

Eric Westhof

List of Publications by Year in descending order

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262
papers

28,227
citations

3721

89
h-index

6454

157
g-index

331
all docs

331
docs citations

331
times ranked

19366
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome evolution in yeasts. <i>Nature</i> , 2004, 430, 35-44.	13.7	1,498
2	Halogen bonds in biological molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16789-16794.	3.3	1,469
3	Modelling of the three-dimensional architecture of group I catalytic introns based on comparative sequence analysis. <i>Journal of Molecular Biology</i> , 1990, 216, 585-610.	2.0	1,253
4	Geometric nomenclature and classification of RNA base pairs. <i>Rna</i> , 2001, 7, 499-512.	1.6	877
5	Single Processing Center Models for Human Dicer and Bacterial RNase III. <i>Cell</i> , 2004, 118, 57-68.	13.5	860
6	The non-Watson-Crick base pairs and their associated isostericity matrices. <i>Nucleic Acids Research</i> , 2002, 30, 3497-3531.	6.5	679
7	A standard reference frame for the description of nucleic acid base-pair geometry 1 Edited by P. E. Wright 2 This is a document of the Nomenclature Committee of IUBMB (NC-IUBMB)/IUPAC-IUBMB Joint Commission on Biochemical Nomenclature (JCBN), whose members are R. Cammack (chairman), A. Bairoch, H.M. Berman, S. Boyce, C.R. Cantor, K. Elliott, D. Horton, M. Kanehisa, A. Kotyk, G.P. Moss, N. Sharon and K.F. Tipton. <i>Journal of Molecular Biology</i> , 2001, 313, 229-237.	2.0	533
8	HIERARCHY AND DYNAMICS OF RNA FOLDING. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 1997, 26, 113-137.	18.3	522
9	Sequence elements outside the hammerhead ribozyme catalytic core enable intracellular activity. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 708-712.	3.6	404
10	Crystal Structure of Paromomycin Docked into the Eubacterial Ribosomal Decoding A Site. <i>Structure</i> , 2001, 9, 647-658.	1.6	363
11	Crystal structures of complexes between aminoglycosides and decoding A site oligonucleotides: role of the number of rings and positive charges in the specific binding leading to miscoding. <i>Nucleic Acids Research</i> , 2005, 33, 5677-5690.	6.5	323
12	Biogenesis of Circular RNAs. <i>Cell</i> , 2014, 159, 13-14.	13.5	309
13	The Dynamic Landscapes of RNA Architecture. <i>Cell</i> , 2009, 136, 604-609.	13.5	303
14	A new understanding of the decoding principle on the ribosome. <i>Nature</i> , 2012, 484, 256-259.	13.7	293
15	New loop-loop tertiary interactions in self-splicing introns of subgroup IC and ID: a complete 3D model of the <i>Tetrahymena thermophila</i> ribozyme. <i>Chemistry and Biology</i> , 1996, 3, 993-1009.	6.2	280
16	Analysis of RNA motifs. <i>Current Opinion in Structural Biology</i> , 2003, 13, 300-308.	2.6	274
17	Topology of three-way junctions in folded RNAs. <i>Rna</i> , 2006, 12, 83-93.	1.6	264
18	Structure of Monomeric Yeast and Mammalian Sec61 Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	6.0	263

