

James R Williamson

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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	Monovalent cation-induced structure of telomeric DNA: the G-quartet model. <i>Cell</i> , 1989 , 59, 871-80	56.2	1080
171	Inhibition of telomerase by G-quartet DNA structures. <i>Nature</i> , 1991 , 350, 718-20	50.4	1002
170	G-quartet structures in telomeric DNA. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1994 , 23, 703-30		638
169	Conformation of the TAR RNA-arginine complex by NMR spectroscopy. <i>Science</i> , 1992 , 257, 76-80	33.3	557
168	Alpha helix-RNA major groove recognition in an HIV-1 rev peptide-RRE RNA complex. <i>Science</i> , 1996 , 273, 1547-51	33.3	556
167	Addressing preferred specimen orientation in single-particle cryo-EM through tilting. <i>Nature Methods</i> , 2017 , 14, 793-796	21.6	368
166	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014 , 24, 165-9	8.1	365
165	Induced fit in RNA-protein recognition. <i>Nature Structural Biology</i> , 2000 , 7, 834-7		355
164	Overflow metabolism in Escherichia coli results from efficient proteome allocation. <i>Nature</i> , 2015 , 528, 99-104	50.4	351
163	Assembly of bacterial ribosomes. <i>Annual Review of Biochemistry</i> , 2011 , 80, 501-26	29.1	325
162	Kinetic intermediates in RNA folding. <i>Science</i> , 1994 , 265, 918-24	33.3	310
161	Preparation of isotopically labeled ribonucleotides for multidimensional NMR spectroscopy of RNA. <i>Nucleic Acids Research</i> , 1992 , 20, 4515-23	20.1	273
160	The catalytic diversity of RNAs. <i>Nature Reviews Molecular Cell Biology</i> , 2005 , 6, 399-412	48.7	270
159	Dual modes of RNA-silencing suppression by Flock House virus protein B2. <i>Nature Structural and Molecular Biology</i> , 2005 , 12, 952-7	17.6	249
158	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, 4284-9	11.5	238
157	Ligand-induced conformational changes observed in single RNA molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 9077-82	11.5	232
156	An assembly landscape for the 30S ribosomal subunit. <i>Nature</i> , 2005 , 438, 628-32	50.4	214

155	Kinetic intermediates trapped by native interactions in RNA folding. <i>Science</i> , 1998 , 279, 1943-6	33.3	201
154	Exposing the kinetic traps in RNA folding. <i>Current Opinion in Structural Biology</i> , 1999 , 9, 339-45	8.1	198
153	Quantitative proteomic analysis reveals a simple strategy of global resource allocation in bacteria. <i>Molecular Systems Biology</i> , 2015 , 11, 784	12.2	191
152	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> , 1993 , 90, 3680-4	11.5	184
151	Structure of the S15,S6,S18-rRNA complex: assembly of the 30S ribosome central domain. <i>Science</i> , 2000 , 288, 107-13	33.3	176
150	Beyond kinetic traps in RNA folding. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 309-14	8.1	172
149	Visualizing ribosome biogenesis: parallel assembly pathways for the 30S subunit. <i>Science</i> , 2010 , 330, 673-7	33.3	153
148	Reduction of translating ribosomes enables Escherichia coli to maintain elongation rates during slow growth. <i>Nature Microbiology</i> , 2016 , 2, 16231	26.6	142
147	Binding of an HIV Rev peptide to Rev responsive element RNA induces formation of purine-purine base pairs. <i>Biochemistry</i> , 1994 , 33, 2741-7	3.2	133
146	Characterization of the overall and internal dynamics of short oligonucleotides by depolarized dynamic light scattering and NMR relaxation measurements. <i>Biochemistry</i> , 1990 , 29, 799-811	3.2	133
145	Solution structure of the HIV-2 TAR-argininamide complex. <i>Journal of Molecular Biology</i> , 1997 , 267, 624-35	3.5	129
144	Quantitative analysis of protein-RNA interactions by gel mobility shift. <i>Methods in Molecular Biology</i> , 2008 , 488, 99-115	1.4	129
143	Preparation of isotopically enriched RNAs for heteronuclear NMR. <i>Methods in Enzymology</i> , 1995 , 261, 300-22	1.7	129
142	RNA helical packing in solution: NMR structure of a 30 kDa GAAA tetraloop-receptor complex. <i>Journal of Molecular Biology</i> , 2005 , 351, 371-82	6.5	128
141	Enthalpy arrays. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 9517-22	11.5	122
140	The universal YrdC/Sua5 family is required for the formation of threonylcarbamoyladenine in tRNA. <i>Nucleic Acids Research</i> , 2009 , 37, 2894-909	20.1	118
139	Guanine quartets. <i>Current Opinion in Structural Biology</i> , 1993 , 3, 357-362	8.1	115
138	Fast folding mutants of the Tetrahymena group I ribozyme reveal a rugged folding energy landscape. <i>Journal of Molecular Biology</i> , 1998 , 281, 609-20	6.5	103

