

# Ivo L Hofacker

## List of Publications by Year in descending order

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187  
papers

30,189  
citations

18436

62  
h-index

5364

164  
g-index

211  
all docs

211  
docs citations

211  
times ranked

30345  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. <i>RNA Biology</i> , 2022, 19, 496-506.	1.5	3
2	Efficient Algorithms for Co-folding of Multiple RNAs. <i>Communications in Computer and Information Science</i> , 2021, , 193-214.	0.4	0
3	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. <i>Bioinformatics</i> , 2021, 37, 2126-2133.	1.8	3
4	Enhancing the Cell-Free Expression of Native Membrane Proteins by In Silico Optimization of the Coding Sequence—An Experimental Study of the Human Voltage-Dependent Anion Channel. <i>Membranes</i> , 2021, 11, 741.	1.4	2
5	Zinc-finger protein CNBP alters the 3-D structure of lncRNA Braveheart in solution. <i>Nature Communications</i> , 2020, 11, 148.	5.8	53
6	The locality dilemma of Sankoff-like RNA alignments. <i>Bioinformatics</i> , 2020, 36, i242-i250.	1.8	0
7	Transcriptional profiling of human macrophages during infection with <i>Bordetella pertussis</i> . <i>RNA Biology</i> , 2020, 17, 731-742.	1.5	15
8	Efficient Computation of Base-pairing Probabilities in Multi-strand RNA Folding. , 2020, , .		4
9	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. <i>Lecture Notes in Computer Science</i> , 2020, , 159-170.	1.0	2
10	Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. <i>Viruses</i> , 2019, 11, 798.	1.5	32
11	Conserved Secondary Structures in Viral mRNAs. <i>Viruses</i> , 2019, 11, 401.	1.5	22
12	Functional RNA Structures in the 3'UTR of Tick-Borne, Insect-Specific and No-Known-Vector Flaviviruses. <i>Viruses</i> , 2019, 11, 298.	1.5	43
13	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. <i>Plant Physiology</i> , 2019, 180, 305-322.	2.3	41
14	IntaRNAhelix-composing RNA-RNA interactions from stable inter-molecular helices boosts bacterial sRNA target prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2019, 17, 1940009.	0.3	5
15	RNA modifications in structure prediction — Status quo and future challenges. <i>Methods</i> , 2019, 156, 32-39.	1.9	31
16	3D based on 2D: Calculating helix angles and stacking patterns using forgi 2.0, an RNA Python library centered on secondary structure elements.. <i>F1000Research</i> , 2019, 8, 287.	0.8	20
17	Constraint Maximal Inter-molecular Helix Lengths within RNA-RNA Interaction Prediction Improves Bacterial sRNA Target Prediction. , 2019, , .		1
18	3D based on 2D: Calculating helix angles and stacking patterns using forgi 2.0, an RNA Python library centered on secondary structure elements.. <i>F1000Research</i> , 2019, 8, 287.	0.8	6

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19	Comparative RNA Genomics. <i>Methods in Molecular Biology</i> , 2018, 1704, 363-400.	0.4	8
20	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. <i>Methods</i> , 2018, 143, 70-76.	1.9	13
21	CMV: visualization for RNA and protein family models and their comparisons. <i>Bioinformatics</i> , 2018, 34, 2676-2678.	1.8	5
22	Comparative genomics of Czech vaccine strains of <i>Bordetella pertussis</i> . <i>Pathogens and Disease</i> , 2018, 76, .	0.8	7
23	In silico design of ligand triggered RNA switches. <i>Methods</i> , 2018, 143, 90-101.	1.9	14
24	RNA Structure Elements Conserved between Mouse and 59 Other Vertebrates. <i>Genes</i> , 2018, 9, 392.	1.0	16
25	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 2018, 7, 1346.	0.8	1
26	MSF: Modulated Sub-graph Finder. <i>F1000Research</i> , 2018, 7, 1346.	0.8	1
27	NMR Structural Profiling of Transcriptional Intermediates Reveals Riboswitch Regulation by Metastable RNA Conformations. <i>Journal of the American Chemical Society</i> , 2017, 139, 2647-2656.	6.6	43
28	microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3' untranslated region: function in replication and influence of RNA secondary structure. <i>Cellular and Molecular Life Sciences</i> , 2017, 74, 747-760.	2.4	28
29	RNAblueprint: flexible multiple target nucleic acid sequence design. <i>Bioinformatics</i> , 2017, 33, 2850-2858.	1.8	17
30	RNA structure prediction: from 2D to 3D. <i>Emerging Topics in Life Sciences</i> , 2017, 1, 275-285.	1.1	13
31	Rlsearch2: suffix array-based large-scale prediction of RNA-RNA interactions and siRNA off-targets. <i>Nucleic Acids Research</i> , 2017, 45, gkw1325.	6.5	75
32	SHAPE directed RNA folding. <i>Bioinformatics</i> , 2016, 32, 145-147.	1.8	91
33	Pseudoknots in RNA folding landscapes. <i>Bioinformatics</i> , 2016, 32, 187-194.	1.8	23
34	RNAlien – Unsupervised RNA family model construction. <i>Nucleic Acids Research</i> , 2016, 44, 8433-8441.	6.5	30
35	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. <i>Scientific Reports</i> , 2016, 6, 34589.	1.6	47
36	Predicting RNA secondary structures from sequence and probing data. <i>Methods</i> , 2016, 103, 86-98.	1.9	110