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19	Plasticity of Animal Genome Architecture Unmasked by Rapid Evolution of a Pelagic Tunicate. <i>Science</i> , 2010, 330, 1381-1385.	6.0	251
20	Water and ion binding around RNA and DNA (C,G) oligomers ¹¹ Edited by I. Tinoco. <i>Journal of Molecular Biology</i> , 2000, 300, 1113-1131.	2.0	248
21	TectoRNA: modular assembly units for the construction of RNA nano-objects. <i>Nucleic Acids Research</i> , 2001, 29, 455-463.	6.5	242
22	<i>RNA-Puzzles</i> : A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	1.6	241
23	Involvement of a GNRA tetraloop in long-range RNA tertiary interactions. <i>Journal of Molecular Biology</i> , 1994, 236, 1271-1276.	2.0	240
24	Tools for the automatic identification and classification of RNA base pairs. <i>Nucleic Acids Research</i> , 2003, 31, 3450-3460.	6.5	240
25	Two conformational states in the crystal structure of the Homo sapiens cytoplasmic ribosomal decoding A site. <i>Nucleic Acids Research</i> , 2006, 34, 676-685.	6.5	235
26	Crystal Structure of a Complex between the Aminoglycoside Tobramycin and an Oligonucleotide Containing the Ribosomal Decoding A Site. <i>Chemistry and Biology</i> , 2002, 9, 747-755.	6.2	229
27	Derivation of the three-dimensional architecture of bacterial ribonuclease P RNAs from comparative sequence analysis. <i>Journal of Molecular Biology</i> , 1998, 279, 773-793.	2.0	227
28	Recurrent structural RNA motifs, Isostericity Matrices and sequence alignments. <i>Nucleic Acids Research</i> , 2005, 33, 2395-2409.	6.5	210
29	Comparative genomics of protoploid <i>Saccharomycetaceae</i> . <i>Genome Research</i> , 2009, 19, 1696-1709.	2.4	207
30	An integrated, structure- and energy-based view of the genetic code. <i>Nucleic Acids Research</i> , 2016, 44, 8020-8040.	6.5	203
31	RNA as a Drug Target: The Case of Aminoglycosides. <i>ChemBioChem</i> , 2003, 4, 1018-1023.	1.3	201
32	Aminoglycoside-RNA interactions. <i>Current Opinion in Chemical Biology</i> , 1999, 3, 694-704.	2.8	200
33	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	3.3	196
34	Frequency and isostericity of RNA base pairs. <i>Nucleic Acids Research</i> , 2009, 37, 2294-2312.	6.5	190
35	Aminoglycoside binding to the hammerhead ribozyme: a general model for the interaction of cationic antibiotics with RNA ¹ Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1998, 276, 903-912.	2.0	181
36	Crystal Structure of Geneticin Bound to a Bacterial 16S Ribosomal RNA A Site Oligonucleotide. <i>Journal of Molecular Biology</i> , 2003, 326, 1175-1188.	2.0	179

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37	Structure of the ribosome-bound cricket paralysis virus IRES RNA. <i>Nature Structural and Molecular Biology</i> , 2006, 13, 1092-1096.	3.6	177
38	Assemble: an interactive graphical tool to analyze and build RNA architectures at the 2D and 3D levels. <i>Bioinformatics</i> , 2010, 26, 2057-2059.	1.8	176
39	A common motif organizes the structure of multi-helix loops in 16 S and 23 S ribosomal RNAs. <i>Journal of Molecular Biology</i> , 1998, 283, 571-583.	2.0	175
40	RNA tectonics: towards RNA design. <i>Folding & Design</i> , 1996, 1, R78-R88.	4.5	166
41	RNA Structure: Advances and Assessment of 3D Structure Prediction. <i>Annual Review of Biophysics</i> , 2017, 46, 483-503.	4.5	166
42	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	1.6	161
43	Correlation between the location of antigenic sites and the prediction of turns in proteins. <i>Immunology Letters</i> , 1993, 36, 83-99.	1.1	159
44	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	1.6	158
45	Rules governing the orientation of the 2'-hydroxyl group in RNA. <i>Journal of Molecular Biology</i> , 1997, 274, 54-63.	2.0	155
46	RNA as a drug target: chemical, modelling, and evolutionary tools. <i>Current Opinion in Biotechnology</i> , 1998, 9, 66-73.	3.3	154
47	A three-dimensional model of hepatitis delta virus ribozyme based on biochemical and mutational analyses. <i>Current Biology</i> , 1994, 4, 488-498.	1.8	150
48	RNA hydration: three nanoseconds of multiple molecular dynamics simulations of the solvated tRNA Asp anticodon hairpin 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 269, 326-341.	2.0	148
49	Computer modeling from solution data of spinach chloroplast and of <i>Xenopus laevis</i> somatic and oocyte 5 S rRNAs. <i>Journal of Molecular Biology</i> , 1989, 207, 417-431.	2.0	144
50	Molecular recognition of aminoglycoside antibiotics by ribosomal RNA and resistance enzymes: An analysis of x-ray crystal structures. <i>Biopolymers</i> , 2003, 70, 42-57.	1.2	142
51	Non-canonical interactions in a kissing loop complex: the dimerization initiation site of HIV-1 genomic RNA. <i>Journal of Molecular Biology</i> , 1997, 270, 36-49.	2.0	141
52	Statistical analysis of atomic contacts at RNA-protein interfaces. <i>Journal of Molecular Recognition</i> , 2001, 14, 199-214.	1.1	141
53	Novel base-pairing interactions at the tRNA wobble position crucial for accurate reading of the genetic code. <i>Nature Communications</i> , 2016, 7, 10457.	5.8	141
54	New metrics for comparing and assessing discrepancies between RNA 3D structures and models. <i>Rna</i> , 2009, 15, 1875-1885.	1.6	138

