Ivo L Hofacker

List of Publications by Year in descending order

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	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
2	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
3	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. Science, 2007, 316, 1484-1488.	6.0	2,250
4	The Vienna RNA Websuite. Nucleic Acids Research, 2008, 36, W70-W74.	6.5	2,012
5	Vienna RNA secondary structure server. Nucleic Acids Research, 2003, 31, 3429-3431.	6.5	2,002
6	Fast folding and comparison of RNA secondary structures. Monatshefte Für Chemie, 1994, 125, 167-188.	0.9	1,862
7	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
8	Secondary Structure Prediction for Aligned RNA Sequences. Journal of Molecular Biology, 2002, 319, 1059-1066.	2.0	545
9	RNAalifold: improved consensus structure prediction for RNA alignments. BMC Bioinformatics, 2008, 9, 474.	1.2	505
10	Complete suboptimal folding of RNA and the stability of secondary structures. , 1999, 49, 145-165.		455
11	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. PLoS Computational Biology, 2007, 3, e65.	1.5	424
12	RNAplex: a fast tool for RNA–RNA interaction search. Bioinformatics, 2008, 24, 2657-2663.	1.8	384
13	Forna (force-directed RNA): Simple and effective online RNA secondary structure diagrams. Bioinformatics, 2015, 31, 3377-3379.	1.8	355
14	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
15	Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182.	1.8	338
16	LocARNA-P: Accurate boundary prediction and improved detection of structural RNAs. Rna, 2012, 18, 900-914.	1.6	326
17	The expansion of the metazoan microRNA repertoire. BMC Genomics, 2006, 7, 25.	1.2	304
18	RNA folding at elementary step resolution. Rna, 2000, 6, 325-338.	1.6	266

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19	The impact of target site accessibility on the design of effective siRNAs. Nature Biotechnology, 2008, 26, 578-583.	9.4	262
20	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
21	Local RNA base pairing probabilities in large sequences. Bioinformatics, 2006, 22, 614-615.	1.8	217
22	Alignment of RNA base pairing probability matrices. Bioinformatics, 2004, 20, 2222-2227.	1.8	205
23	RNA folding and combinatory landscapes. Physical Review E, 1993, 47, 2083-2099.	0.8	202
24	miRNAMap: genomic maps of microRNA genes and their target genes in mammalian genomes. Nucleic Acids Research, 2006, 34, D135-D139.	6.5	199
25	Oxygen and proton pathways in cytochrome c oxidase. , 1998, 30, 100-107.		197
26	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	1.6	188
27	Memory efficient folding algorithms for circular RNA secondary structures. Bioinformatics, 2006, 22, 1172-1176.	1.8	183
28	Conserved RNA secondary structures in Flaviviridae genomes. Journal of General Virology, 2004, 85, 1113-1124.	1.3	165
29	Small ncRNA transcriptome analysis from Aspergillus fumigatus suggests a novel mechanism for regulation of protein synthesis. Nucleic Acids Research, 2008, 36, 2677-2689.	6.5	162
30	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
31	Primary relaxation in a hard-sphere system. Physical Review A, 1992, 45, 898-912.	1.0	149
32	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
33	Prediction of locally stable RNA secondary structures for genome-wide surveys. Bioinformatics, 2004, 20, 186-190.	1.8	145
34	AREsite: a database for the comprehensive investigation of AU-rich elements. Nucleic Acids Research, 2011, 39, D66-D69.	6.5	140
35	Design of multistable RNA molecules. Rna, 2001, 7, 254-265.	1.6	138
36	RNAz 2.0: improved noncoding RNA detection. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2010, , 69-79.	0.7	135

