Peter F F Stadler

List of Publications by Year
in descending order

679 papers	57,529 citations	3449 93 h-index	1875 215 g-index
732 all docs	732 docs citations	732 times ranked	63384 citing authors

#	Article	IF	Citations
1	Best Match Graphs With Binary Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1679-1690.	1.9	0
2	Generic Context-Aware Group Contributions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 429-442.	1.9	1
3	44 Current Challenges in miRNomics. Methods in Molecular Biology, 2022, 2257, 423-438.	0.4	6
4	Multiomics reveal unique signatures of human epiploic adipose tissue related to systemic insulin resistance. Gut, 2022, 71, 2179-2193.	6.1	12
5	Evolution and Phylogeny of MicroRNAs â€" Protocols, Pitfalls, and Problems. Methods in Molecular Biology, 2022, 2257, 211-233.	0.4	2
6	From modular decomposition trees to rooted median graphs. Discrete Applied Mathematics, 2022, 310, 1-9.	0.5	6
7	Synthetic Riboswitches for the Analysis of tRNA Processing by eukaryotic RNase P Enzymes. Rna, 2022, , rna.078814.121.	1.6	3
8	Evolution of DNA Methylation Across Ecdysozoa. Journal of Molecular Evolution, 2022, 90, 56-72.	0.8	12
9	Chromosomeâ€level *Thlaspi arvense* genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. Plant Biotechnology Journal, 2022, 20, 944-963.	4.1	18
10	PredicTF: prediction of bacterial transcription factors in complex microbial communities using deep learning. Environmental Microbiomes, 2022, 17, 7.	2.2	6
11	ExceS-A: an exon-centric split aligner. Journal of Integrative Bioinformatics, 2022, 19, .	1.0	0
12	Small integral membrane protein 10 like 1 downregulation enhances differentiation of adipose progenitor cells. Biochemical and Biophysical Research Communications, 2022, 604, 57-62.	1.0	1
13	Compatibility of partitions with trees, hierarchies, and split systems. Discrete Applied Mathematics, 2022, 314, 265-283.	0.5	4
14	Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair. Frontiers in Microbiology, 2022, 13, 822304.	1.5	3
15	The genomic and transcriptional landscape of primary central nervous system lymphoma. Nature Communications, 2022, 13, 2558.	5.8	52
16	Bi-alignments with affine gaps costs. Algorithms for Molecular Biology, 2022, 17, 10.	0.3	2
17	Complete edge-colored permutation graphs. Advances in Applied Mathematics, 2022, 139, 102377.	0.4	2
18	RNA Design Principles for Riboswitches that Regulate RNase P-Mediated tRNA Processing. Methods in Molecular Biology, 2022, , 179-202.	0.4	1

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19	BioAutoML: automated feature engineering and metalearning to predict noncoding RNAs in bacteria. Briefings in Bioinformatics, 2022, 23, .	3.2	10
20	Alzheimer-related genes show accelerated evolution. Molecular Psychiatry, 2021, 26, 5790-5796.	4.1	10
21	Superbubbles as an empirical characteristic of directed networks. Network Science, 2021, 9, 49-58.	0.8	0
22	Proteomics reveals sex-specific heat shock response of Baikal amphipod Eulimnogammarus cyaneus. Science of the Total Environment, 2021, 763, 143008.	3.9	4
23	HumanMetagenomeDB: a public repository of curated and standardized metadata for human metagenomes. Nucleic Acids Research, 2021, 49, D743-D750.	6.5	37
24	Beyond Plug and Pray: Context Sensitivity and *in silico* Design of Artificial Neomycin Riboswitches. RNA Biology, 2021, 18, 457-467.	1.5	6
25	MCPIP1 ribonuclease can bind and cleave *AURKA* mRNA in *MYCN*-amplified neuroblastoma cells. RNA Biology, 2021, 18, 144-156.	1.5	5
26	Efficient Algorithms for Co-folding of Multiple RNAs. Communications in Computer and Information Science, 2021, , 193-214.	0.4	0
27	Cut Vertex Transit Functions of Hypergraphs. Lecture Notes in Computer Science, 2021, , 222-233.	1.0	0
28	Ligand-dependent tRNA processing by a rationally designed RNase P riboswitch. Nucleic Acids Research, 2021, 49, 1784-1800.	6.5	4
29	Best Match Graphs with Binary Trees. Lecture Notes in Computer Science, 2021, , 82-93.	1.0	3
30	Comprehensive benchmarking of software for mapping whole genome bisulfite data: from read alignment to DNA methylation analysis. Briefings in Bioinformatics, 2021, 22, .	3.2	14
31	Thermal reaction norms of key metabolic enzymes reflect divergent physiological and behavioral adaptations of closely related amphipod species. Scientific Reports, 2021, 11, 4562.	1.6	7
32	FORMAN–RICCI CURVATURE FOR HYPERGRAPHS. International Journal of Modeling, Simulation, and Scientific Computing, 2021, 24, .	0.9	3
33	miRNAture–Computational Detection of microRNA Candidates. Genes, 2021, 12, 348.	1.0	3
34	Weighted Consensus Segmentations. Computation, 2021, 9, 17.	1.0	0
35	Complete Characterization of Incorrect Orthology Assignments in Best Match Graphs. Journal of Mathematical Biology, 2021, 82, 20.	0.8	13
36	Human pathways in animal models: possibilities and limitations. Nucleic Acids Research, 2021, 49, 1859-1871.	6.5	35