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55	Visualization of macromolecular structures. <i>Nature Methods</i> , 2010, 7, S42-S55.	9.0	137
56	Assembly of core helices and rapid tertiary folding of a small bacterial group I ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 1574-1579.	3.3	136
57	Recent Advances in Mitochondrial Aminoacyl-tRNA Synthetases and Disease. <i>Trends in Molecular Medicine</i> , 2017, 23, 693-708.	3.5	132
58	Conserved geometrical base-pairing patterns in RNA. <i>Quarterly Reviews of Biophysics</i> , 1998, 31, 399-455.	2.4	130
59	The Molecular Basis for A-Site Mutations Conferring Aminoglycoside Resistance: Relationship between Ribosomal Susceptibility and X-ray Crystal Structures. <i>ChemBioChem</i> , 2003, 4, 1078-1088.	1.3	130
60	Yeast tRNA ^{Asp} tertiary structure in solution and areas of interaction of the tRNA with aspartyl-tRNA synthetase. <i>Journal of Molecular Biology</i> , 1985, 184, 455-471.	2.0	129
61	Sequence to Structure (S2S): display, manipulate and interconnect RNA data from sequence to structure. <i>Bioinformatics</i> , 2005, 21, 3320-3321.	1.8	127
62	iSpinach: a fluorogenic RNA aptamer optimized for <i>in vitro</i> applications. <i>Nucleic Acids Research</i> , 2016, 44, 2491-2500.	6.5	126
63	Mutations in signal recognition particle SRP54 cause syndromic neutropenia with Shwachman-Diamond-like features. <i>Journal of Clinical Investigation</i> , 2017, 127, 4090-4103.	3.9	126
64	Docking of Cationic Antibiotics to Negatively Charged Pockets in RNA Folds. <i>Journal of Medicinal Chemistry</i> , 1999, 42, 1250-1261.	2.9	124
65	Anion Binding to Nucleic Acids. <i>Structure</i> , 2004, 12, 379-388.	1.6	124
66	Importance of potassium ions for ribosome structure and function revealed by long-wavelength X-ray diffraction. <i>Nature Communications</i> , 2019, 10, 2519.	5.8	124
67	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19754-19759.	3.3	122
68	High-resolution cryo-electron microscopy structure of the <i>Trypanosoma brucei</i> ribosome. <i>Nature</i> , 2013, 494, 385-389.	13.7	122
69	Unusual helical packing in crystals of DNA bearing a mutation hot spot. <i>Nature</i> , 1989, 341, 459-462.	13.7	121
70	A pH-responsive riboregulator. <i>Genes and Development</i> , 2009, 23, 2650-2662.	2.7	119
71	Deciphering RNA recognition: aminoglycoside binding to the hammerhead ribozyme. <i>Chemistry and Biology</i> , 1998, 5, R277-R283.	6.2	117
72	Structural basis for the specificity of the initiation of HIV-1 reverse transcription. <i>EMBO Journal</i> , 1999, 18, 1038-1048.	3.5	116