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37	Transcriptome-wide effects of inverted SINEs on gene expression and their impact on RNA polymerase II activity. <i>Genome Biology</i> , 2016, 17, 220.	3.8	20
38	Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammation resolution. <i>Molecular Systems Biology</i> , 2016, 12, 868.	3.2	74
39	RNA folding with hard and soft constraints. <i>Algorithms for Molecular Biology</i> , 2016, 11, 8.	0.3	89
40	AREsite2: an enhanced database for the comprehensive investigation of AU/GU/U-rich elements. <i>Nucleic Acids Research</i> , 2016, 44, D90-D95.	6.5	77
41	Computational Design of a Circular RNA with Prionlike Behavior. <i>Artificial Life</i> , 2016, 22, 172-184.	1.0	3
42	Practical Guidelines for Incorporating Knowledge-Based and Data-Driven Strategies into the Inference of Gene Regulatory Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 64-75.	1.9	3
43	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. <i>PLoS ONE</i> , 2015, 10, e0139900.	1.1	11
44	Optimizing RNA structures by sequence extensions using RNAcop. <i>Nucleic Acids Research</i> , 2015, 43, 8135-8145.	6.5	5
45	Product Grammars for Alignment and Folding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 507-519.	1.9	12
46	Sequence-controlled RNA self-processing: computational design, biochemical analysis, and visualization by AFM. <i>Rna</i> , 2015, 21, 1249-1260.	1.6	18
47	Forna (force-directed RNA): Simple and effective online RNA secondary structure diagrams. <i>Bioinformatics</i> , 2015, 31, 3377-3379.	1.8	355
48	Thermodynamic and Kinetic Folding of Riboswitches. <i>Methods in Enzymology</i> , 2015, 553, 193-213.	0.4	19
49	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. <i>PLoS Computational Biology</i> , 2015, 11, e1004126.	1.5	45
50	Predicting RNA 3D structure using a coarse-grain helix-centered model. <i>Rna</i> , 2015, 21, 1110-1121.	1.6	69
51	Impact of Hfq on the <i>Bacillus subtilis</i> Transcriptome. <i>PLoS ONE</i> , 2014, 9, e98661.	1.1	40
52	Basin Hopping Graph: a computational framework to characterize RNA folding landscapes. <i>Bioinformatics</i> , 2014, 30, 2009-2017.	1.8	39
53	Challenges in RNA virus bioinformatics. <i>Bioinformatics</i> , 2014, 30, 1793-1799.	1.8	47
54	Predicting RNA Structure: Advances and Limitations. <i>Methods in Molecular Biology</i> , 2014, 1086, 1-19.	0.4	18

