuclear NMR studies of DNA hairpins. 1. Structure and dynamics of d(CGCGTTGTTCCGCG). <i>Biochemistry</i> , <b>1989</b> , 28, 2819-31	3.2	85
3	Multinuclear NMR studies of DNA hairpins. 2. Sequence-dependent structural variations. <i>Biochemistry</i> , <b>1989</b> , 28, 2831-6	3.2	38
2	Synthesis of a thymidine phosphoramidite labelled with <sup>13</sup> C at C6: relaxation studies of the loop region in a <sup>13</sup> C labelled DNA hairpin. <i>Nucleic Acids Research</i> , <b>1988</b> , 16, 1529-40	20.1	24
1	Role of Era in Assembly and Homeostasis of the Ribosomal Small Subunit		1