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73	The viral protein NSP1 acts as a ribosome gatekeeper for shutting down host translation and fostering SARS-CoV-2 translation. <i>Rna</i> , 2021, 27, 253-264.	1.6	112
74	Exploration of metal ion binding sites in RNA folds by Brownian-dynamics simulations. <i>Structure</i> , 1998, 6, 1303-1314.	1.6	110
75	A Tyrosyl-tRNA Synthetase Recognizes a Conserved tRNA-like Structural Motif in the Group I Intron Catalytic Core. <i>Cell</i> , 1996, 87, 1135-1145.	13.5	109
76	Singly and Bifurcated Hydrogen-bonded Base-pairs in tRNA Anticodon Hairpins and Ribozymes. <i>Journal of Molecular Biology</i> , 1999, 292, 467-483.	2.0	109
77	RNA folding: beyond Watson-Crick pairs. <i>Structure</i> , 2000, 8, R55-R65.	1.6	109
78	Effects of magnesium ions on the stabilization of RNA oligomers of defined structures. <i>Rna</i> , 2002, 8, 307-323.	1.6	109
79	Water and ion binding around r(U _p A) ₁₂ and d(T _p A) ₁₂ Oligomers - comparison with RNA and DNA (C _p G) ₁₂ duplexes. <i>Journal of Molecular Biology</i> , 2001, 305, 1057-1072.	2.0	108
80	The 5S rRNA loop E: Chemical probing and phylogenetic data versus crystal structure. <i>Rna</i> , 1998, 4, 1134-1153.	1.6	107
81	On the wobble G _o U and related pairs. <i>Rna</i> , 2000, 6, 9-15.	1.6	107
82	Monitoring of the Cooperative Unfolding of the sunY Group I Intron of Bacteriophage T4. <i>Journal of Molecular Biology</i> , 1993, 234, 331-346.	2.0	106
83	Molecular Modeling of the Three-dimensional Structure of the Bacterial RNase P Holoenzyme. <i>Journal of Molecular Biology</i> , 2003, 325, 661-675.	2.0	105
84	Structural insights into the translational infidelity mechanism. <i>Nature Communications</i> , 2015, 6, 7251.	5.8	100
85	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	1.6	100
86	Binding of Escherichia coli ribosomal protein S8 to 16 S rRNA. <i>Journal of Molecular Biology</i> , 1987, 198, 91-107.	2.0	99
87	Three-dimensional model of Escherichia coli ribosomal 5 S RNA as deduced from structure probing in solution and computer modeling. <i>Journal of Molecular Biology</i> , 1991, 221, 293-308.	2.0	96
88	Inter-domain cross-linking and molecular modelling of the hairpin ribozyme. <i>Journal of Molecular Biology</i> , 1997, 274, 197-212.	2.0	96
89	Unique secondary and tertiary structural features of the eucaryotic selenocysteine tRNA ^{Sec} . <i>Nucleic Acids Research</i> , 1993, 21, 1073-1079.	6.5	94
90	Non-Watson-Crick base pairs in RNA-protein recognition. <i>Chemistry and Biology</i> , 1999, 6, R335-R343.	6.2	94

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91	Symmetric K ⁺ and Mg ²⁺ Ion-binding Sites in the 5S rRNA Loop E Inferred from Molecular Dynamics Simulations. <i>Journal of Molecular Biology</i> , 2004, 335, 555-571.	2.0	93
92	Docking of Aminoglycosides to Hydrated and Flexible RNA. <i>Journal of Medicinal Chemistry</i> , 2006, 49, 1023-1033.	2.9	93
93	Molecular Dynamics Simulations of the Anticodon Hairpin of tRNA ^{Asp} : Structuring Effects of C ⁺ H ⁺ O Hydrogen Bonds and of Long-Range Hydration Forces. <i>Journal of the American Chemical Society</i> , 1996, 118, 1181-1189.	6.6	91
94	RNAML: A standard syntax for exchanging RNA information. <i>Rna</i> , 2002, 8, 707-717.	1.6	91
95	The Mg ²⁺ Binding Sites of the 5S rRNA Loop E Motif as Investigated by Molecular Dynamics Simulations. <i>Chemistry and Biology</i> , 2003, 10, 551-561.	6.2	91
96	A potential RNA drug target in the hepatitis C virus internal ribosomal entry site. <i>Rna</i> , 2000, 6, 1423-1431.	1.6	88
97	Antibacterial Aminoglycosides with a Modified Mode of Binding to the Ribosomal-RNA Decoding Site. <i>Angewandte Chemie - International Edition</i> , 2004, 43, 6735-6738.	7.2	88
98	Multiple Molecular Dynamics Simulations of the Anticodon Loop of tRNA ^{Asp} in Aqueous Solution with Counterions. <i>Journal of the American Chemical Society</i> , 1995, 117, 6720-6726.	6.6	87
99	The RNA polymerase III-dependent family of genes in hemiascomycetes: comparative RNomics, decoding strategies, transcription and evolutionary implications. <i>Nucleic Acids Research</i> , 2006, 34, 1816-1835.	6.5	86
100	In-line alignment and Mg ²⁺ coordination at the cleavage site of the env22 twister ribozyme. <i>Nature Communications</i> , 2014, 5, 5534.	5.8	84
101	Dimerization of HIV-1 genomic RNA of subtypes A and B: RNA loop structure and magnesium binding. <i>Rna</i> , 1999, 5, 1222-1234.	1.6	83
102	A quantitative RNA code for mRNA target selection by the germline fate determinant GLD-1. <i>EMBO Journal</i> , 2011, 30, 533-545.	3.5	81
103	Sequence-based identification of 3D structural modules in RNA with RMDetect. <i>Nature Methods</i> , 2011, 8, 513-519.	9.0	80
104	Hydration of RNA Base Pairs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1998, 16, 693-707.	2.0	78
105	Functional Hammerhead Ribozymes Naturally Encoded in the Genome of <i>Arabidopsis thaliana</i> . <i>Plant Cell</i> , 2005, 17, 1877-1885.	3.1	78
106	An extended structural signature for the tRNA anticodon loop. <i>Rna</i> , 2001, 7, 334-341.	1.6	76
107	A PNPase Dependent CRISPR System in <i>Listeria</i> . <i>PLoS Genetics</i> , 2014, 10, e1004065.	1.5	76
108	The ribozyme core of group II introns: a structure in want of partners. <i>Trends in Biochemical Sciences</i> , 2009, 34, 189-199.	3.7	74

