

Peter F F Stadler

List of Publications by Year in descending order

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679
papers

57,529
citations

2963

93
h-index

1627

215
g-index

732
all docs

732
docs citations

732
times ranked

57002
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	MITOS: Improved de novo metazoan mitochondrial genome annotation. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 313-319.	1.2	3,919
3	ViennaRNA Package 2.0. <i>Algorithms for Molecular Biology</i> , 2011, 6, 26.	0.3	3,719
4	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. <i>Science</i> , 2007, 316, 1484-1488.	6.0	2,250
5	Pan-cancer analysis of whole genomes. <i>Nature</i> , 2020, 578, 82-93.	13.7	1,966
6	Fast folding and comparison of RNA secondary structures. <i>Monatshefte für Chemie</i> , 1994, 125, 167-188.	0.9	1,862
7	Analyses of pig genomes provide insight into porcine demography and evolution. <i>Nature</i> , 2012, 491, 393-398.	13.7	1,190
8	The primary transcriptome of the major human pathogen <i>Helicobacter pylori</i> . <i>Nature</i> , 2010, 464, 250-255.	13.7	1,115
9	Proteinortho: Detection of (Co-)orthologs in large-scale analysis. <i>BMC Bioinformatics</i> , 2011, 12, 124.	1.2	1,091
10	Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.	6.0	895
11	tRNAdb 2009: compilation of tRNA sequences and tRNA genes. <i>Nucleic Acids Research</i> , 2009, 37, D159-D162.	6.5	751
12	The African coelacanth genome provides insights into tetrapod evolution. <i>Nature</i> , 2013, 496, 311-316.	13.7	612
13	From The Cover: Fast and reliable prediction of noncoding RNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 2454-2459.	3.3	599
14	Interleukin-6-dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. <i>Blood</i> , 2007, 110, 1330-1333.	0.6	597
15	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	13.7	569
16	Molecular Evolution of a MicroRNA Cluster. <i>Journal of Molecular Biology</i> , 2004, 339, 327-335.	2.0	554
17	Secondary Structure Prediction for Aligned RNA Sequences. <i>Journal of Molecular Biology</i> , 2002, 319, 1059-1066.	2.0	545
18	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. <i>Nature Genetics</i> , 2016, 48, 427-437.	9.4	545

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19	RNAalifold: improved consensus structure prediction for RNA alignments. BMC Bioinformatics, 2008, 9, 474.	1.2	505
20	Fast Mapping of Short Sequences with Mismatches, Insertions and Deletions Using Index Structures. PLoS Computational Biology, 2009, 5, e1000502.	1.5	487
21	Smoothness within ruggedness: the role of neutrality in adaptation.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 397-401.	3.3	473
22	Dual RNA-seq unveils noncoding RNA functions in host-pathogen interactions. Nature, 2016, 529, 496-501.	13.7	450
23	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. PLoS Computational Biology, 2007, 3, e65.	1.5	424
24	Recurrent mutation of the ID3 gene in Burkitt lymphoma identified by integrated genome, exome and transcriptome sequencing. Nature Genetics, 2012, 44, 1316-1320.	9.4	389
25	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	2.6	380
26	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
27	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
28	EVOLUTION: Transitions from Nonliving to Living Matter. Science, 2004, 303, 963-965.	6.0	339
29	Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182.	1.8	338
30	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. Genome Research, 2016, 26, 256-262.	2.4	331
31	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. Nature Genetics, 2013, 45, 776-783.	9.4	327
32	LocARNA-P: Accurate boundary prediction and improved detection of structural RNAs. Rna, 2012, 18, 900-914.	1.6	326
33	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. Nucleic Acids Research, 2019, 47, 10543-10552.	6.5	324
34	Alu Elements in ANRIL Non-Coding RNA at Chromosome 9p21 Modulate Atherogenic Cell Functions through Trans-Regulation of Gene Networks. PLoS Genetics, 2013, 9, e1003588.	1.5	323
35	Centers of complex networks. Journal of Theoretical Biology, 2003, 223, 45-53.	0.8	317
36	The expansion of the metazoan microRNA repertoire. BMC Genomics, 2006, 7, 25.	1.2	304