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37	Arc-Completion of 2-Colored Best Match Graphs to Binary-Explainable Best Match Graphs. Algorithms, 2021, 14, 110.	1.2	2
38	Lifestyle weight-loss intervention may attenuate methylation aging: the CENTRAL MRI randomized controlled trial. Clinical Epigenetics, 2021, 13, 48.	1.8	22
39	Complexity of modification problems for best match graphs. Theoretical Computer Science, 2021, 865, 63-84.	0.5	8
40	Changes of the tRNA Modification Pattern during the Development of Dictyostelium discoideum. Non-coding RNA, 2021, 7, 32.	1.3	1
41	Accelerated Evolution of Tissue-Specific Genes Mediates Divergence Amidst Gene Flow in European Green Lizards. Genome Biology and Evolution, 2021, 13, .	1.1	1
42	A workflow to identify novel proteins based on the direct mapping of peptide-spectrum-matches to genomic locations. BMC Bioinformatics, 2021, 22, 277.	1.2	4
43	Effects of lifestyle interventions on epigenetic signatures of liver fat: Central randomized controlled trial. Liver International, 2021, 41, 2101-2111.	1.9	15
44	Mutational mechanisms shaping the coding and noncoding genome of germinal center derived B-cell lymphomas. Leukemia, 2021, 35, 2002-2016.	3.3	34
45	LazyB: fast and cheap genome assembly. Algorithms for Molecular Biology, 2021, 16, 8.	0.3	4
46	Alignments of biomolecular contact maps. Interface Focus, 2021, 11, 20200066.	1.5	3
47	Ryūtō: improved multi-sample transcript assembly for differential transcript expression analysis and more. Bioinformatics, 2021, 37, 4307-4313.	1.8	3
48	Indirect identification of horizontal gene transfer. Journal of Mathematical Biology, 2021, 83, 10.	0.8	8
49	PTEN regulates adipose progenitor cell growth, differentiation, and replicative aging. Journal of Biological Chemistry, 2021, 297, 100968.	1.6	8
50	Heuristic algorithms for best match graph editing. Algorithms for Molecular Biology, 2021, 16, 19.	0.3	2
51	OrtSuite: from genomes to prediction of microbial interactions within targeted ecosystem processes. Life Science Alliance, 2021, 4, e202101167.	1.3	4
52	Different ways to play it cool: Transcriptomic analysis sheds light on different activity patterns of three amphipod species under long‐term cold exposure. Molecular Ecology, 2021, 30, 5735-5751.	2.0	11
53	Machine Learning Studies of Non-coding RNAs based on Artificially Constructed Training Data. , 2021, , .		0
54	Compositional Properties of Alignments. Mathematics in Computer Science, 2021, 15, 609.	0.2	3

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55	RNA Secondary Structures with Limited Base Pair Span: Exact Backtracking and an Application. Genes, 2021, 12, 14.	1.0	7
56	Efficient Laplacian spectral density computations for networks with arbitrary degree distributions. Network Science, 2021, 9, 312-327.	0.8	2
57	Disturbance of phylogenetic layer-specific adaptation of human brain gene expression in Alzheimer's disease. Scientific Reports, 2021, 11, 20200.	1.6	1
58	cyPhyRNA-seq: a genome-scale RNA-seq method to detect active self-cleaving ribozymes by capturing RNAs with 2Ê¹,3Ê¹ <u>cy</u>clic <u>p</u>hosphates and 5Ê¹ <u>hy</u>droxyl ends. RNA Biology, 2021, 18, 818-831.	1.5	5
59	A simpler linear-time algorithm for the common refinement of rooted phylogenetic trees on a common leaf set. Algorithms for Molecular Biology, 2021, 16, 23.	0.3	3
60	Common Features in lncRNA Annotation and Classification: A Survey. Non-coding RNA, 2021, 7, 77.	1.3	13
61	The Genome of the â€œSea Vomitâ€•Didemnum vexillum. Life, 2021, 11, 1377.	1.1	0
62	EpiDiverse Toolkit: a pipeline suite for the analysis of bisulfite sequencing data in ecological plant epigenetics. NAR Genomics and Bioinformatics, 2021, 3, lqab106.	1.5	7
63	TerrestrialMetagenomeDB: a public repository of curated and standardized metadata for terrestrial metagenomes. Nucleic Acids Research, 2020, 48, D626-D632.	6.5	25
64	Average Fitness Differences on NK Landscapes. Theory in Biosciences, 2020, 139, 1-7.	0.6	5
65	Transit sets of -point crossover operators. AKCE International Journal of Graphs and Combinatorics, 2020, 17, 519-533.	0.4	1
66	LOTTE-seq (Long hairpin oligonucleotide based tRNA high-throughput sequencing): specific selection of tRNAs with 3â€™-CCA end for high-throughput sequencing. RNA Biology, 2020, 17, 23-32.	1.5	22
67	Reciprocal best match graphs. Journal of Mathematical Biology, 2020, 80, 865-953.	0.8	10
68	Transcriptome-level effects of the model organic pollutant phenanthrene and its solvent acetone in three amphipod species. Comparative Biochemistry and Physiology Part D: Genomics and Proteomics, 2020, 33, 100630.	0.4	2
69	Complexity of modification problems for reciprocal best match graphs. Theoretical Computer Science, 2020, 809, 384-393.	0.5	4
70	Enrichment and identification of small proteins in a simplified human gut microbiome. Journal of Proteomics, 2020, 213, 103604.	1.2	32
71	DNA methylation signature in blood mirrors successful weight-loss during lifestyle interventions: the CENTRAL trial. Genome Medicine, 2020, 12, 97.	3.6	28
72	Unusual Occurrence of Two Bona-Fide CCA-Adding Enzymes in Dictyostelium discoideum. International Journal of Molecular Sciences, 2020, 21, 5210.	1.8	4

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73	Exact-2-relation graphs. Discrete Applied Mathematics, 2020, 285, 212-226.	0.5	3
74	Convexity Deficit of Benzenoids. Croatica Chemica Acta, 2020, 92, 457-466.	0.1	2
75	Clustering Improves the Goemans–Williamson Approximation for the Max-Cut Problem. Computation, 2020, 8, 75.	1.0	0
76	Splicing Endonuclease Is an Important Player in rRNA and tRNA Maturation in Archaea. Frontiers in Microbiology, 2020, 11, 594838.	1.5	11
77	Street Name Data as a Reflection of Migration and Settlement History. Urban Science, 2020, 4, 74.	1.1	0
78	Are spliced ncRNA host genes distinct classes of lncRNAs?. Theory in Biosciences, 2020, 139, 349-359.	0.6	1
79	Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing. Genome Biology, 2020, 21, 299.	3.8	6
80	A probabilistic version of Sankoff's maximum parsimony algorithm. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050004.	0.3	1
81	Best match graphs and reconciliation of gene trees with species trees. Journal of Mathematical Biology, 2020, 80, 1459-1495.	0.8	14
82	A guide to naming human non‐coding RNA genes. EMBO Journal, 2020, 39, e103777.	3.5	77
83	Distinct abdominal and gluteal adipose tissue transcriptome signatures are altered by exercise training in African women with obesity. Scientific Reports, 2020, 10, 10240.	1.6	15
84	Generalized Fitch graphs II: Sets of binary relations that are explained by edge-labeled trees. Discrete Applied Mathematics, 2020, 283, 495-511.	0.5	5
85	Master and servant: LINC00152 â€“ a STAT3-induced long noncoding RNA regulates STAT3 in a positive feedback in human multiple myeloma. BMC Medical Genomics, 2020, 13, 22.	0.7	11
86	Identification of RNA 3´ ends and termination sites in <i>Haloferax volcanii</i>. RNA Biology, 2020, 17, 663-676.	1.5	16
87	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
88	From pairs of most similar sequences to phylogenetic best matches. Algorithms for Molecular Biology, 2020, 15, 5.	0.3	12
89	Splicing conservation signals in plant long noncoding RNAs. Rna, 2020, 26, 784-793.	1.6	16
90	Developmentally Driven Changes in Adipogenesis in Different Fat Depots Are Related to Obesity. Frontiers in Endocrinology, 2020, 11, 138.	1.5	12