137	RNA target specificity of the STAR/GSG domain post-transcriptional regulatory protein GLD-1. <i>Nature Structural and Molecular Biology</i> , 2004 , 11, 20-8	17.6	100
136	A novel loop-loop recognition motif in the yeast ribosomal protein L30 autoregulatory RNA complex. <i>Nature Structural Biology</i> , 1999 , 6, 1139-47		99
135	Modular Assembly of the Bacterial Large Ribosomal Subunit. <i>Cell</i> , 2016 , 167, 1610-1622.e15	56.2	97
134	A global resource allocation strategy governs growth transition kinetics of Escherichia coli. <i>Nature</i> , 2017 , 551, 119-123	50.4	96
133	A CCHC metal-binding domain in Nanos is essential for translational regulation. <i>EMBO Journal</i> , 1997 , 16, 834-43	13	93
132	Cooperativity in macromolecular assembly. <i>Nature Chemical Biology</i> , 2008 , 4, 458-65	11.7	93
131	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> , 2000 , 28, 1585-93	20.1	93
130	The kinetic folding pathway of the Tetrahymena ribozyme reveals possible similarities between RNA and protein folding. <i>Nature Structural Biology</i> , 1996 , 3, 432-8		93
129	Characterization of the ribosome biogenesis landscape in E. coli using quantitative mass spectrometry. <i>Journal of Molecular Biology</i> , 2013 , 425, 767-79	6.5	87
128	Cooperativity in RNA-protein interactions: global analysis of RNA binding specificity. <i>Cell Reports</i> , 2012 , 1, 570-81	10.6	86
127	Multinuclear NMR studies of DNA hairpins. 1. Structure and dynamics of d(CGCGTTGTTGCG). <i>Biochemistry</i> , 1989 , 28, 2819-31	3.2	85
126	Systematic chromosomal deletion of bacterial ribosomal protein genes. <i>Journal of Molecular Biology</i> , 2011 , 413, 751-61	6.5	81
125	A complex assembly landscape for the 30S ribosomal subunit. <i>Annual Review of Biophysics</i> , 2009 , 38, 197-215	21.1	79
124	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, 453-64	6.5	78
123	The PUMILIO-RNA interaction: a single RNA-binding domain monomer recognizes a bipartite target sequence. <i>Biochemistry</i> , 1999 , 38, 596-604	3.2	78
122	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	16.4	78
121	3D 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	16.4	76
120	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> , 1999 , 96, 12471-6	11.5	75