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37	Barrier Trees of Degenerate Landscapes. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	130
38	<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
39	Combinatorics of RNA secondary structures. Discrete Applied Mathematics, 1998, 88, 207-237.	0.5	120
40	RNApredator: fast accessibility-based prediction of sRNA targets. Nucleic Acids Research, 2011, 39, W149-W154.	6.5	117
41	The RNAsnp web server: predicting SNP effects on local RNA secondary structure. Nucleic Acids Research, 2013, 41, W475-W479.	6.5	117
42	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. Bioinformatics, 2008, 24, 158-164.	1.8	116
43	Comments on the alpha -peak shapes for relaxation in supercooled liquids. Journal of Physics Condensed Matter, 1991, 3, 5047-5071.	0.7	115
44	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. Nucleic Acids Research, 1998, 26, 3825-3836.	6.5	115
45	Tristetraprolinâ€driven regulatory circuit controls quality and timing of mRNA decay in inflammation. Molecular Systems Biology, 2011, 7, 560.	3.2	110
46	Predicting RNA secondary structures from sequence and probing data. Methods, 2016, 103, 86-98.	1.9	110
47	R NA Secondary Structure Analysis Using the Vienna RNA Package. Current Protocols in Bioinformatics, 2003, 4, Unit 12.2.	25.8	107
48	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. Nucleic Acids Research, 2012, 40, 4261-4272.	6.5	106
49	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
50	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
51	Efficient computation of RNA folding dynamics. Journal of Physics A, 2004, 37, 4731-4741.	1.6	99
52	Analysis of RNA sequence structure maps by exhaustive enumeration II. Structures of neutral networks and shape space covering. Monatshefte FÃ¼r Chemie, 1996, 127, 375-389.	0.9	94
53	R<scp>NA</scp> Secondary Structure Analysis Using the Vienna <scp>RNA</scp> Package. Current Protocols in Bioinformatics, 2009, 26, Unit12.2.	25.8	91
54	SHAPE directed RNA folding. Bioinformatics, 2016, 32, 145-147.	1.8	91

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55	RNA folding with hard and soft constraints. Algorithms for Molecular Biology, 2016, 11, 8.	0.3	89
56	Conserved RNA secondary structures in Picornaviridae genomes. Nucleic Acids Research, 2001, 29, 5079-5089.	6.5	84
57	The RNAz web server: prediction of thermodynamically stable and evolutionarily conserved RNA structures. Nucleic Acids Research, 2007, 35, W335-W338.	6.5	84
58	Algorithm independent properties of RNA secondary structure predictions. European Biophysics Journal, 1996, 25, 115-130.	1.2	79
59	Folding Kinetics of Large RNAs. Journal of Molecular Biology, 2008, 379, 160-173.	2.0	77
60	AREsite2: an enhanced database for the comprehensive investigation of AU/GU/U-rich elements. Nucleic Acids Research, 2016, 44, D90-D95.	6.5	77
61	RIsearch2: suffix array-based large-scale prediction of RNA–RNA interactions and siRNA off-targets. Nucleic Acids Research, 2017, 45, gkw1325.	6.5	75
62	Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammationÂresolution. Molecular Systems Biology, 2016, 12, 868.	3.2	74
63	TSSAR: TSS annotation regime for dRNA-seq data. BMC Bioinformatics, 2014, 15, 89.	1.2	73
64	Predicting RNA 3D structure using a coarse-grain helix-centered model. Rna, 2015, 21, 1110-1121.	1.6	69
65	RNAZ 2.0:. , 2009, , 69-79.		68
66	Variations on RNA folding and alignment: lessons from Benasque. Journal of Mathematical Biology, 2007, 56, 129-144.	0.8	65
67	Evolutionary patterns of non-coding RNAs. Theory in Biosciences, 2005, 123, 301-369.	0.6	64
68	Strategies for measuring evolutionary conservation of RNA secondary structures. BMC Bioinformatics, 2008, 9, 122.	1.2	63
69	A folding algorithm for extended RNA secondary structures. Bioinformatics, 2011, 27, i129-i136.	1.8	59
70	De novo prediction of structured RNAs from genomic sequences. Trends in Biotechnology, 2010, 28, 9-19.	4.9	58
71	Automatic detection of conserved base pairing patterns in RNA virus genomes. Computers & Chemistry, 1999, 23, 401-414.	1.2	53
72	BarMap: RNA folding on dynamic energy landscapes. Rna, 2010, 16, 1308-1316.	1.6	53