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91	Cograph editing: Merging modules is equivalent to editing P_4s. Art of Discrete and Applied Mathematics, 2020, 3, #P2.01.	0.2	3
92	Efficient Computation of Base-pairing Probabilities in Multi-strand RNA Folding. , 2020, , .		4
93	Bi-alignments as Models of Incongruent Evolution of RNA Sequence and Secondary Structure. Lecture Notes in Computer Science, 2020, , 159-170.	1.0	2
94	Computational Simulations for Cyclizations Catalyzed by Plant Monoterpene Synthases. Lecture Notes in Computer Science, 2020, , 247-258.	1.0	0
95	Anti-CD3 Stimulated T Cell Transcriptome Reveals Novel ncRNAs and Correlates with a Suppressive Profile. Lecture Notes in Computer Science, 2020, , 180-191.	1.0	0
96	Indication of ongoing amphipod speciation in Lake Baikal by genetic structures within endemic species. BMC Evolutionary Biology, 2019, 19, 138.	3.2	12
97	Gene expression profile of human T cells following a single stimulation of peripheral blood mononuclear cells with anti-CD3 antibodies. BMC Genomics, 2019, 20, 593.	1.2	12
98	Selection Pressures on RNA Sequences and Structures. Evolutionary Bioinformatics, 2019, 15, 117693431987191.	0.6	9
99	Improved annotation of protein-coding genes boundaries in metazoan mitochondrial genomes. Nucleic Acids Research, 2019, 47, 10543-10552.	6.5	324
100	DREAM and RB cooperate to induce gene repression and cell-cycle arrest in response to p53 activation. Nucleic Acids Research, 2019, 47, 9087-9103.	6.5	61
101	A streamlined protocol for the detection of mRNAâ€"sRNA interactions using AMT-crosslinking <i>in vitro</i>. BioTechniques, 2019, 67, 178-183.	0.8	4
102	Comparison between transcriptomic responses to short-term stress exposures of a common Holarctic and endemic Lake Baikal amphipods. BMC Genomics, 2019, 20, 712.	1.2	17
103	Description of strongly heat-inducible heat shock protein 70 transcripts from Baikal endemic amphipods. Scientific Reports, 2019, 9, 8907.	1.6	7
104	Best match graphs. Journal of Mathematical Biology, 2019, 78, 2015-2057.	0.8	18
105	Exploration of the chemical space and its three historical regimes. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12660-12665.	3.3	64
106	Direct Superbubble Detection. Algorithms, 2019, 12, 81.	1.2	1
107	The RNA workbench 2.0: next generation RNA data analysis. Nucleic Acids Research, 2019, 47, W511-W515.	6.5	13
108	Exploring Plant Sesquiterpene Diversity by Generating Chemical Networks. Processes, 2019, 7, 240.	1.3	4

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109	Big Data Competence Center ScaDS Dresden/Leipzig: Overview and selected research activities. Datenbank-Spektrum, 2019, 19, 5-16.	1.2	5
110	Automatic curation of large comparative animal MicroRNA datasets. Bioinformatics, 2019, 35, 4553-4559.	1.8	5
111	RyÅ«tÅ network-flow based transcriptome reconstruction. BMC Bioinformatics, 2019, 20, 190.	1.2	20
112	Genomic and transcriptomic changes complement each other in the pathogenesis of sporadic Burkitt lymphoma. Nature Communications, 2019, 10, 1459.	5.8	99
113	SSS-test: a novel test for detecting positive selection on RNA secondary structure. BMC Bioinformatics, 2019, 20, 151.	1.2	12
114	Within-population genome size variation is mediated by multiple genomic elements that segregate independently during meiosis. Genome Biology and Evolution, 2019, 11, 3424-3435.	1.1	13
115	Genome analyses of a placozoan rickettsial endosymbiont show a combination of mutualistic and parasitic traits. Scientific Reports, 2019, 9, 17561.	1.6	11
116	flowEMMi: an automated model-based clustering tool for microbial cytometric data. BMC Bioinformatics, 2019, 20, 643.	1.2	16
117	RNApuzzler: efficient outerplanar drawing of RNA-secondary structures. Bioinformatics, 2019, 35, 1342-1349.	1.8	12
118	RNAcentral: a hub of information for non-coding RNA sequences. Nucleic Acids Research, 2019, 47, D221-D229.	6.5	153
119	Chemical Transformation Motifsâ€"Modelling Pathways as Integer Hyperflows. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 510-523.	1.9	31
120	Axiomatic characterization of transit functions of weak hierarchies. Art of Discrete and Applied Mathematics, 2019, 2, #P1.01.	0.2	4
121	A General Framework for Exact Partially Local Alignments. , 2019, , .		0
122	In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors. Genome Research, 2018, 28, 699-713.	2.4	62
123	Toward a mechanistic explanation of phenotypic evolution: The need for a theory of theory integration. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2018, 330, 5-14.	0.6	12
124	The fungal snoRNAome. Rna, 2018, 24, 342-360.	1.6	10
125	Gene Phylogenies and Orthologous Groups. Methods in Molecular Biology, 2018, 1704, 1-28.	0.4	11
126	Comparative RNA Genomics. Methods in Molecular Biology, 2018, 1704, 363-400.	0.4	8