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109	Solution structure of human U1 snRNA. Derivation of a possible three-dimensional model. <i>Nucleic Acids Research</i> , 1990, 18, 3803-3811.	6.5	73
110	Mapping in Three Dimensions of Regions in a Catalytic RNA Protected from Attack by an Fe(II)-EDTA Reagent. <i>Journal of Molecular Biology</i> , 1996, 258, 600-613.	2.0	73
111	Classification of pseudo pairs between nucleotide bases and amino acids by analysis of nucleotide-protein complexes. <i>Nucleic Acids Research</i> , 2011, 39, 8628-8637.	6.5	71
112	An mRNA Is Capped by a 2', 5' Lariat Catalyzed by a Group I-Like Ribozyme. <i>Science</i> , 2005, 309, 1584-1587.	6.0	70
113	Molecular Dynamics Simulations of Solvated Yeast tRNA ^{Asp} . <i>Biophysical Journal</i> , 1999, 76, 50-64.	0.2	68
114	Crystal structure of the bacterial ribosomal decoding site complexed with amikacin containing the 3-amino-1-hydroxybutyryl (haba) group. <i>Biochimie</i> , 2006, 88, 1027-1031.	1.3	68
115	An unusual structure formed by antisense-target RNA binding involves an extended kissing complex with a four-way junction and a side-by-side helical alignment. <i>Rna</i> , 2000, 6, 311-324.	1.6	66
116	Molecular Contacts Between Antibiotics and the 30S Ribosomal Particle. <i>Methods in Enzymology</i> , 2006, 415, 180-202.	0.4	66
117	Analysis of the Contribution of Individual Substituents in 4,6-Aminoglycoside-Ribosome Interaction. <i>Antimicrobial Agents and Chemotherapy</i> , 2005, 49, 5112-5118.	1.4	64
118	New Structural Insights into Translational Miscoding. <i>Trends in Biochemical Sciences</i> , 2016, 41, 798-814.	3.7	64
119	Binding of Neomycin-Class Aminoglycoside Antibiotics to Mutant Ribosomes with Alterations in the A Site of 16S rRNA. <i>Antimicrobial Agents and Chemotherapy</i> , 2006, 50, 1489-1496.	1.4	63
120	Crystal structure and fluorescence properties of the iSpinach aptamer in complex with DFHBI. <i>Rna</i> , 2017, 23, 1788-1795.	1.6	63
121	Dimerization confers increased stability to nucleases in 5' halves from glycine and glutamic acid tRNAs. <i>Nucleic Acids Research</i> , 2018, 46, 9081-9093.	6.5	63
122	Transcriptome-wide identification of A > I RNA editing sites by inosine specific cleavage. <i>Rna</i> , 2013, 19, 257-270.	1.6	62
123	A Large-Scale Assessment of Nucleic Acids Binding Site Prediction Programs. <i>PLoS Computational Biology</i> , 2015, 11, e1004639.	1.5	62
124	Using droplet-based microfluidics to improve the catalytic properties of RNA under multiple-turnover conditions. <i>Rna</i> , 2015, 21, 458-469.	1.6	62
125	Importance of Conserved Residues for the Conformation of the T-Loop in tRNAs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1987, 5, 669-687.	2.0	60
126	The RNA Ontology Consortium: An open invitation to the RNA community. <i>Rna</i> , 2006, 12, 533-541.	1.6	59