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37	Soundâ€™meaning association biases evidenced across thousands of languages. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10818-10823.	3.3	285
38	Ecological plant epigenetics: Evidence from model and nonâ€™model species, and the way forward. Ecology Letters, 2017, 20, 1576-1590.	3.0	279
39	CREx: inferring genomic rearrangements based on common intervals. Bioinformatics, 2007, 23, 2957-2958.	1.8	276
40	Statistics of RNA secondary structures. Biopolymers, 1993, 33, 1389-1404.	1.2	265
41	The Topology of the Possible: Formal Spaces Underlying Patterns of Evolutionary Change. Journal of Theoretical Biology, 2001, 213, 241-274.	0.8	265
42	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. Genome Biology, 2014, 15, R34.	13.9	242
43	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
44	Improved systematic tRNA gene annotation allows new insights into the evolution of mitochondrial tRNA structures and into the mechanisms of mitochondrial genome rearrangements. Nucleic Acids Research, 2012, 40, 2833-2845.	6.5	218
45	Local RNA base pairing probabilities in large sequences. Bioinformatics, 2006, 22, 614-615.	1.8	217
46	An updated human snoRNAome. Nucleic Acids Research, 2016, 44, 5068-5082.	6.5	216
47	Landscapes and their correlation functions. Journal of Mathematical Chemistry, 1996, 20, 1-45.	0.7	214
48	Genetic aspects of mitochondrial genome evolution. Molecular Phylogenetics and Evolution, 2013, 69, 328-338.	1.2	206
49	Alignment of RNA base pairing probability matrices. Bioinformatics, 2004, 20, 2222-2227.	1.8	205
50	RNA folding and combinatorial landscapes. Physical Review E, 1993, 47, 2083-2099.	0.8	202
51	Combinatorial Landscapes. SIAM Review, 2002, 44, 3-54.	4.2	201
52	miRNAMap: genomic maps of microRNA genes and their target genes in mammalian genomes. Nucleic Acids Research, 2006, 34, D135-D139.	6.5	199
53	Generic properties of combinatorial maps: Neutral networks of RNA secondary structures. Bulletin of Mathematical Biology, 1997, 59, 339-397.	0.9	189
54	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	1.6	188

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55	Spontaneous and Engineered Deletions in the 3' Noncoding Region of Tick-Borne Encephalitis Virus: Construction of Highly Attenuated Mutants of a Flavivirus. <i>Journal of Virology</i> , 1998, 72, 2132-2140.	1.5	187
56	Memory efficient folding algorithms for circular RNA secondary structures. <i>Bioinformatics</i> , 2006, 22, 1172-1176.	1.8	183
57	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. <i>Molecular Phylogenetics and Evolution</i> , 2013, 69, 352-364.	1.2	183
58	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. <i>Bioinformatics</i> , 2006, 22, e197-e202.	1.8	180
59	RNAcentral: a comprehensive database of non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2017, 45, D128-D134.	6.5	174
60	The 'Fish-Specific' Hox Cluster Duplication Is Coincident with the Origin of Teleosts. <i>Molecular Biology and Evolution</i> , 2006, 23, 121-136.	3.5	170
61	Conserved RNA secondary structures in Flaviviridae genomes. <i>Journal of General Virology</i> , 2004, 85, 1113-1124.	1.3	165
62	De novo design of a synthetic riboswitch that regulates transcription termination. <i>Nucleic Acids Research</i> , 2013, 41, 2541-2551.	6.5	163
63	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
64	Noisy: Identification of problematic columns in multiple sequence alignments. <i>Algorithms for Molecular Biology</i> , 2008, 3, 7.	0.3	154
65	RNAcentral: a hub of information for non-coding RNA sequences. <i>Nucleic Acids Research</i> , 2019, 47, D221-D229.	6.5	153
66	Structured RNAs in the ENCODE selected regions of the human genome. <i>Genome Research</i> , 2007, 17, 852-864.	2.4	150
67	Prediction of locally stable RNA secondary structures for genome-wide surveys. <i>Bioinformatics</i> , 2004, 20, 186-190.	1.8	145
68	Widespread purifying selection on RNA structure in mammals. <i>Nucleic Acids Research</i> , 2013, 41, 8220-8236.	6.5	144
69	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. <i>Current Biology</i> , 2012, 22, 1309-1313.	1.8	140
70	Evolution of microRNAs located within Hox gene clusters. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2005, 304B, 75-85.	0.6	139
71	Structure of transfer RNAs: similarity and variability. <i>Wiley Interdisciplinary Reviews RNA</i> , 2012, 3, 37-61.	3.2	139
72	Design of multistable RNA molecules. <i>Rna</i> , 2001, 7, 254-265.	1.6	138