119	Specificity of the STAR/GSG domain protein Qk1: implications for the regulation of myelination. <i>Rna</i> , 2004 , 10, 1449-58	5.8	72
118	Chemical Probe for Glycosidic Conformation in Telomeric DNAs. <i>Journal of the American Chemical Society</i> , 1994 , 116, 4479-4480	16.4	72
117	Quantitative analysis of rRNA modifications using stable isotope labeling and mass spectrometry. <i>Journal of the American Chemical Society</i> , 2014 , 136, 2058-69	16.4	71
116	Base flexibility in HIV-2 TAR RNA mapped by solution (15)N, (13)C NMR relaxation. <i>Journal of Molecular Biology</i> , 2002 , 317, 263-78	6.5	70
115	Interaction of the Bacillus stearothermophilus ribosomal protein S15 with 16 S rRNA: I. Defining the minimal RNA site. <i>Journal of Molecular Biology</i> , 1996 , 261, 536-49	6.5	69
114	Pathway engineered enzymatic de novo purine nucleotide synthesis. <i>ACS Chemical Biology</i> , 2008 , 3, 499-511	5.1	68
113	Synthesis of 5-fluoropyrimidine nucleotides as sensitive NMR probes of RNA structure. <i>Journal of the American Chemical Society</i> , 2007 , 129, 14911-21	16.4	58
112	Measurement of long-range 1H-19F scalar coupling constants and their glycosidic torsion dependence in 5-fluoropyrimidine-substituted RNA. <i>Journal of the American Chemical Society</i> , 2006 , 128, 5851-8	16.4	58
111	Effects of polyvalent cations on the folding of an rRNA three-way junction and binding of ribosomal protein S15. <i>Rna</i> , 1998 , 4, 984-97	5.8	58
110	Joint X-ray and NMR refinement of the yeast L30e-mRNA complex. <i>Structure</i> , 2004 , 12, 1165-76	5.2	56
109	RNA tertiary structure and cooperative assembly of a large ribonucleoprotein complex. <i>Journal of Molecular Biology</i> , 2004 , 344, 395-407	6.5	56
108	Preparation of specifically 2H- and 13C-labeled ribonucleotides. <i>Methods in Enzymology</i> , 2000 , 317, 18-38	3.7	56
107	Measuring Food Intake and Nutrient Absorption in Caenorhabditis elegans. <i>Genetics</i> , 2015 , 200, 443-54	4	55
106	Discovery of a small molecule that inhibits bacterial ribosome biogenesis. <i>ELife</i> , 2014 , 3, e03574	8.9	55
105	The effect of ribosome assembly cofactors on in vitro 30S subunit reconstitution. <i>Journal of Molecular Biology</i> , 2010 , 398, 1-7	6.5	55
104	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	6.5	53
103	Enzymatic de novo pyrimidine nucleotide synthesis. <i>Journal of the American Chemical Society</i> , 2011 , 133, 297-304	16.4	53
102	Structure and dynamics of bacterial ribosome biogenesis. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017 , 372,	5.8	52

101	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> , 1996 , 261, 550-67	6.5	52
100	Central domain assembly: thermodynamics and kinetics of S6 and S18 binding to an S15-RNA complex. <i>Journal of Molecular Biology</i> , 2001 , 313, 35-48	6.5	51
99	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> , 1994 , 91, 11467-71	11.5	51
98	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, 6503-14	20.1	50
97	The RNA Ontology Consortium: an open invitation to the RNA community. <i>Rna</i> , 2006 , 12, 533-41	5.8	49
96	After the ribosome structures: how are the subunits assembled?. <i>Rna</i> , 2003 , 9, 165-7	5.8	49
95	Synergy of NMR, computation, and X-ray crystallography for structural biology. <i>Structure</i> , 2009 , 17, 499-507	5.0	48
94	Enzymatic synthesis and 19F NMR studies of 2-fluoroadenine-substituted RNA. <i>Journal of the American Chemical Society</i> , 2004 , 126, 11776-7	16.4	48
93	Functional domains of the 50S subunit mature late in the assembly process. <i>Nucleic Acids Research</i> , 2014 , 42, 3419-35	20.1	47
92	Application of NMR SHAPES screening to an RNA target. <i>Journal of the American Chemical Society</i> , 2003 , 125, 15724-5	16.4	47
91	A three-fluorophore FRET assay for high-throughput screening of small-molecule inhibitors of ribosome assembly. <i>Nucleic Acids Research</i> , 2004 , 32, 2707-15	20.1	46
90	Preparation of Specifically Deuterated and 13C-Labeled RNA for NMR Studies Using Enzymatic Synthesis. <i>Journal of the American Chemical Society</i> , 1997 , 119, 12100-12108	16.4	44
89	A combined quantitative mass spectrometry and electron microscopy analysis of ribosomal 30S subunit assembly in <i>E. coli</i> . <i>ELife</i> , 2014 , 3,	8.9	42
88	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, 959-71	6.5	41
87	Quantitative analysis of isotope distributions in proteomic mass spectrometry using least-squares Fourier transform convolution. <i>Analytical Chemistry</i> , 2008 , 80, 4906-17	7.8	41
86	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, 5417-22	11.5	40
85	Concerted kinetic folding of a multidomain ribozyme with a disrupted loop-receptor interaction. <i>Journal of Molecular Biology</i> , 2001 , 305, 11-21	6.5	40
84	A universal trade-off between growth and lag in fluctuating environments. <i>Nature</i> , 2020 , 584, 470-474	50.4	40