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127	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. Journal of Mathematical Biology, 2018, 77, 313-341.	0.8	1
128	Accurate mapping of tRNA reads. Bioinformatics, 2018, 34, 1116-1124.	1.8	33
129	Tracing the evolution of the heterotrimeric G protein α subunit in Metazoa. BMC Evolutionary Biology, 2018, 18, 51.	3.2	17
130	Finding the K best synthesis plans. Journal of Cheminformatics, 2018, 10, 19.	2.8	9
131	Partially Local Multi-way Alignments. Mathematics in Computer Science, 2018, 12, 207-234.	0.2	4
132	Temporal ordering of substitutions in RNA evolution: Uncovering the structural evolution of the Human Accelerated Region 1. Journal of Theoretical Biology, 2018, 438, 143-150.	0.8	7
133	Detailed secondary structure models of invertebrate 7SK RNAs. RNA Biology, 2018, 15, 158-164.	1.5	14
134	Inferring phylogenetic trees from the knowledge of rare evolutionary events. Journal of Mathematical Biology, 2018, 76, 1623-1653.	0.8	6
135	Identification and characterization of novel conserved RNA structures in Drosophila. BMC Genomics, 2018, 19, 899.	1.2	6
136	Superbubbles revisited. Algorithms for Molecular Biology, 2018, 13, 16.	0.3	3
137	Split-inducing indels in phylogenomic analysis. Algorithms for Molecular Biology, 2018, 13, 12.	0.3	11
138	Patterning the insect eye: From stochastic to deterministic mechanisms. PLoS Computational Biology, 2018, 14, e1006363.	1.5	9
139	Divergent evolution in the genomes of closely-related lacertids, Lacerta viridis and L. bilineata and implications for speciation. GigaScience, 2018, 8, .	3.3	10
140	Combined Experimental and System-Level Analyses Reveal the Complex Regulatory Network of miR-124 during Human Neurogenesis. Cell Systems, 2018, 7, 438-452.e8.	2.9	41
141	Coordinate systems for supergenomes. Algorithms for Molecular Biology, 2018, 13, 15.	0.3	10
142	Noncoding RNA Transcripts during Differentiation of Induced Pluripotent Stem Cells into Hepatocytes. Stem Cells International, 2018, 2018, 1-15.	1.2	5
143	Reconstructing gene trees from Fitch's xenology relation. Journal of Mathematical Biology, 2018, 77, 1459-1491.	0.8	23
144	Moderate weather extremes alter phytoplankton diversity—A microcosm study. Freshwater Biology, 2018, 63, 1211-1224.	1.2	21

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145	Studying language evolution in the age of big data. Journal of Language Evolution, 2018, 3, 94-129.	2.2	10
146	Phylogenetics beyond biology. Theory in Biosciences, 2018, 137, 133-143.	0.6	5
147	The Sierra Platinum Service for generating peak-calls for replicated ChIP-seq experiments. BMC Research Notes, 2018, 11, 512.	0.6	3
148	TERribly Difficult: Searching for Telomerase RNAs in Saccharomycetes. Genes, 2018, 9, 372.	1.0	12
149	Nonprotein-Coding RNAs as Regulators of Development in Tunicates. Results and Problems in Cell Differentiation, 2018, 65, 197-225.	0.2	5
150	Cover-Encodings of Fitness Landscapes. Bulletin of Mathematical Biology, 2018, 80, 2154-2176.	0.9	1
151	Time-consistent reconciliation maps and forbidden time travel. Algorithms for Molecular Biology, 2018, 13, 2.	0.3	9
152	Trichoplax genomes reveal profound admixture and suggest stable wild populations without bisexual reproduction. Scientific Reports, 2018, 8, 11168.	1.6	36
153	Beyond the 3â€²UTR binding-microRNA-induced protein truncation via DNA binding. Oncotarget, 2018, 9, 32855-32867.	0.8	17
154	Axiomatic characterization of transit functions of hierarchies. Ars Mathematica Contemporanea, 2018, 14, 117-128.	0.3	1
155	A short note on undirected Fitch graphs. Art of Discrete and Applied Mathematics, 2018, 1, #1.08.	0.2	9
156	Applicability of a computational design approach for synthetic riboswitches. Nucleic Acids Research, 2017, 45, gkw1267.	6.5	52
157	The complete mitochondrial genome of <i>Lacerta bilineata</i> and comparison with its closely related congener <i>L. Viridis</i>. Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2017, 28, 116-118.	0.7	5
158	Towards a Consistent, Quantitative Evaluation of MicroRNA Evolution. Journal of Integrative Bioinformatics, 2017, 14, .	1.0	7
159	ceRNAs in plants: computational approaches and associated challenges for target mimic research. Briefings in Bioinformatics, 2017, 19, 1273-1289.	3.2	16
160	The RNA workbench: best practices for RNA and high-throughput sequencing bioinformatics in Galaxy. Nucleic Acids Research, 2017, 45, W560-W566.	6.5	38
161	RNA-bioinformatics: Tools, services and databases for the analysis of RNA-based regulation. Journal of Biotechnology, 2017, 261, 76-84.	1.9	21
162	The mathematics of xenology: di-cographs, symbolic ultrametrics, 2-structures and tree-representable systems of binary relations. Journal of Mathematical Biology, 2017, 75, 199-237.	0.8	26

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163	Keeping it complicated: Mitochondrial genome plasticity across diplonemids. Scientific Reports, 2017, 7, 14166.	1.6	18
164	Similarity-Based Segmentation of Multi-Dimensional Signals. Scientific Reports, 2017, 7, 12355.	1.6	15
165	Ecological plant epigenetics: Evidence from model and nonâ€model species, and the way forward. Ecology Letters, 2017, 20, 1576-1590.	3.0	279
166	STAT3-induced long noncoding RNAs in multiple myeloma cells display different properties in cancer. Scientific Reports, 2017, 7, 7976.	1.6	26
167	An intermediate level of abstraction for computational systems chemistry. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2017, 375, 20160354.	1.6	13
168	Recent advances in RNA folding. Journal of Biotechnology, 2017, 261, 97-104.	1.9	66
169	Do genome size differences within Brachionus asplanchnoidis (Rotifera, Monogononta) cause reproductive barriers among geographic populations?. Hydrobiologia, 2017, 796, 59-75.	1.0	14
170	Accurate annotation of protein-coding genes in mitochondrial genomes. Molecular Phylogenetics and Evolution, 2017, 106, 209-216.	1.2	22
171	Evolutionary clues in <scp>lncRNAs</scp>. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1376.	3.2	60
172	RNAcentral: a comprehensive database of non-coding RNA sequences. Nucleic Acids Research, 2017, 45, D128-D134.	6.5	174
173	Multidimensional segmentation of heterogeneous data. , 2017, , .		0
174	Evolution of Fungal U3 snoRNAs: Structural Variation and Introns. Non-coding RNA, 2017, 3, 3.	1.3	4
175	Rare Splice Variants in Long Non-Coding RNAs. Non-coding RNA, 2017, 3, 23.	1.3	8
176	Design of Artificial Riboswitches as Biosensors. Sensors, 2017, 17, 1990.	2.1	50
177	A Support Vector Machine based method to distinguish long non-coding RNAs from protein coding transcripts. BMC Genomics, 2017, 18, 804.	1.2	47
178	Algebraic Dynamic Programming on Trees. Algorithms, 2017, 10, 135.	1.2	4
179	RIsearch2: suffix array-based large-scale prediction of RNAâ€"RNA interactions and siRNA off-targets. Nucleic Acids Research, 2017, 45, gkw1325.	6.5	75
180	Uncovering missing pieces: duplication and deletion history of arrestins in deuterostomes. BMC Evolutionary Biology, 2017, 17, 163.	3.2	39