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73	Topology and prediction of RNA pseudoknots. <i>Bioinformatics</i> , 2011, 27, 1076-1085.	1.8	137
74	RNAz 2.0: improved noncoding RNA detection. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2010, , 69-79.	0.7	135
75	Barrier Trees of Degenerate Landscapes. <i>Zeitschrift Fur Physikalische Chemie</i> , 2002, 216, .	1.4	130
76	Evolution of Vault RNAs. <i>Molecular Biology and Evolution</i> , 2009, 26, 1975-1991.	3.5	130
77	Partition function and base pairing probabilities for RNA-RNA interaction prediction. <i>Bioinformatics</i> , 2009, 25, 2646-2654.	1.8	124
78	<scp>RNA</scp> snp: Efficient Detection of Local <scp>RNA</scp> Secondary Structure Changes Induced by <scp>SNP</scp> s. <i>Human Mutation</i> , 2013, 34, 546-556.	1.1	121
79	The landscape of the traveling salesman problem. <i>Physics Letters, Section A: General, Atomic and Solid State Physics</i> , 1992, 161, 337-344.	0.9	120
80	Combinatorics of RNA secondary structures. <i>Discrete Applied Mathematics</i> , 1998, 88, 207-237.	0.5	120
81	Evidence for human microRNA-offset RNAs in small RNA sequencing data. <i>Bioinformatics</i> , 2009, 25, 2298-2301.	1.8	120
82	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. <i>Nature Genetics</i> , 2015, 47, 1316-1325.	9.4	119
83	RNApredator: fast accessibility-based prediction of sRNA targets. <i>Nucleic Acids Research</i> , 2011, 39, W149-W154.	6.5	117
84	The RNAsnp web server: predicting SNP effects on local RNA secondary structure. <i>Nucleic Acids Research</i> , 2013, 41, W475-W479.	6.5	117
85	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. <i>Bioinformatics</i> , 2008, 24, 158-164.	1.8	116
86	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. <i>Nucleic Acids Research</i> , 1998, 26, 3825-3836.	6.5	115
87	Evolution of the let-7 microRNA Family. <i>RNA Biology</i> , 2012, 9, 231-241.	1.5	115
88	HLA-DRB1 [∗] —0401 and HLA-DRB1 [∗] —0408 Are Strongly Associated with the Development of Antibodies against Interferon- β Therapy in Multiple Sclerosis. <i>American Journal of Human Genetics</i> , 2008, 83, 219-227.	2.6	114
89	Analysis of RNA sequence structure maps by exhaustive enumeration I. Neutral networks. <i>Monatshefte Für Chemie</i> , 1996, 127, 355-374.	0.9	112
90	Laplacian Eigenvectors of Graphs. <i>Lecture Notes in Mathematics</i> , 2007, , .	0.1	112