83	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, 1347-53	4.9	38
82	Multinuclear NMR studies of DNA hairpins. 2. Sequence-dependent structural variations. <i>Biochemistry</i> , 1989 , 28, 2831-6	3.2	38
81	Measuring the dynamics of E. coli ribosome biogenesis using pulse-labeling and quantitative mass spectrometry. <i>Molecular BioSystems</i> , 2012 , 8, 3325-34		37
80	Quantitative proteomic analysis of ribosome assembly and turnover in vivo. <i>Journal of Molecular Biology</i> , 2010 , 403, 331-45	6.5	37
79	A hierarchy of RNA subdomains in assembly of the central domain of the 30 S ribosomal subunit. <i>Rna</i> , 2000 , 6, 402-8	5.8	37
78	Slowdown of Translational Elongation in under Hyperosmotic Stress. <i>MBio</i> , 2018 , 9,	7.8	34
77	Identification of a conserved interface between PUF and CPEB proteins. <i>Journal of Biological Chemistry</i> , 2012 , 287, 18854-62	5.4	33
76	Inherent protein structural flexibility at the RNA-binding interface of L30e. <i>Journal of Molecular Biology</i> , 2003 , 326, 999-1004	6.5	31
75	RNA-protein interactions promote asymmetric sorting of the ASH1 mRNA ribonucleoprotein complex. <i>Rna</i> , 2003 , 9, 1383-99	5.8	31
74	Transient Protein-RNA Interactions Guide Nascent Ribosomal RNA Folding. <i>Cell</i> , 2019 , 179, 1357-1369.e16.2	16.2	31
73	Translation attenuation by minocycline enhances longevity and proteostasis in old post-stress-responsive organisms. <i>ELife</i> , 2018 , 7,	8.9	30
72	Protein structure and oligomerization are important for the formation of export-competent HIV-1 Rev-RRE complexes. <i>Protein Science</i> , 2008 , 17, 420-30	6.3	28
71	Local folding coupled to RNA binding in the yeast ribosomal protein L30. <i>Journal of Molecular Biology</i> , 1999 , 292, 345-59	6.5	28
70	Differential Sensitivity of Target Genes to Translational Repression by miR-17~92. <i>PLoS Genetics</i> , 2017 , 13, e1006623	6	26
69	Enzymatic synthesis and structural characterization of ¹³ C, ¹⁵ N-poly(ADP-ribose). <i>Journal of the American Chemical Society</i> , 2009 , 131, 14571-8	16.4	26
68	Interaction of the Bacillus stearothermophilus ribosomal protein S15 with its 5Rtranslational operator mRNA. <i>Journal of Molecular Biology</i> , 2001 , 314, 413-22	6.5	26
67	NMR evidence for a base triple in the HIV-2 TAR C-G.C+ mutant-argininamide complex. <i>Nucleic Acids Research</i> , 1998 , 26, 1991-5	20.1	26
66	Binding properties of YjeQ (RsgA), RbfA, RimM and Era to assembly intermediates of the 30S subunit. <i>Nucleic Acids Research</i> , 2016 , 44, 9918-9932	20.1	26