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55	TSSAR: TSS annotation regime for dRNA-seq data. BMC Bioinformatics, 2014, 15, 89.	1.2	73
56	Concepts and Introduction to RNA Bioinformatics. Methods in Molecular Biology, 2014, 1097, 1-31.	0.4	2
57	Energy-Directed RNA Structure Prediction. Methods in Molecular Biology, 2014, 1097, 71-84.	0.4	29
58	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 832-844.	1.9	37
59	Identification of new protein coding sequences and signal peptidase cleavage sites of Helicobacter pylori strain 26695 by proteogenomics. Journal of Proteomics, 2013, 86, 27-42.	1.2	37
60	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. Nucleic Acids Research, 2013, 41, 9999-10009.	6.5	14
61	CMCompare webserver: comparing RNA families via covariance models. Nucleic Acids Research, 2013, 41, W499-W503.	6.5	10
62	<scp>RNA</scp> snp: Efficient Detection of Local <scp>RNA</scp> Secondary Structure Changes Induced by <scp>SNP</scp> s. Human Mutation, 2013, 34, 546-556.	1.1	121
63	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	1.2	27
64	The RNAsnp web server: predicting SNP effects on local RNA secondary structure. Nucleic Acids Research, 2013, 41, W475-W479.	6.5	117
65	Alterations of the Transcriptome of Sulfolobus acidocaldarius by Exoribonuclease aCPSF2. PLoS ONE, 2013, 8, e76569.	1.1	21
66	The Trouble with Long-Range Base Pairs in RNA Folding. Lecture Notes in Computer Science, 2013, , 1-11.	1.0	7
67	How to Multiply Dynamic Programming Algorithms. Lecture Notes in Computer Science, 2013, , 82-93.	1.0	4
68	Modelling Translation Initiation under the Influence of sRNA. International Journal of Molecular Sciences, 2012, 13, 16223-16240.	1.8	9
69	Folding RNA/DNA hybrid duplexes. Bioinformatics, 2012, 28, 2530-2531.	1.8	17
70	LocARNA-P: Accurate boundary prediction and improved detection of structural RNAs. Rna, 2012, 18, 900-914.	1.6	326
71	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. Nucleic Acids Research, 2012, 40, 4261-4272.	6.5	106
72	Symmetric circular matchings and RNA folding. Discrete Mathematics, 2012, 312, 100-112.	0.4	8

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73	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.0	7
74	AREsite: a database for the comprehensive investigation of AU-rich elements. Nucleic Acids Research, 2011, 39, D66-D69.	6.5	140
75	Tristetraprolinâ€driven regulatory circuit controls quality and timing of mRNA decay in inflammation. Molecular Systems Biology, 2011, 7, 560.	3.2	110
76	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
77	RNA Accessibility in cubic time. Algorithms for Molecular Biology, 2011, 6, 3.	0.3	43
78	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. Journal of Biotechnology, 2011, 153, 62-75.	1.9	102
79	Animal snRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	1.5	30
80	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	1.6	188
81	Fast accessibility-based prediction of RNAâ€RNA interactions. Bioinformatics, 2011, 27, 1934-1940.	1.8	48
82	A folding algorithm for extended RNA secondary structures. Bioinformatics, 2011, 27, i129-i136.	1.8	59
83	RNApredator: fast accessibility-based prediction of sRNA targets. Nucleic Acids Research, 2011, 39, W149-W154.	6.5	117
84	From Structure Prediction to Genomic Screens for Novel Non-Coding RNAs. PLoS Computational Biology, 2011, 7, e1002100.	1.5	40
85	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	0.8	32
86	De novo prediction of structured RNAs from genomic sequences. Trends in Biotechnology, 2010, 28, 9-19.	4.9	58
87	Hybridization thermodynamics of NimbleGen Microarrays. BMC Bioinformatics, 2010, 11, 35.	1.2	19
88	Bcheck: a wrapper tool for detecting RNase P RNA genes. BMC Genomics, 2010, 11, 432.	1.2	23
89	Evolution of metabolic networks: a computational frame-work. Journal of Systems Chemistry, 2010, 1, 4.	1.7	15
90	BarMap: RNA folding on dynamic energy landscapes. Rna, 2010, 16, 1308-1316.	1.6	53