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91	Accurate and efficient reconstruction of deep phylogenies from structured RNAs. <i>Nucleic Acids Research</i> , 2009, 37, 6184-6193.	6.5	108
92	Fitness landscapes. , 2002, , 183-204.		106
93	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. <i>Nucleic Acids Research</i> , 2012, 40, 4261-4272.	6.5	106
94	Lacking alignments? The next-generation sequencing mapper segemehl revisited. <i>Bioinformatics</i> , 2014, 30, 1837-1843.	1.8	105
95	Independent Hox-cluster duplications in lampreys. <i>The Journal of Experimental Zoology</i> , 2003, 299B, 18-25.	1.4	102
96	Neutral networks in protein space: a computational study based on knowledge-based potentials of mean force. <i>Folding & Design</i> , 1997, 2, 261-269.	4.5	100
97	Efficient computation of RNA folding dynamics. <i>Journal of Physics A</i> , 2004, 37, 4731-4741.	1.6	99
98	Detection of small RNAs in <i>Pseudomonas aeruginosa</i> by RNomics and structure-based bioinformatic tools. <i>Microbiology (United Kingdom)</i> , 2008, 154, 3175-3187.	0.7	99
99	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. <i>Nature Communications</i> , 2019, 10, 1459.	5.8	99
100	Discrete nodal domain theorems. <i>Linear Algebra and Its Applications</i> , 2001, 336, 51-60.	0.4	97
101	Third Report on Chicken Genes and Chromosomes 2015. <i>Cytogenetic and Genome Research</i> , 2015, 145, 78-179.	0.6	97
102	Analysis of RNA sequence structure maps by exhaustive enumeration II. Structures of neutral networks and shape space covering. <i>Monatshefte für Chemie</i> , 1996, 127, 375-389.	0.9	94
103	Genome-wide transcriptome analysis of the plant pathogen <i>Xanthomonas</i> identifies sRNAs with putative virulence functions. <i>Nucleic Acids Research</i> , 2012, 40, 2020-2031.	6.5	93
104	Genomic organization of eukaryotic tRNAs. <i>BMC Genomics</i> , 2010, 11, 270.	1.2	91
105	SHAPE directed RNA folding. <i>Bioinformatics</i> , 2016, 32, 145-147.	1.8	91
106	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E5261-70.	3.3	91
107	Neutrality in fitness landscapes. <i>Applied Mathematics and Computation</i> , 2001, 117, 321-350.	1.4	89
108	Bichir HoxA Cluster Sequence Reveals Surprising Trends in Ray-Finned Fish Genomic Evolution. <i>Genome Research</i> , 2003, 14, 11-17.	2.4	89

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109	FRANz: reconstruction of wild multi-generation pedigrees. <i>Bioinformatics</i> , 2009, 25, 2134-2139.	1.8	89
110	RNA folding with hard and soft constraints. <i>Algorithms for Molecular Biology</i> , 2016, 11, 8.	0.3	89
111	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. <i>Molecular Cell</i> , 2014, 56, 389-399.	4.5	88
112	Changes of bivalent chromatin coincide with increased expression of developmental genes in cancer. <i>Scientific Reports</i> , 2016, 6, 37393.	1.6	88
113	Orthology Detection Combining Clustering and Synteny for Very Large Datasets. <i>PLoS ONE</i> , 2014, 9, e105015.	1.1	86
114	Conserved RNA secondary structures in Picornaviridae genomes. <i>Nucleic Acids Research</i> , 2001, 29, 5079-5089.	6.5	84
115	Phylogenomics with paralogs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 2058-2063.	3.3	83
116	Comparison of splice sites reveals that long noncoding RNAs are evolutionarily well conserved. <i>Rna</i> , 2015, 21, 801-812.	1.6	83
117	A Graph-Based Toy Model of Chemistry. <i>Journal of Chemical Information and Computer Sciences</i> , 2003, 43, 1085-1093.	2.8	82
118	Evidence for independent Hox gene duplications in the hagfish lineage: a PCR-based gene inventory of <i>Eptatretus stoutii</i> . <i>Molecular Phylogenetics and Evolution</i> , 2004, 32, 686-694.	1.2	82
119	DARIO: a ncRNA detection and analysis tool for next-generation sequencing experiments. <i>Nucleic Acids Research</i> , 2011, 39, W112-W117.	6.5	82
120	The CHR site: definition and genome-wide identification of a cell cycle transcriptional element. <i>Nucleic Acids Research</i> , 2014, 42, 10331-10350.	6.5	82
121	RNA Structures with Pseudo-knots: Graph-theoretical, Combinatorial, and Statistical Properties. <i>Bulletin of Mathematical Biology</i> , 1999, 61, 437-467.	0.9	81
122	Algorithm independent properties of RNA secondary structure predictions. <i>European Biophysics Journal</i> , 1996, 25, 115-130.	1.2	79
123	Evolution of Spliceosomal snRNA Genes in Metazoan Animals. <i>Journal of Molecular Evolution</i> , 2008, 67, 594-607.	0.8	79
124	Structure and Function of the Smallest Vertebrate Telomerase RNA from Teleost Fish. <i>Journal of Biological Chemistry</i> , 2008, 283, 2049-2059.	1.6	78
125	Temperature-responsive in vitro RNA structurome of <i>Yersinia pseudotuberculosis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 7237-7242.	3.3	78
126	Mutation in autocatalytic reaction networks. <i>Journal of Mathematical Biology</i> , 1992, 30, 597-631.	0.8	77