65	Structural analysis of the quaking homodimerization interface. <i>Journal of Molecular Biology</i> , 2012 , 423, 766-81	6.5	24
64	Structural mimicry in the phage phi21 N peptide-boxB RNA complex. <i>Rna</i> , 2003 , 9, 663-76	5.8	24
63	Synthesis of a thymidine phosphoramidite labelled with ¹³ C at C6: relaxation studies of the loop region in a ¹³ C labelled DNA hairpin. <i>Nucleic Acids Research</i> , 1988 , 16, 1529-40	20.1	24
62	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> , 2016 , 44, 8442-55	20.1	23
61	Structure of the GLD-1 homodimerization domain: insights into STAR protein-mediated translational regulation. <i>Structure</i> , 2010 , 18, 377-89	5.2	23
60	Biophysical studies of bacterial ribosome assembly. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 299-304		23
59	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, 1357-71	6.5	23
58	Rapid procedure for chemical sequencing of small oligonucleotides without ethanol precipitation. <i>Nucleic Acids Research</i> , 1990 , 18, 379	20.1	23
57	Real-time assembly of ribonucleoprotein complexes on nascent RNA transcripts. <i>Nature Communications</i> , 2018 , 9, 5087	17.4	23
56	Numerical Matrices Method for nonlinear system identification and description of dynamics of biochemical reaction networks. <i>Biophysical Journal</i> , 2007 , 92, 3459-73	2.9	22
55	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, 13614-9	11.5	21
54	Quantitative ESI-TOF analysis of macromolecular assembly kinetics. <i>Analytical Chemistry</i> , 2008 , 80, 9379-86		21
53	UHM-ULM interactions in the RBM39-U2AF65 splicing-factor complex. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016 , 72, 497-511	5.5	21
52	Toward a Whole-Cell Model of Ribosome Biogenesis: Kinetic Modeling of SSU Assembly. <i>Biophysical Journal</i> , 2015 , 109, 1117-35	2.9	20
51	Role of Era in assembly and homeostasis of the ribosomal small subunit. <i>Nucleic Acids Research</i> , 2019 , 47, 8301-8317	20.1	20
50	Functional interaction between ribosomal protein L6 and RbgA during ribosome assembly. <i>PLoS Genetics</i> , 2014 , 10, e1004694	6	20
49	RNA-protein binding kinetics in an automated microfluidic reactor. <i>Nucleic Acids Research</i> , 2009 , 37, e1420.1	20.1	20
48	The spectroscopic basis of fluorescence triple correlation spectroscopy. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 1908-19	3.4	19

47	The binding interface between <i>Bacillus stearothermophilus</i> ribosomal protein S15 and its 5Rtranslational operator mRNA. <i>Journal of Molecular Biology</i> , 2005 , 351, 280-90	6.5	19
46	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, 41-6	3	18
45	Assembly of the 30S ribosomal subunit. <i>Quarterly Reviews of Biophysics</i> , 2005 , 38, 397-403	7	18
44	ArcA overexpression induces fermentation and results in enhanced growth rates of <i>E. coli</i> . <i>Scientific Reports</i> , 2017 , 7, 11866	4.9	17
43	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, 649-65	6.5	17
42	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	3	17
41	NMR pulse schemes for the sequential assignment of arginine side-chain H epsilon protons. <i>Journal of Magnetic Resonance Series B</i> , 1996 , 113, 272-6		16
40	New RNA labeling methods offer dramatic sensitivity enhancements in ² H NMR relaxation spectra. <i>Journal of the American Chemical Society</i> , 2006 , 128, 9346-7	16.4	15
39	Improvement in the apparent mass resolution of oligonucleotides by using ¹² C/ ¹⁴ N-enriched samples. <i>Analytical Chemistry</i> , 2002 , 74, 226-31	7.8	15
38	Solution NMR studies of the maturation intermediates of a 13 MDa viral capsid. <i>Journal of the American Chemical Society</i> , 2007 , 129, 7867-76	16.4	14
37	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	3	14
36	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> , 2001 , 123, 3395-6	16.4	14
35	Quantitation of the ribosomal protein autoregulatory network using mass spectrometry. <i>Analytical Chemistry</i> , 2010 , 82, 5038-45	7.8	13
34	Kinetic oligonucleotide hybridization for monitoring kinetic folding of large RNAs. <i>Methods in Enzymology</i> , 2000 , 317, 330-53	1.7	13
33	A Survey of DDX21 Activity During Rev/RRE Complex Formation. <i>Journal of Molecular Biology</i> , 2018 , 430, 537-553	6.5	12
32	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	4.5	12
31	Novel Intersubunit Interaction Critical for HIV-1 Core Assembly Defines a Potentially Targetable Inhibitor Binding Pocket. <i>MBio</i> , 2019 , 10,	7.8	11
30	Biochemical characterization of the <i>Caenorhabditis elegans</i> FBF.CPB-1 translational regulation complex identifies conserved protein interaction hotspots. <i>Journal of Molecular Biology</i> , 2013 , 425, 725-37	6.5	11