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73	Zinc-finger protein CNBP alters the 3-D structure of lncRNA Braveheart in solution. Nature Communications, 2020, 11, 148.	5.8	53
74	Prediction of consensus RNA secondary structures including pseudoknots. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 66-77.	1.9	51
75	How microRNAs choose their targets. Nature Genetics, 2007, 39, 1191-1192.	9.4	51
76	Exploring Protein Sequence Space Using Knowledge-based Potentials. Journal of Theoretical Biology, 2001, 212, 35-46.	0.8	49
77	Beyond energy minimization: approaches to the kinetic folding of RNA. Monatshefte Für Chemie, 2008, 139, 447-457.	0.9	49
78	<tt>RNAsnoop</tt>: efficient target prediction for H/ACA snoRNAs. Bioinformatics, 2010, 26, 610-616.	1.8	49
79	Fast accessibility-based prediction of RNA–RNA interactions. Bioinformatics, 2011, 27, 1934-1940.	1.8	48
80	RNA Consensus Structure Prediction With RNAalifold. Methods in Molecular Biology, 2007, 395, 527-543.	0.4	48
81	Challenges in RNA virus bioinformatics. Bioinformatics, 2014, 30, 1793-1799.	1.8	47
82	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. Scientific Reports, 2016, 6, 34589.	1.6	47
83	RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25.	0.6	46
84	Arthropod 7SK RNA. Molecular Biology and Evolution, 2008, 25, 1923-1930.	3.5	45
85	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. PLoS Computational Biology, 2015, 11, e1004126.	1.5	45
86	Conserved RNA secondary structures in viral genomes: a survey. Bioinformatics, 2004, 20, 1495-1499.	1.8	43
87	RNA Accessibility in cubic time. Algorithms for Molecular Biology, 2011, 6, 3.	0.3	43
88	NMR Structural Profiling of Transcriptional Intermediates Reveals Riboswitch Regulation by Metastable RNA Conformations. Journal of the American Chemical Society, 2017, 139, 2647-2656.	6.6	43
89	Functional RNA Structures in the 3′UTR of Tick-Borne, Insect-Specific and No-Known-Vector Flaviviruses. Viruses, 2019, 11, 298.	1.5	43
90	Control of Cognate Sense mRNA Translation by cis-Natural Antisense RNAs. Plant Physiology, 2019, 180, 305-322.	2.3	41

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91	From Structure Prediction to Genomic Screens for Novel Non-Coding RNAs. PLoS Computational Biology, 2011, 7, e1002100.	1.5	40
92	Impact of Hfq on the Bacillus subtilis Transcriptome. PLoS ONE, 2014, 9, e98661.	1.1	40
93	RNPomics: Defining the ncRNA transcriptome by cDNA library generation from ribonucleo-protein particles. Nucleic Acids Research, 2010, 38, e113-e113.	6.5	39
94	Basin Hopping Graph: a computational framework to characterize RNA folding landscapes. Bioinformatics, 2014, 30, 2009-2017.	1.8	39
95	Invertebrate 7SK snRNAs. Journal of Molecular Evolution, 2008, 66, 107-115.	0.8	37
96	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
97	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
98	Algebraic comparison of metabolic networks, phylogenetic inference, and metabolic innovation. BMC Bioinformatics, 2006, 7, 67.	1.2	33
99	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	0.8	32
100	Updated Phylogeny of Chikungunya Virus Suggests Lineage-Specific RNA Architecture. Viruses, 2019, 11, 798.	1.5	32
101	RNA modifications in structure prediction â€" Status quo and future challenges. Methods, 2019, 156, 32-39.	1.9	31
102	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	1.5	30
103	RNAlien â€" Unsupervised RNA family model construction. Nucleic Acids Research, 2016, 44, 8433-8441.	6.5	30
104	Energy-Directed RNA Structure Prediction. Methods in Molecular Biology, 2014, 1097, 71-84.	0.4	29
105	microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3â€² untranslated region: function in replication and influence of RNA secondary structure. Cellular and Molecular Life Sciences, 2017, 74, 747-760.	2.4	28
106	Prediction of RNA Base Pairing Probabilities on Massively Parallel Computers. Journal of Computational Biology, 2000, 7, 171-182.	0.8	27
107	From consensus structure prediction to RNA gene finding. Briefings in Functional Genomics & Proteomics, 2009, 8, 461-471.	3.8	27
108	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	1.2	27