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181	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. Algorithms for Molecular Biology, 2017, 12, 22.	0.3	7
182	Tractable RNA–ligand interaction kinetics. BMC Bioinformatics, 2017, 18, 424.	1.2	10
183	SMORE: Synteny Modulator of Repetitive Elements. Life, 2017, 7, 42.	1.1	2
184	Chemical Graph Transformation with Stereo-Information. Lecture Notes in Computer Science, 2017, , 54-69.	1.0	7
185	Oriented components and their separations. Applied General Topology, 2017, 18, 255.	0.1	1
186	SHAPE directed RNA folding. Bioinformatics, 2016, 32, 145-147.	1.8	91
187	Pseudoknots in RNA folding landscapes. Bioinformatics, 2016, 32, 187-194.	1.8	23
188	Orthologs, turn-over, and remolding of tRNAs in primates and fruit flies. BMC Genomics, 2016, 17, 617.	1.2	20
189	Molecular Phylogenetics 2016. BioMed Research International, 2016, 2016, 1-2.	0.9	2
190	Never Ending Analysis of a Century Old Evolutionary Debate: "Unringing" the Urmetazoon Bell. Frontiers in Ecology and Evolution, 2016, 4, .	1.1	15
191	Automatic Inference of Graph Transformation Rules Using the Cyclic Nature of Chemical Reactions. Lecture Notes in Computer Science, 2016, , 206-222.	1.0	2
192	A Software Package for Chemically Inspired Graph Transformation. Lecture Notes in Computer Science, 2016, , 73-88.	1.0	31
193	Automated detection of ncRNAs in the draft genome sequence of a colonial tunicate: the carpet sea squirt Didemnum vexillum. BMC Genomics, 2016, 17, 691.	1.2	10
194	Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells. Scientific Reports, 2016, 6, 34589.	1.6	47
195	Alterations of microRNA and microRNA-regulated messenger RNA expression in germinal center B-cell lymphomas determined by integrative sequencing analysis. Haematologica, 2016, 101, 1380-1389.	1.7	43
196	Assessing Greenness of Chemical Reactions and Synthesis Plans through Posetic Landscapes. ACS Sustainable Chemistry and Engineering, 2016, 4, 2191-2199.	3.2	4
197	Associativity and Non-Associativity of Some Hypergraph Products. Mathematics in Computer Science, 2016, 10, 403-408.	0.2	1
198	Changes of bivalent chromatin coincide with increased expression of developmental genes in cancer. Scientific Reports, 2016, 6, 37393.	1.6	88

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199	Sound–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
200	Design specifications for cellular regulation. Theory in Biosciences, 2016, 135, 231-240.	0.6	6
201	Phylogenetic distribution of plant snoRNA families. BMC Genomics, 2016, 17, 969.	1.2	15
202	An updated human snoRNAome. Nucleic Acids Research, 2016, 44, 5068-5082.	6.5	216
203	Algebraic dynamic programming for multiple context-free grammars. Theoretical Computer Science, 2016, 639, 91-109.	0.5	8
204	The paralog-to-contig assignment problem: high quality gene models from fragmented assemblies. Algorithms for Molecular Biology, 2016, 11, 1.	0.3	28
205	Temperature-responsive in vitro RNA structurome of *Yersinia pseudotuberculosis*. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 7237-7242.	3.3	78
206	RNA folding with hard and soft constraints. Algorithms for Molecular Biology, 2016, 11, 8.	0.3	89
207	Read mapping. IT - Information Technology, 2016, 58, 119-125.	0.6	0
208	Dual RNA-seq unveils noncoding RNA functions in host–pathogen interactions. Nature, 2016, 529, 496-501.	13.7	450
209	U6 snRNA intron insertion occurred multiple times during fungi evolution. RNA Biology, 2016, 13, 119-127.	1.5	7
210	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	9.4	545
211	metilene: fast and sensitive calling of differentially methylated regions from bisulfite sequencing data. Genome Research, 2016, 26, 256-262.	2.4	331
212	Spectral classes of regular, random, and empirical graphs. Linear Algebra and Its Applications, 2016, 489, 30-49.	0.4	14
213	Algebraic Dynamic Programming over general data structures. BMC Bioinformatics, 2015, 16, S2.	1.2	10
214	Evolution of 3'UTR-associated RNAs. BMC Bioinformatics, 2015, 16, .	1.2	1
215	*In silico* Support for Eschenmoser's Glyoxylate Scenario. Israel Journal of Chemistry, 2015, 55, 919-933.	1.0	10
216	Unusual Novel SnoRNA-Like RNAs in Drosophila melanogaster. Non-coding RNA, 2015, 1, 139-150.	1.3	3

#	Article	IF	Citations
217	Conservation and Losses of Non-Coding RNAs in Avian Genomes. PLoS ONE, 2015, 10, e0121797.	1.1	18
218	Molecular Phylogenetics 2014. BioMed Research International, 2015, 2015, 1-2.	0.9	1
219	Spiders can be Recognized by Counting Their Legs. Mathematics in Computer Science, 2015, 9, 437-441.	0.2	0
220	The Expansion of Animal MicroRNA Families Revisited. Life, 2015, 5, 905-920.	1.1	44
221	Optimizing RNA structures by sequence extensions using RNAcop. Nucleic Acids Research, 2015, 43, 8135-8145.	6.5	5
222	Product Grammars for Alignment and Folding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 507-519.	1.9	12
223	The relativity of biological function. Theory in Biosciences, 2015, 134, 143-147.	0.6	14
224	The ancestor of modern Holozoa acquired the CCA-adding enzyme from Alphaproteobacteria by horizontal gene transfer. Nucleic Acids Research, 2015, 43, 6739-6746.	6.5	14
225	Connectivity Spaces. Mathematics in Computer Science, 2015, 9, 409-436.	0.2	3
226	Design of Transcription Regulating Riboswitches. Methods in Enzymology, 2015, 550, 1-22.	0.4	8
227	Developmentally regulated expression and expression strategies of Drosophila snoRNAs. Insect Biochemistry and Molecular Biology, 2015, 61, 69-78.	1.2	8
228	Phylogenomics with paralogs. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 2058-2063.	3.3	83
229	Prevalent and distinct spliceosomal 3â€²-end processing mechanisms for fungal telomerase RNA. Nature Communications, 2015, 6, 6105.	5.8	21
230	Kiwi genome provides insights into evolution of a nocturnal lifestyle. Genome Biology, 2015, 16, 147.	3.8	68
231	Third Report on Chicken Genes and Chromosomes 2015. Cytogenetic and Genome Research, 2015, 145, 78-179.	0.6	97
232	A simple data-adaptive probabilistic variant calling model. Algorithms for Molecular Biology, 2015, 10, 10.	0.3	3
233	Comparison of splice sites reveals that long noncoding RNAs are evolutionarily well conserved. Rna, 2015, 21, 801-812.	1.6	83
234	Design criteria for synthetic riboswitches acting on transcription. RNA Biology, 2015, 12, 221-231.	1.5	41