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127	Folding Kinetics of Large RNAs. <i>Journal of Molecular Biology</i> , 2008, 379, 160-173.	2.0	77
128	A guide to naming human non-coding RNA genes. <i>EMBO Journal</i> , 2020, 39, e103777.	3.5	77
129	Evolution of 7SK RNA and Its Protein Partners in Metazoa. <i>Molecular Biology and Evolution</i> , 2009, 26, 2821-2830.	3.5	76
130	Rsearch2: 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
131	Generalized Topological Spaces in Evolutionary Theory and Combinatorial Chemistry. <i>Journal of Chemical Information and Computer Sciences</i> , 2002, 42, 577-585.	2.8	73
132	Evolution of mitochondrial gene orders in echinoderms. <i>Molecular Phylogenetics and Evolution</i> , 2008, 47, 855-864.	1.2	73
133	TSSAR: TSS annotation regime for dRNA-seq data. <i>BMC Bioinformatics</i> , 2014, 15, 89.	1.2	73
134	Generic properties of combinatory maps: Neutral networks of RNA secondary structures. <i>Bulletin of Mathematical Biology</i> , 1997, 59, 339-397.	0.9	72
135	Landscapes: Complex optimization problems and biopolymer structures. <i>Computers & Chemistry</i> , 1994, 18, 295-324.	1.2	70
136	The common ancestral core of vertebrate and fungal telomerase RNAs. <i>Nucleic Acids Research</i> , 2013, 41, 450-462.	6.5	70
137	Algebraic Theory of Recombination Spaces. <i>Evolutionary Computation</i> , 1997, 5, 241-275.	2.3	68
138	Viral RNA and evolved mutational robustness. , 1999, 285, 119-127.		68
139	RNAZ 2.0.: , 2009, , 69-79.		68
140	Kiwi genome provides insights into evolution of a nocturnal lifestyle. <i>Genome Biology</i> , 2015, 16, 147.	3.8	68
141	Effect of pH on growth, cell volume, and production of freshwater ciliates, and implications for their distribution. <i>Limnology and Oceanography</i> , 2006, 51, 1708-1715.	1.6	67
142	RNAcentral: A vision for an international database of RNA sequences. <i>Rna</i> , 2011, 17, 1941-1946.	1.6	67
143	Random catalytic reaction networks. <i>Physica D: Nonlinear Phenomena</i> , 1993, 63, 378-392.	1.3	66
144	Quasi-Independence, Homology and the Unity of Type: A Topological Theory of Characters. <i>Journal of Theoretical Biology</i> , 2003, 220, 505-527.	0.8	66