29	A protein-protein interaction platform involved in recruitment of GLD-3 to the FBF.fem-3 mRNA complex. <i>Journal of Molecular Biology</i> , 2013 , 425, 738-54	6.5	10
28	RNA Recognition by HIV-1 Tat and Rev. <i>Seminars in Virology</i> , 1997 , 8, 186-193		10
27	PACE analysis of RNA-peptide interactions. <i>Methods in Molecular Biology</i> , 1999 , 118, 129-41	1.4	10
26	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	6.5	9
25	A DEAD-box protein acts through RNA to promote HIV-1 Rev-RRE assembly. <i>Nucleic Acids Research</i> , 2017 , 45, 4632-4641	20.1	9
24	Envelope: interactive software for modeling and fitting complex isotope distributions. <i>BMC Bioinformatics</i> , 2008 , 9, 446	3.6	9
23	Shape-specific nucleotide binding of single-stranded RNA by the GLD-1 STAR domain. <i>Journal of Molecular Biology</i> , 2005 , 346, 91-104	6.5	9
22	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	3.7	9
21	Monitoring assembly of ribonucleoprotein complexes by isothermal titration calorimetry. <i>Methods in Molecular Biology</i> , 2008 , 488, 117-27	1.4	9
20	The acidic domain is a unique structural feature of the splicing factor SYNCRIP. <i>Protein Science</i> , 2016 , 25, 1545-50	6.3	7
19	SrmB Rescues Trapped Ribosome Assembly Intermediates. <i>Journal of Molecular Biology</i> , 2020 , 432, 978-990	6.9	6
18	An alternative resource allocation strategy in the chemolithoautotrophic archaeon. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	6
17	The ribosome at atomic resolution. <i>Cell</i> , 2009 , 139, 1041-3	56.2	5
16	Stable isotope pulse-chase monitored by quantitative mass spectrometry applied to E. coli 30S ribosome assembly kinetics. <i>Methods</i> , 2009 , 49, 136-41	4.6	5
15	Combinatorial crystallization of an RNA-protein complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003 , 59, 466-73		5
14	Global coordination of metabolic pathways in Escherichia coli by active and passive regulation. <i>Molecular Systems Biology</i> , 2021 , 17, e10064	12.2	5
13	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> , 2012 , 415, 489-502	6.5	4
12	A simple method for preparing pools of synthetic oligonucleotides with random point deletions. <i>Nucleic Acids Research</i> , 1995 , 23, 3603-4	20.1	4

11	Discrimination between Functional and Non-functional Cellular Gag Complexes involved in HIV-1 Assembly. <i>Journal of Molecular Biology</i> , 2021 , 433, 166842	6.5	4
10	NMR assignments of HIV-2 TAR RNA. <i>Biomolecular NMR Assignments</i> , 2008 , 2, 167-9	0.7	3
9	Really exasperating viral protein from HIV. <i>ELife</i> , 2015 , 4,	8.9	3
8	Vectorized data acquisition and fast triple-correlation integrals for Fluorescence Triple Correlation Spectroscopy. <i>Computer Physics Communications</i> , 2013 , 184, 1322-1332	4.2	1
7	Role of Era in Assembly and Homeostasis of the Ribosomal Small Subunit		1
6	Pytheas: a software package for the automated analysis of RNA sequences and modifications via tandem mass spectrometry.. <i>Nature Communications</i> , 2022 , 13, 2424	17.4	1
5	Balancing teaching and research in obtaining a faculty position at a predominantly undergraduate institution. <i>ACS Chemical Biology</i> , 2007 , 2, 521-4	4.9	0
4	The Histone H1-Like Protein AlgP Facilitates Even Spacing of Polyphosphate Granules in <i>Pseudomonas aeruginosa</i> .. <i>MBio</i> , 2022 , e0246321	7.8	0
3	A higher degree of difficulty. <i>ACS Chemical Biology</i> , 2007 , 2, 197-9	4.9	
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