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91	RNPomics: Defining the ncRNA transcriptome by cDNA library generation from ribonucleo-protein particles. <i>Nucleic Acids Research</i> , 2010, 38, e113-e113.	6.5	39
92	<tt>RNAsnoop</tt>: efficient target prediction for H/ACA snoRNAs. <i>Bioinformatics</i> , 2010, 26, 610-616.	1.8	49
93	Discriminatory power of RNA family models. <i>Bioinformatics</i> , 2010, 26, i453-i459.	1.8	17
94	Nucleic Acid Sequence and Structure Databases. <i>Methods in Molecular Biology</i> , 2010, 609, 3-15.	0.4	3
95	Designing Optimal siRNA Based on Target Site Accessibility. <i>Methods in Molecular Biology</i> , 2010, 623, 137-154.	0.4	11
96	RNAz 2.0: improved noncoding RNA detection. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010, , 69-79.	0.7	135
97	R<scp>NA</scp> Secondary Structure Analysis Using the Vienna <scp>RNA</scp> Package. <i>Current Protocols in Bioinformatics</i> , 2009, 26, Unit12.2.	25.8	91
98	RNAZ 2.0: , 2009, , 69-79.		68
99	Model-based probe set optimization for high-performance microarrays. <i>Nucleic Acids Research</i> , 2009, 37, e18-e18.	6.5	22
100	From consensus structure prediction to RNA gene finding. <i>Briefings in Functional Genomics &amp; Proteomics</i> , 2009, 8, 461-471.	3.8	27
101	COMPUTATIONAL STUDIES OF NON-CODING RNAs – Session Introduction. , 2009, , 54-56.		0
102	Invertebrate 7SK snRNAs. <i>Journal of Molecular Evolution</i> , 2008, 66, 107-115.	0.8	37
103	Beyond energy minimization: approaches to the kinetic folding of RNA. <i>Monatshefte F&amp;Auml;r Chemie</i> , 2008, 139, 447-457.	0.9	49
104	The impact of target site accessibility on the design of effective siRNAs. <i>Nature Biotechnology</i> , 2008, 26, 578-583.	9.4	262
105	Strategies for measuring evolutionary conservation of RNA secondary structures. <i>BMC Bioinformatics</i> , 2008, 9, 122.	1.2	63
106	RNAalifold: improved consensus structure prediction for RNA alignments. <i>BMC Bioinformatics</i> , 2008, 9, 474.	1.2	505
107	www.rnaworkbench.com: A new program for analyzing RNA interference. <i>Computer Methods and Programs in Biomedicine</i> , 2008, 90, 89-94.	2.6	8
108	Folding Kinetics of Large RNAs. <i>Journal of Molecular Biology</i> , 2008, 379, 160-173.	2.0	77

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109	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. <i>Bioinformatics</i> , 2008, 24, 158-164.	1.8	116
110	Arthropod 7SK RNA. <i>Molecular Biology and Evolution</i> , 2008, 25, 1923-1930.	3.5	45
111	The Vienna RNA Websuite. <i>Nucleic Acids Research</i> , 2008, 36, W70-W74.	6.5	2,012
112	Small ncRNA transcriptome analysis from <i>Aspergillus fumigatus</i> suggests a novel mechanism for regulation of protein synthesis. <i>Nucleic Acids Research</i> , 2008, 36, 2677-2689.	6.5	162
113	RNAplex: a fast tool for RNA-RNA interaction search. <i>Bioinformatics</i> , 2008, 24, 2657-2663.	1.8	384
114	Translational Control by RNA-RNA Interaction: Improved Computation of RNA-RNA Binding Thermodynamics. <i>Communications in Computer and Information Science</i> , 2008, , 114-127.	0.4	21
115	Visualization of Barrier Tree Sequences Revisited. <i>Mathematics and Visualization</i> , 2008, , 275-290.	0.4	1
116	The RNAz web server: prediction of thermodynamically stable and evolutionarily conserved RNA structures. <i>Nucleic Acids Research</i> , 2007, 35, W335-W338.	6.5	84
117	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. <i>PLoS Computational Biology</i> , 2007, 3, e65.	1.5	424
118	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
119	Identifying Structural Noncoding RNAs Using RNAz. <i>Current Protocols in Bioinformatics</i> , 2007, 19, Unit 12.7.	25.8	15
120	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	6.0	2,250
121	RNAs everywhere: genome-wide annotation of structured RNAs. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 1-25.	0.6	46
122	How microRNAs choose their targets. <i>Nature Genetics</i> , 2007, 39, 1191-1192.	9.4	51
123	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	13.7	4,709
124	Detection of RNA structures in porcine EST data and related mammals. <i>BMC Genomics</i> , 2007, 8, 316.	1.2	11
125	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , 2007, 56, 129-144.	0.8	65
126	RNA Consensus Structure Prediction With RNAalifold. <i>Methods in Molecular Biology</i> , 2007, 395, 527-543.	0.4	48