#	Article	IF	Citations
235	DNA methylome analysis in Burkitt and follicular lymphomas identifies differentially methylated regions linked to somatic mutation and transcriptional control. Nature Genetics, 2015, 47, 1316-1325.	9.4	119
236	Evolution of the unspliced transcriptome. BMC Evolutionary Biology, 2015, 15, 166.	3.2	7
237	Knowledge-based reasoning to annotate noncoding RNA using multi-agent system. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550021.	0.3	0
238	Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. Nucleic Acids Research, 2015, 43, 8044-8056.	6.5	22
239	MINCR is a MYC-induced lncRNA able to modulate MYC's transcriptional network in Burkitt lymphoma cells. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5261-70.	3.3	91
240	Evolution of RNA-Based Networks. Current Topics in Microbiology and Immunology, 2015, 392, 43-59.	0.7	9
241	The Grid Property and Product-Like Hypergraphs. Graphs and Combinatorics, 2015, 31, 757-770.	0.2	0
242	Indications for Potential Parent-of-Origin Effects within the FTO Gene. PLoS ONE, 2015, 10, e0119206.	1.1	7
243	Processed Small RNAs in Archaea and BHB Elements. Genomics and Computational Biology, 2015, 1, 18.	0.7	2
244	Generalized Topologies: Hypergraphs, Chemical Reactions, and Biological Evolution. , 2015, , 300-328.		4
245	Identification of Blut, a Novel Long-Noncoding RNA Differentially Expressed in Burkitt Lymphoma. Blood, 2015, 126, 3875-3875.	0.6	0
246	Orthology Detection Combining Clustering and Synteny for Very Large Datasets. PLoS ONE, 2014, 9, e105015.	1.1	86
247	Atom mapping with constraint programming. Algorithms for Molecular Biology, 2014, 9, 23.	0.3	14
248	Bioinformatics of prokaryotic RNAs. RNA Biology, 2014, 11, 470-483.	1.5	12
249	23 RNA in phylogenetic reconstruction. , 2014, , 531-538.		1
250	plantDARIO: web based quantitative and qualitative analysis of small RNA-seq data in plants. Frontiers in Plant Science, 2014, 5, 708.	1.7	20
251	22 Computational methods for the analysis of mitochondrial genome rearrangements. , 2014, , 515-530.		4
252	24 Intron positions and near intron pairs. , 2014, , 539-548.		0

#	Article	IF	Citations
253	25 Molecular morphology: Higher order characters derivable from sequence information. , 2014, , 549-562.		5
254	Atypical RNAs in the coelacanth transcriptome. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 342-351.	0.6	43
255	<tt>snoStrip</tt>: a snoRNA annotation pipeline. Bioinformatics, 2014, 30, 115-116.	1.8	23
256	Comparative genomics reveals insights into avian genome evolution and adaptation. Science, 2014, 346, 1311-1320.	6.0	895
257	Basin Hopping Graph: a computational framework to characterize RNA folding landscapes. Bioinformatics, 2014, 30, 2009-2017.	1.8	39
258	Graph-distance distribution of the Boltzmann ensemble of RNA secondary structures. Algorithms for Molecular Biology, 2014, 9, 19.	0.3	0
259	The CHR site: definition and genome-wide identification of a cell cycle transcriptional element. Nucleic Acids Research, 2014, 42, 10331-10350.	6.5	82
260	17 Deuterostome phylogeny â€" a molecular perspective. , 2014, , 413-424.		0
261	Cell cycle, oncogenic and tumor suppressor pathways regulate numerous long and macro non-protein-coding RNAs. Genome Biology, 2014, 15, R48.	13.9	37
262	A first Glimpse at the genome of the Baikalian amphipod <i>Eulimnogammarus verrucosus</i>. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2014, 322, 177-189.	0.6	27
263	Unique square property, equitable partitions, and product-like graphs. Discrete Mathematics, 2014, 320, 92-103.	0.4	2
264	Challenges in RNA virus bioinformatics. Bioinformatics, 2014, 30, 1793-1799.	1.8	47
265	Biological evidence for the world's smallest tRNAs. Biochimie, 2014, 100, 151-158.	1.3	57
266	The genome of the recently domesticated crop plant sugar beet (Beta vulgaris). Nature, 2014, 505, 546-549.	13.7	569
267	Matching of Soulmates: Coevolution of snoRNAs and Their Targets. Molecular Biology and Evolution, 2014, 31, 455-467.	3.5	51
268	The Coilin Interactome Identifies Hundreds of Small Noncoding RNAs that Traffic through Cajal Bodies. Molecular Cell, 2014, 56, 389-399.	4.5	88
269	Structured RNAs and synteny regions in the pig genome. BMC Genomics, 2014, 15, 459.	1.2	20
270	A multi-split mapping algorithm for circular RNA, splicing, trans-splicing and fusion detection. Genome Biology, 2014, 15, R34.	13.9	242

#	Article	IF	Citations
271	Lacking alignments? The next-generation sequencing mapper segemehl revisited. Bioinformatics, 2014, 30, 1837-1843.	1.8	105
272	TSSAR: TSS annotation regime for dRNA-seq data. BMC Bioinformatics, 2014, 15, 89.	1.2	73
273	Simulation of gene family histories. BMC Bioinformatics, 2014, 15, .	1.2	2
274	GC skew and mitochondrial origins of replication. Mitochondrion, 2014, 17, 56-66.	1.6	35
275	A priori assessment of data quality in molecular phylogenetics. Algorithms for Molecular Biology, 2014, 9, .	0.3	23
276	Draft Genome Sequence of FT9, a Novel Bacillus cereus Strain Isolated from a Brazilian Thermal Spring. Genome Announcements, 2014, 2, .	0.8	1
277	Generic strategies for chemical space exploration. International Journal of Computational Biology and Drug Design, 2014, 7, 225.	0.3	26
278	Class-Specific Prediction of ncRNAs. Methods in Molecular Biology, 2014, 1097, 199-213.	0.4	12
279	Computational Prediction of MicroRNA Genes. Methods in Molecular Biology, 2014, 1097, 437-456.	0.4	15
280	50 Shades of Rule Composition. Lecture Notes in Computer Science, 2014, , 117-135.	1.0	9
281	Dynamic Programming for Set Data Types. Lecture Notes in Computer Science, 2014, , 57-64.	1.0	4
282	Rugged and Elementary Landscapes. Natural Computing Series, 2014, , 41-61.	2.2	5
283	Geometry and Coarse-Grained Representations of Landscapes. Emergence, Complexity and Computation, 2014, , 153-176.	0.2	10
284	Convex cycle bases. Ars Mathematica Contemporanea, 2014, 7, 123-140.	0.3	6
285	A Common Framework for Linear and Cyclic Multiple Sequence Alignment Problems. Lecture Notes in Computer Science, 2014, , 135-147.	1.0	1
286	Genome-Wide Identification of Non-coding RNAs in Komagatella pastoris str. GS115. Lecture Notes in Computer Science, 2014, , 115-122.	1.0	0
287	SOUND SYMBOLISM AND THE ORIGINS OF LANGUAGE. , 2014, , .		1
288	LocARNAscan: Incorporating thermodynamic stability in sequence and structure-based RNA homology search. Algorithms for Molecular Biology, 2013, 8, 14.	0.3	14