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109	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
110	Interactions in Oligonucleotide Hybrid Duplexes on Microarrays. Journal of Physical Chemistry B, 2004, 108, 18015-18025.	1.2	25
111	Multiple sequence alignments of partially coding nucleic acid sequences. BMC Bioinformatics, 2005, 6, 160.	1.2	25
112	Bcheck: a wrapper tool for detecting RNase P RNA genes. BMC Genomics, 2010, 11, 432.	1.2	23
113	Pseudoknots in RNA folding landscapes. Bioinformatics, 2016, 32, 187-194.	1.8	23
114	Model-based probe set optimization for high-performance microarrays. Nucleic Acids Research, 2009, 37, e18-e18.	6.5	22
115	Conserved Secondary Structures in Viral mRNAs. Viruses, 2019, 11, 401.	1.5	22
116	Alterations of the Transcriptome of Sulfolobus acidocaldarius by Exoribonuclease aCPSF2. PLoS ONE, 2013, 8, e76569.	1.1	21
117	Translational Control by RNA-RNA Interaction: Improved Computation of RNA-RNA Binding Thermodynamics. Communications in Computer and Information Science, 2008, , 114-127.	0.4	21
118	On the evolution of primitive genetic codes. Origins of Life and Evolution of Biospheres, 2003, 33, 491-514.	0.8	20
119	Transcriptome-wide effects of inverted SINEs on gene expression and their impact on RNA polymerase II activity. Genome Biology, 2016, 17, 220.	3.8	20
120	3D based on 2D: Calculating helix angles and stacking patterns using forgi 2.0, an RNA Python library centered on secondary structure elements.. F1000Research, 2019, 8, 287.	0.8	20
121	Exploring the lower part of discrete polymer model energy landscapes. Europhysics Letters, 2006, 74, 726-732.	0.7	19
122	Hybridization thermodynamics of NimbleGen Microarrays. BMC Bioinformatics, 2010, 11, 35.	1.2	19
123	Thermodynamic and Kinetic Folding of Riboswitches. Methods in Enzymology, 2015, 553, 193-213.	0.4	19
124	Predicting RNA Structure: Advances and Limitations. Methods in Molecular Biology, 2014, 1086, 1-19.	0.4	18
125	Sequence-controlled RNA self-processing: computational design, biochemical analysis, and visualization by AFM. Rna, 2015, 21, 1249-1260.	1.6	18
126	Concurrent Neutral Evolution of mRNA Secondary Structures and Encoded Proteins. Journal of Molecular Evolution, 2000, 50, 238-242.	0.8	17

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127	Structural parameters affecting the kinetics of RNA hairpin formation. Nucleic Acids Research, 2006, 34, 3568-3576.	6.5	17
128	Discriminatory power of RNA family models. Bioinformatics, 2010, 26, i453-i459.	1.8	17
129	Folding RNA/DNA hybrid duplexes. Bioinformatics, 2012, 28, 2530-2531.	1.8	17
130	RNAblueprint: flexible multiple target nucleic acid sequence design. Bioinformatics, 2017, 33, 2850-2858.	1.8	17
131	RNA Structure Elements Conserved between Mouse and 59 Other Vertebrates. Genes, 2018, 9, 392.	1.0	16
132	Identifying Structural Noncoding RNAs Using RNAz. Current Protocols in Bioinformatics, 2007, 19, Unit 12.7.	25.8	15
133	Evolution of metabolic networks: a computational frame-work. Journal of Systems Chemistry, 2010, 1, 4.	1.7	15
134	Transcriptional profiling of human macrophages during infection with *Bordetella pertussis*. RNA Biology, 2020, 17, 731-742.	1.5	15
135	The Hepatitis B Virus Pregenome: Prediction of RNA Structure and Implications for the Emergence of Deletions. Intervirology, 2000, 43, 154-164.	1.2	14
136	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. Nucleic Acids Research, 2013, 41, 9999-10009.	6.5	14
137	In silico design of ligand triggered RNA switches. Methods, 2018, 143, 90-101.	1.9	14
138	Visualization of Barrier Tree Sequences. IEEE Transactions on Visualization and Computer Graphics, 2006, 12, 781-788.	2.9	13
139	RNA structure prediction: from 2D to 3D. Emerging Topics in Life Sciences, 2017, 1, 275-285.	1.1	13
140	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. Methods, 2018, 143, 70-76.	1.9	13
141	Product Grammars for Alignment and Folding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 507-519.	1.9	12
142	Detection of RNA structures in porcine EST data and related mammals. BMC Genomics, 2007, 8, 316.	1.2	11
143	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. PLoS ONE, 2015, 10, e0139900.	1.1	11
144	Designing Optimal siRNA Based on Target Site Accessibility. Methods in Molecular Biology, 2010, 623, 137-154.	0.4	11