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127	Saddles and Barrier in Landscapes of Generalized Search Operators. Lecture Notes in Computer Science, 2007, , 194-212.	1.0	10
128	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
129	Visualization of Barrier Tree Sequences. IEEE Transactions on Visualization and Computer Graphics, 2006, 12, 781-788.	2.9	13
130	Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182.	1.8	338
131	Algebraic comparison of metabolic networks, phylogenetic inference, and metabolic innovation. BMC Bioinformatics, 2006, 7, 67.	1.2	33
132	The expansion of the metazoan microRNA repertoire. BMC Genomics, 2006, 7, 25.	1.2	304
133	Structural parameters affecting the kinetics of RNA hairpin formation. Nucleic Acids Research, 2006, 34, 3568-3576.	6.5	17
134	Exploring the lower part of discrete polymer model energy landscapes. Europhysics Letters, 2006, 74, 726-732.	0.7	19
135	Memory efficient folding algorithms for circular RNA secondary structures. Bioinformatics, 2006, 22, 1172-1176.	1.8	183
136	miRNAMap: genomic maps of microRNA genes and their target genes in mammalian genomes. Nucleic Acids Research, 2006, 34, D135-D139.	6.5	199
137	Local RNA base pairing probabilities in large sequences. Bioinformatics, 2006, 22, 614-615.	1.8	217
138	Modeling RNA Folding. , 2006, , 227-245.		0
139	RNAs everywhere: genome-wide annotation of structured RNAs. Genome Informatics, 2006, 17, 281-2.	0.4	2
140	RNA Folding in silico. , 2005, , 177-190.		1
141	Evolutionary patterns of non-coding RNAs. Theory in Biosciences, 2005, 123, 301-369.	0.6	64
142	Mapping of conserved RNA secondary structures predicts thousands of functional noncoding RNAs in the human genome. Nature Biotechnology, 2005, 23, 1383-1390.	9.4	352
143	Multiple sequence alignments of partially coding nucleic acid sequences. BMC Bioinformatics, 2005, 6, 160.	1.2	25
144	Unorthodox mRNA start site to extend the highly structured leader of retrotransposon Tto1 mRNA increases transposition rate. Rna, 2005, 11, 1181-1191.	1.6	7

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145	From The Cover: Fast and reliable prediction of noncoding RNAs. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2454-2459.	3.3	599
146	Efficient computation of RNA folding dynamics. Journal of Physics A, 2004, 37, 4731-4741.	1.6	99
147	Conserved RNA secondary structures in Flaviviridae genomes. Journal of General Virology, 2004, 85, 1113-1124.	1.3	165
148	Alignment of RNA base pairing probability matrices. Bioinformatics, 2004, 20, 2222-2227.	1.8	205
149	Prediction of locally stable RNA secondary structures for genome-wide surveys. Bioinformatics, 2004, 20, 186-190.	1.8	145
150	Prediction of consensus RNA secondary structures including pseudoknots. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 66-77.	1.9	51
151	Interactions in Oligonucleotide Hybrid Duplexes on Microarrays. Journal of Physical Chemistry B, 2004, 108, 18015-18025.	1.2	25
152	Conserved RNA secondary structures in viral genomes: a survey. Bioinformatics, 2004, 20, 1495-1499.	1.8	43
153	Structural and evolutionary analysis of the transcribed sequence of Boudicca, a Schistosoma mansoni retrotransposon. Gene, 2004, 329, 103-114.	1.0	6
154	Consensus Folding of Aligned Sequences as a New Measure for the Detection of Functional RNAs by Comparative Genomics. Journal of Molecular Biology, 2004, 342, 19-30.	2.0	146
155	On the evolution of primitive genetic codes. Origins of Life and Evolution of Biospheres, 2003, 33, 491-514.	0.8	20
156	Vienna RNA secondary structure server. Nucleic Acids Research, 2003, 31, 3429-3431.	6.5	2,002
157	RNA Secondary Structure Analysis Using the Vienna RNA Package. Current Protocols in Bioinformatics, 2003, 4, Unit 12.2.	25.8	107
158	Barrier Trees of Degenerate Landscapes. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	130
159	Secondary Structure Prediction for Aligned RNA Sequences. Journal of Molecular Biology, 2002, 319, 1059-1066.	2.0	545
160	Design of multistable RNA molecules. Rna, 2001, 7, 254-265.	1.6	138
161	Exploring Protein Sequence Space Using Knowledge-based Potentials. Journal of Theoretical Biology, 2001, 212, 35-46.	0.8	49
162	Conserved RNA secondary structures in Picornaviridae genomes. Nucleic Acids Research, 2001, 29, 5079-5089.	6.5	84