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145	Mitochondrial genome evolution in Ophiuroidea, Echinoidea, and Holothuroidea: Insights in phylogenetic relationships of Echinodermata. <i>Molecular Phylogenetics and Evolution</i> , 2010, 56, 201-211.	1.2	66
146	Recent advances in RNA folding. <i>Journal of Biotechnology</i> , 2017, 261, 97-104.	1.9	66
147	Full characterization of a strange attractor. <i>Physica D: Nonlinear Phenomena</i> , 1991, 48, 65-90.	1.3	65
148	RNA multi-structure landscapes. <i>European Biophysics Journal</i> , 1993, 22, 13-24.	1.2	65
149	Variations on RNA folding and alignment: lessons from Benasque. <i>Journal of Mathematical Biology</i> , 2007, 56, 129-144.	0.8	65
150	Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3622-3627.	3.3	65
151	Evolutionary patterns of non-coding RNAs. <i>Theory in Biosciences</i> , 2005, 123, 301-369.	0.6	64
152	Exploration of the chemical space and its three historical regimes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 12660-12665.	3.3	64
153	Structural profiles of human miRNA families from pairwise clustering. <i>Bioinformatics</i> , 2009, 25, 291-294.	1.8	62
154	Orthology relations, symbolic ultrametrics, and cographs. <i>Journal of Mathematical Biology</i> , 2013, 66, 399-420.	0.8	62
155	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. <i>Genome Research</i> , 2018, 28, 699-713.	2.4	62
156	RELEVANT CYCLES IN CHEMICAL REACTION NETWORKS. <i>International Journal of Modeling, Simulation, and Scientific Computing</i> , 2001, 04, 207-226.	0.9	61
157	DREAM and RB cooperate to induce gene repression and cell-cycle arrest in response to p53 activation. <i>Nucleic Acids Research</i> , 2019, 47, 9087-9103.	6.5	61
158	Random field models for fitness landscapes. <i>Journal of Mathematical Biology</i> , 1999, 38, 435-478.	0.8	60
159	Solvent Exposure Imparts Similar Selective Pressures across a Range of Yeast Proteins. <i>Molecular Biology and Evolution</i> , 2009, 26, 1155-1161.	3.5	60
160	Evolutionary clues in <scp>lncRNAs</scp>. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1376.	3.2	60
161	Towards a theory of landscapes. , 1995, , 78-163.		59
162	A folding algorithm for extended RNA secondary structures. <i>Bioinformatics</i> , 2011, 27, i129-i136.	1.8	59

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163	RNA structures and folding: from conventional to new issues in structure predictions. <i>Current Opinion in Structural Biology</i> , 1997, 7, 229-235.	2.6	58
164	Target prediction and a statistical sampling algorithm for RNA-RNA interaction. <i>Bioinformatics</i> , 2010, 26, 175-181.	1.8	57
165	Biological evidence for the world's smallest tRNAs. <i>Biochimie</i> , 2014, 100, 151-158.	1.3	57
166	Non-coding RNA annotation of the genome of <i>Trichoplax adhaerens</i> . <i>Nucleic Acids Research</i> , 2009, 37, 1602-1615.	6.5	56
167	The challenges and scope of theoretical biology. <i>Journal of Theoretical Biology</i> , 2011, 276, 269-276.	0.8	56
168	Dicer-Processed Small RNAs: Rules and Exceptions. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2013, 320, 35-46.	0.6	56
169	The tedious task of finding homologous noncoding RNA genes. <i>Rna</i> , 2009, 15, 2075-2082.	1.6	55
170	Evolution of the vertebrate Y RNA cluster. <i>Theory in Biosciences</i> , 2007, 126, 9-14.	0.6	54
171	Traces of post-transcriptional RNA modifications in deep sequencing data. <i>Biological Chemistry</i> , 2011, 392, 305-13.	1.2	54
172	Automatic detection of conserved base pairing patterns in RNA virus genomes. <i>Computers & Chemistry</i> , 1999, 23, 401-414.	1.2	53
173	BarMap: RNA folding on dynamic energy landscapes. <i>Rna</i> , 2010, 16, 1308-1316.	1.6	53
174	PLEXY: efficient target prediction for box C/D snoRNAs. <i>Bioinformatics</i> , 2011, 27, 279-280.	1.8	53
175	Armless mitochondrial tRNAs in Enoplea (Nematoda). <i>RNA Biology</i> , 2012, 9, 1161-1166.	1.5	53
176	Why Some Fitness Landscapes are Fractal. <i>Journal of Theoretical Biology</i> , 1993, 163, 255-275.	0.8	52
177	Multiple sequence alignment with user-defined anchor points. <i>Algorithms for Molecular Biology</i> , 2006, 1, 6.	0.3	52
178	Applicability of a computational design approach for synthetic riboswitches. <i>Nucleic Acids Research</i> , 2017, 45, gkw1267.	6.5	52
179	The genomic and transcriptional landscape of primary central nervous system lymphoma. <i>Nature Communications</i> , 2022, 13, 2558.	5.8	52
180	Prediction of consensus RNA secondary structures including pseudoknots. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 66-77.	1.9	51

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