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127	The ribosome prohibits the Gâ€U wobble geometry at the first position of the codonâ€anticodon helix. <i>Nucleic Acids Research</i> , 2016, 44, gkw431.	6.5	59
128	Mutation in a primate-conserved retrotransposon reveals a noncoding RNA as a mediator of infantile encephalopathy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4980-4985.	3.3	58
129	Hydrophobic Groups Stabilize the Hydration Shell of 2â€-O-Methylated RNA Duplexes. <i>Angewandte Chemie - International Edition</i> , 2001, 40, 4648-4650.	7.2	57
130	Somatic Mutation in Human T-Cell Leukemia Virus Type 1 Provirus and Flanking Cellular Sequences During Clonal Expansion In Vivo. <i>Journal of the National Cancer Institute</i> , 2001, 93, 367-377.	3.0	57
131	Binding of manganese(II) to a tertiary stabilized hammerhead ribozyme as studied by electron paramagnetic resonance spectroscopy. <i>Rna</i> , 2005, 11, 1-6.	1.6	57
132	Structure of a Folding Intermediate Reveals the Interplay Between Core and Peripheral Elements in RNA Folding. <i>Journal of Molecular Biology</i> , 2005, 352, 712-722.	2.0	57
133	RNA structure analysis of human spliceosomes reveals a compact 3D arrangement of snRNAs at the catalytic core. <i>EMBO Journal</i> , 2013, 32, 2804-2818.	3.5	57
134	The complete genome of <i>Blastobotrys (Arxula) adenivorans</i> LS3 - a yeast of biotechnological interest. <i>Biotechnology for Biofuels</i> , 2014, 7, 66.	6.2	57
135	Function of P11, a tertiary base pairing in self-splicing introns of subgroup IA. <i>Journal of Molecular Biology</i> , 1991, 221, 1153-1164.	2.0	56
136	Architecture and folding mechanism of the <i>Azoarcus</i> Group I Pre-tRNA. <i>Journal of Molecular Biology</i> , 2004, 339, 41-51.	2.0	56
137	Differential Selectivity of Natural and Synthetic Aminoglycosides towards the Eukaryotic and Prokaryotic Decoding A Sites. <i>ChemBioChem</i> , 2007, 8, 1700-1709.	1.3	56
138	Advances in RNA 3D Structure Modeling Using Experimental Data. <i>Frontiers in Genetics</i> , 2020, 11, 574485.	1.1	56
139	Structure-Based Design, Synthesis, and A-Site rRNA Cocrystal Complexes of Functionally Novel Aminoglycoside Antibiotics:â C2â€ Ether Analogues of Paromomycin. <i>Journal of Medicinal Chemistry</i> , 2007, 50, 2352-2369.	2.9	54
140	Isostericity and tautomerism of base pairs in nucleic acids. <i>FEBS Letters</i> , 2014, 588, 2464-2469.	1.3	53
141	An Interactive Framework for RNA Secondary Structure Prediction with a Dynamical Treatment of Constraints. <i>Journal of Molecular Biology</i> , 1995, 254, 163-174.	2.0	52
142	Ribose Conformations in the Common Purine(â)ribosides, in Some Antibiotic Nucleosides, and in Some Isopropylidene Derivatives: A Comparison. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 1975, 30, 131-140.	0.6	51
143	Determination of thermodynamic parameters for HIV DIS type loop-loop kissing complexes. <i>Nucleic Acids Research</i> , 2004, 32, 5126-5133.	6.5	50
144	New structural insights into the decoding mechanism: Translation infidelity via a Gâ€U pair with Watsonâ€Crick geometry. <i>FEBS Letters</i> , 2013, 587, 1848-1857.	1.3	50

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145	Prediction of nucleic acid binding probability in proteins: a neighboring residue network based score. <i>Nucleic Acids Research</i> , 2015, 43, 5340-5351.	6.5	50
146	Protein-dependent transition states for ribonucleoprotein assembly. <i>Journal of Molecular Biology</i> , 2001, 309, 1087-1100.	2.0	49
147	Pronounced instability of tandem IU base pairs in RNA. <i>Nucleic Acids Research</i> , 2004, 32, 1824-1828.	6.5	49
148	Distinctive structures between chimpanzee and human in a brain noncoding RNA. <i>Rna</i> , 2008, 14, 1270-1275.	1.6	49
149	Architecture of a Diels-Alderase Ribozyme with a Preformed Catalytic Pocket. <i>Chemistry and Biology</i> , 2004, 11, 1217-1227.	6.2	48
150	Proximity of conserved U6 and U2 snRNA elements to the 5' splice site region in activated spliceosomes. <i>EMBO Journal</i> , 2006, 25, 2475-2486.	3.5	48
151	Binding of tobramycin leads to conformational changes in yeast tRNA ^{Asp} and inhibition of aminoacylation. <i>EMBO Journal</i> , 2002, 21, 760-768.	3.5	47
152	Speciation of a group I intron into a lariat capping ribozyme. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 7659-7664.	3.3	47
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