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163	Concurrent Neutral Evolution of mRNA Secondary Structures and Encoded Proteins. Journal of Molecular Evolution, 2000, 50, 238-242.	0.8	17
164	RNA folding at elementary step resolution. Rna, 2000, 6, 325-338.	1.6	266
165	Prediction of RNA Base Pairing Probabilities on Massively Parallel Computers. Journal of Computational Biology, 2000, 7, 171-182.	0.8	27
166	The Hepatitis B Virus Pregenome: Prediction of RNA Structure and Implications for the Emergence of Deletions. Intervirology, 2000, 43, 154-164.	1.2	14
167	RNA In Silico The Computational Biology of RNA Secondary Structures. International Journal of Modeling, Simulation, and Scientific Computing, 1999, 02, 65-90.	0.9	25
168	Automatic detection of conserved base pairing patterns in RNA virus genomes. Computers & Chemistry, 1999, 23, 401-414.	1.2	53
169	Complete suboptimal folding of RNA and the stability of secondary structures. , 1999, 49, 145-165.		455
170	Complete suboptimal folding of RNA and the stability of secondary structures. , 1999, 49, 145.		2
171	Oxygen and proton pathways in cytochrome c oxidase. , 1998, 30, 100-107.		197
172	Combinatorics of RNA secondary structures. Discrete Applied Mathematics, 1998, 88, 207-237.	0.5	120
173	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. Nucleic Acids Research, 1998, 26, 3825-3836.	6.5	115
174	Oxygen and proton pathways in cytochrome c oxidase. , 1998, 30, 100.		4
175	Neutral networks in protein space: a computational study based on knowledge-based potentials of mean force. Folding & Design, 1997, 2, 261-269.	4.5	100
176	Algorithm independent properties of RNA secondary structure predictions. European Biophysics Journal, 1996, 25, 115-130.	1.2	79
177	Analysis of RNA sequence structure maps by exhaustive enumeration II. Structures of neutral networks and shape space covering. Monatshefte Für Chemie, 1996, 127, 375-389.	0.9	94
178	Fast folding and comparison of RNA secondary structures. Monatshefte Für Chemie, 1994, 125, 167-188.	0.9	1,862
179	The inverse folding problem for RNA secondary structures. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 1127-1127.	0.9	0
180	RNA folding and combinatorial landscapes. Physical Review E, 1993, 47, 2083-2099.	0.8	202

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181	Primary relaxation in a hard-sphere system. Physical Review A, 1992, 45, 898-912.	1.0	149
182	Comments on the alpha -peak shapes for relaxation in supercooled liquids. Journal of Physics Condensed Matter, 1991, 3, 5047-5071.	0.7	115
183	An ESS-analysis for ensembles of Prisoner's dilemma strategies. Journal of Theoretical Biology, 1990, 142, 189-200.	0.8	7
184	RNA Secondary Structures. , 0, , 439-489.		6
185	Computational Design of a Circular RNA with Prion-Like Behavior. , 0, , .		1
186	RNA Consensus Structure Prediction With RNAalifold. , 0, , 527-544.		1
187	Caveats to Deep Learning Approaches to RNA Secondary Structure Prediction. Frontiers in Bioinformatics, 0, 2, .	1.0	11