#	Article	IF	Citations
289	Chromatin computation: Epigenetic inheritance as a pattern reconstruction problem. Journal of Theoretical Biology, 2013, 336, 61-74.	0.8	11
290	The correlation of genome size and DNA methylation rate in metazoans. Theory in Biosciences, 2013, 132, 47-60.	0.6	43
291	Orthology relations, symbolic ultrametrics, and cographs. Journal of Mathematical Biology, 2013, 66, 399-420.	0.8	62
292	Mitogenomics and metazoan evolution. Molecular Phylogenetics and Evolution, 2013, 69, 311-312.	1.2	7
293	Identification of purple sea urchin telomerase RNA using a next-generation sequencing based approach. Rna, 2013, 19, 852-860.	1.6	12
294	On the Complexity of Reconstructing Chemical Reaction Networks. Mathematics in Computer Science, 2013, 7, 275-292.	0.2	2
295	Inferring chemical reaction patterns using rule composition in graph grammars. Journal of Systems Chemistry, 2013, 4, .	1.7	28
296	ncRNA-Agents: A Multiagent System for Non-coding RNA Annotation. Lecture Notes in Computer Science, 2013, , 136-147.	1.0	0
297	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
298	Dicer€Processed Small RNAs: Rules and Exceptions. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2013, 320, 35-46.	0.6	56
299	Computational biology of RNA interactions. Wiley Interdisciplinary Reviews RNA, 2013, 4, 107-120.	3.2	24
300	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2013, 23, 1388.	1.8	1
301	Genetic aspects of mitochondrial genome evolution. Molecular Phylogenetics and Evolution, 2013, 69, 328-338.	1.2	206
302	Bioinformatics methods for the comparative analysis of metazoan mitochondrial genome sequences. Molecular Phylogenetics and Evolution, 2013, 69, 320-327.	1.2	31
303	The African coelacanth genome provides insights into tetrapod evolution. Nature, 2013, 496, 311-316.	13.7	612
304	Mapping the RNA-Seq trash bin. RNA Biology, 2013, 10, 1204-1210.	1.5	13
305	A comprehensive analysis of bilaterian mitochondrial genomes and phylogeny. Molecular Phylogenetics and Evolution, 2013, 69, 352-364.	1.2	183
306	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

#	Article	IF	Citations
307	MITOS: Improved de novo metazoan mitochondrial genome annotation. Molecular Phylogenetics and Evolution, 2013, 69, 313-319.	1.2	3,919
308	The duck genome and transcriptome provide insight into an avian influenza virus reservoir species. Nature Genetics, 2013, 45, 776-783.	9.4	327
309	Near intron pairs and the metazoan tree. Molecular Phylogenetics and Evolution, 2013, 66, 811-823.	1.2	11
310	Navigating the Chemical Space of HCN Polymerization and Hydrolysis: Guiding Graph Grammars by Mass Spectrometry Data. Entropy, 2013, 15, 4066-4083.	1.1	38
311	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
312	Widespread purifying selection on RNA structure in mammals. Nucleic Acids Research, 2013, 41, 8220-8236.	6.5	144
313	The common ancestral core of vertebrate and fungal telomerase RNAs. Nucleic Acids Research, 2013, 41, 450-462.	6.5	70
314	Translation in Mammalian Mitochondria: Order and Disorder Linked to tRNAs and Aminoacyl-tRNA Synthetases. , 2013, , 55-83.		2
315	De novo design of a synthetic riboswitch that regulates transcription termination. Nucleic Acids Research, 2013, 41, 2541-2551.	6.5	163
316	<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
317	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	1.2	27
318	The RNAsnp web server: predicting SNP effects on local RNA secondary structure. Nucleic Acids Research, 2013, 41, W475-W479.	6.5	117
319	The Trouble with Long-Range Base Pairs in RNA Folding. Lecture Notes in Computer Science, 2013, , 1-11.	1.0	7
320	Atom Mapping with Constraint Programming. Lecture Notes in Computer Science, 2013, , 805-822.	1.0	2
321	Distribution of Graph-Distances in Boltzmann Ensembles of RNA Secondary Structures. Lecture Notes in Computer Science, 2013, , 112-125.	1.0	1
322	Relations between graphs. Ars Mathematica Contemporanea, 2013, 6, 323-350.	0.3	0
323	How to Multiply Dynamic Programming Algorithms. Lecture Notes in Computer Science, 2013, , 82-93.	1.0	4
324	In-Depth miRNA Profiling Of Germinal Center Derived B-Cell Lymphomas By Next Generation Sequencing: A Report From The German Icgc-Mmml-Seq Project. Blood, 2013, 122, 2500-2500.	0.6	4