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145	Caveats to Deep Learning Approaches to RNA Secondary Structure Prediction. Frontiers in Bioinformatics, 0, 2, .	1.0	11
146	CMCompare webserver: comparing RNA families via covariance models. Nucleic Acids Research, 2013, 41, W499-W503.	6.5	10
147	Saddles and Barrier in Landscapes of Generalized Search Operators. Lecture Notes in Computer Science, 2007, , 194-212.	1.0	10
148	Modelling Translation Initiation under the Influence of sRNA. International Journal of Molecular Sciences, 2012, 13, 16223-16240.	1.8	9
149	www.rnaworkbench.com: A new program for analyzing RNA interference. Computer Methods and Programs in Biomedicine, 2008, 90, 89-94.	2.6	8
150	Symmetric circular matchings and RNA folding. Discrete Mathematics, 2012, 312, 100-112.	0.4	8
151	Comparative RNA Genomics. Methods in Molecular Biology, 2018, 1704, 363-400.	0.4	8
152	An ESS-analysis for ensembles of Prisoner's dilemma strategies. Journal of Theoretical Biology, 1990, 142, 189-200.	0.8	7
153	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
154	Comparative genomics of Czech vaccine strains of Bordetella pertussis. Pathogens and Disease, 2018, 76, .	0.8	7
155	The Trouble with Long-Range Base Pairs in RNA Folding. Lecture Notes in Computer Science, 2013, , 1-11.	1.0	7
156	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.0	7
157	Structural and evolutionary analysis of the transcribed sequence of Boudicca, a Schistosoma mansoni retrotransposon. Gene, 2004, 329, 103-114.	1.0	6
158	RNA Secondary Structures. , 0, , 439-489.		6
159	3D based on 2D: Calculating helix angles and stacking patterns using forgi 2.0, an RNA Python library centered on secondary structure elements.. F1000Research, 2019, 8, 287.	0.8	6
160	Optimizing RNA structures by sequence extensions using RNAcop. Nucleic Acids Research, 2015, 43, 8135-8145.	6.5	5
161	CMV: visualization for RNA and protein family models and their comparisons. Bioinformatics, 2018, 34, 2676-2678.	1.8	5
162	IntaRNAhelix-composing RNA–RNA interactions from stable inter-molecular helices boosts bacterial sRNA target prediction. Journal of Bioinformatics and Computational Biology, 2019, 17, 1940009.	0.3	5

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163	Oxygen and proton pathways in cytochrome c oxidase. , 1998, 30, 100.		4
164	Efficient Computation of Base-pairing Probabilities in Multi-strand RNA Folding. , 2020, , .		4
165	How to Multiply Dynamic Programming Algorithms. Lecture Notes in Computer Science, 2013, , 82-93.	1.0	4
166	Nucleic Acid Sequence and Structure Databases. Methods in Molecular Biology, 2010, 609, 3-15.	0.4	3
167	Computational Design of a Circular RNA with Prionlike Behavior. Artificial Life, 2016, 22, 172-184.	1.0	3
168	Practical Guidelines for Incorporating Knowledge-Based and Data-Driven Strategies into the Inference of Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 64-75.	1.9	3
169	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. Bioinformatics, 2021, 37, 2126-2133.	1.8	3
170	Insights into the secondary and tertiary structure of the Bovine Viral Diarrhea Virus Internal Ribosome Entry Site. RNA Biology, 2022, 19, 496-506.	1.5	3
171	Enhancing the Cell-Free Expression of Native Membrane Proteins by In Silico Optimization of the Coding Sequenceâ€"An Experimental Study of the Human Voltage-Dependent Anion Channel. Membranes, 2021, 11, 741.	1.4	2
172	Complete suboptimal folding of RNA and the stability of secondary structures. , 1999, 49, 145.		2
173	Concepts and Introduction to RNA Bioinformatics. Methods in Molecular Biology, 2014, 1097, 1-31.	0.4	2
174	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. Lecture Notes in Computer Science, 2020, , 159-170.	1.0	2
175	RNAs everywhere: genome-wide annotation of structured RNAs. Genome Informatics, 2006, 17, 281-2.	0.4	2
176	RNA Folding in silico. , 2005, , 177-190.		1
177	MSF: Modulated Sub-graph Finder. F1000Research, 2018, 7, 1346.	0.8	1
178	Constraint Maximal Inter-molecular Helix Lengths within RNA-RNA Interaction Prediction Improves Bacterial sRNA Target Prediction. , 2019, , .		1
179	Visualization of Barrier Tree Sequences Revisited. Mathematics and Visualization, 2008, , 275-290.	0.4	1
180	Computational Design of a Circular RNA with Prion-Like Behavior. , 0, , .		1

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181	MSF: Modulated Sub-graph Finder. F1000Research, 2018, 7, 1346.	0.8	1
182	RNA Consensus Structure Prediction With RNAalifold. , 0, , 527-544.		1
183	The inverse folding problem for RNA secondary structures. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 1127-1127.	0.9	0
184	The locality dilemma of Sankoff-like RNA alignments. Bioinformatics, 2020, 36, i242-i250.	1.8	0
185	Efficient Algorithms for Co-folding of Multiple RNAs. Communications in Computer and Information Science, 2021, , 193-214.	0.4	0
186	COMPUTATIONAL STUDIES OF NON-CODING RNAS â€" Session Introduction. , 2009, , 54-56.		0
187	Modeling RNA Folding. , 2006, , 227-245.		0