#	Article	IF	Citations
325	Genome-wide transcriptome analysis of the plant pathogen Xanthomonas identifies sRNAs with putative virulence functions. Nucleic Acids Research, 2012, 40, 2020-2031.	6.5	93
326	deepBlockAlign: a tool for aligning RNA-seq profiles of read block patterns. Bioinformatics, 2012, 28, 17-24.	1.8	19
327	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
328	A Visual Cross-Database Comparison of Metabolic Networks. Lecture Notes in Computer Science, 2012, , 678-687.	1.0	0
329	LocARNA-P: Accurate boundary prediction and improved detection of structural RNAs. Rna, 2012, 18, 900-914.	1.6	326
330	Armless mitochondrial tRNAs in Enoplea (Nematoda). RNA Biology, 2012, 9, 1161-1166.	1.5	53
331	Evolution of the let-7 microRNA Family. RNA Biology, 2012, 9, 231-241.	1.5	115
332	RNA folding with soft constraints: reconciliation of probing data and thermodynamic secondary structure prediction. Nucleic Acids Research, 2012, 40, 4261-4272.	6.5	106
333	Addendum: topology and prediction of RNA pseudoknots. Bioinformatics, 2012, 28, 300-300.	1.8	3
334	Chromatin measurements reveal contributions of synthesis and decay to steady‑state mRNA levels. Molecular Systems Biology, 2012, 8, 593.	3.2	48
335	Maximizing output and recognizing autocatalysis in chemical reaction networks is NP-complete. Journal of Systems Chemistry, 2012, 3, .	1.7	39
336	Analyses of pig genomes provide insight into porcine demography and evolution. Nature, 2012, 491, 393-398.	13.7	1,190
337	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2012, 22, 1309-1313.	1.8	140
338	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
339	From event-labeled gene trees to species trees. BMC Bioinformatics, 2012, 13, .	1.2	29
340	Landscape Encodings Enhance Optimization. PLoS ONE, 2012, 7, e34780.	1.1	8
341	Clustering Rfam 10.1: Clans, Families, and Classes. Genes, 2012, 3, 378-390.	1.0	3
342	Structure of transfer RNAs: similarity and variability. Wiley Interdisciplinary Reviews RNA, 2012, 3, 37-61.	3.2	139

#	Article	IF	Citations
343	Fast and sensitive mapping of bisulfite-treated sequencing data. Bioinformatics, 2012, 28, 1698-1704.	1.8	51
344	A Survey on Hypergraph Products. Mathematics in Computer Science, 2012, 6, 1-32.	0.2	16
345	Hidden treasures in unspliced EST data. Theory in Biosciences, 2012, 131, 49-57.	0.6	6
346	Diagonalized Cartesian products of <mml:math altimg="si42.gif" display="inline" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="htt. Discrete Mathematics,	0.4	4
347	Symmetric circular matchings and RNA folding. Discrete Mathematics, 2012, 312, 100-112.	0.4	8
348	The Cartesian product of hypergraphs. Journal of Graph Theory, 2012, 70, 180-196.	0.5	10
349	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.0	7
350	Minimum cycle bases of lexicographic products. Ars Mathematica Contemporanea, 2012, 5, 223-234.	0.3	0
351	DARIO: a ncRNA detection and analysis tool for next-generation sequencing experiments. Nucleic Acids Research, 2011, 39, W112-W117.	6.5	82
352	MicroRNA or Not MicroRNA?. Lecture Notes in Computer Science, 2011, , 1-9.	1.0	14
353	Traces of post-transcriptional RNA modifications in deep sequencing data. Biological Chemistry, 2011, 392, 305-13.	1.2	54
354	The Use and Abuse of -Omes. Methods in Molecular Biology, 2011, 719, 173-196.	0.4	8
355	Protein-coding structured RNAs: A computational survey of conserved RNA secondary structures overlapping coding regions in drosophilids. Biochimie, 2011, 93, 2019-2023.	1.3	9
356	RNA Interactions. Advances in Experimental Medicine and Biology, 2011, 722, 20-38.	0.8	6
357	Molecular Evolution of the Non-Coding Eosinophil Granule Ontogeny Transcript. Frontiers in Genetics, 2011, 2, 69.	1.1	12
358	Evolution and Quantitative Comparison of Genome-Wide Protein Domain Distributions. Genes, 2011, 2, 912-924.	1.0	9
359	A Pipeline for Computational Historical Linguistics. Language Dynamics and Change, 2011, 1, 89-127.	0.4	35
360	Deletion analysis of the 3â€² long terminal repeat sequence of plant retrotransposon Tto1 identifies 125 base pairs redundancy as sufficient for first strand transfer. Virology, 2011, 412, 75-82.	1.1	1

#	Article	IF	Citations
361	Proteinortho: Detection of (Co-)orthologs in large-scale analysis. BMC Bioinformatics, 2011, 12, 124.	1.2	1,091
362	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
363	"Hypothesis for the Modern RNA World" A pervasive Non-coding RNA-Based Genetic Regulation is a Prerequisite for the Emergence of Multicellular Complexity. Origins of Life and Evolution of Biospheres, 2011, 41, 587-607.	0.8	22
364	The challenges and scope of theoretical biology. Journal of Theoretical Biology, 2011, 276, 269-276.	0.8	56
365	Fast local fragment chaining using sum-of-pair gap costs. Algorithms for Molecular Biology, 2011, 6, 4.	0.3	15
366	The enigmatic mitochondrial genome of Rhabdopleura compacta(Pterobranchia) reveals insights into selection of an efficient tRNA system and supports monophyly of Ambulacraria. BMC Evolutionary Biology, 2011, 11, 134.	3.2	19
367	Genome size evolution at the speciation level: The cryptic species complex Brachionus plicatilis(Rotifera). BMC Evolutionary Biology, 2011, 11, 90.	3.2	42
368	<i>Hox</i> clusters of the bichir (Actinopterygii, <i>Polypterus senegalus</i>) highlight unique patterns of sequence evolution in gnathostome phylogeny. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2011, 316B, 451-464.	0.6	13
369	In Silico Evolution of Early Metabolism. Artificial Life, 2011, 17, 87-108.	1.0	10
370	<tt>PLEXY</tt>: efficient target prediction for box C/D snoRNAs. Bioinformatics, 2011, 27, 279-280.	1.8	53
371	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	1.5	30
372	RNAcode: Robust discrimination of coding and noncoding regions in comparative sequence data. Rna, 2011, 17, 578-594.	1.6	188
373	Topology and prediction of RNA pseudoknots. Bioinformatics, 2011, 27, 1076-1085.	1.8	137
374	RNAcentral: A vision for an international database of RNA sequences. Rna, 2011, 17, 1941-1946.	1.6	67
375	The Reality of Pervasive Transcription. PLoS Biology, 2011, 9, e1000625.	2.6	380
376	Fast accessibility-based prediction of RNA–RNA interactions. Bioinformatics, 2011, 27, 1934-1940.	1.8	48
377	A folding algorithm for extended RNA secondary structures. Bioinformatics, 2011, 27, i129-i136.	1.8	59
378	maxAlike: maximum likelihood-based sequence reconstruction with application to improved primer design for unknown sequences. Bioinformatics, 2011, 27, 317-325.	1.8	25

#	Article	IF	Citations
379	Computational discovery of human coding and non-coding transcripts with conserved splice sites. Bioinformatics, 2011, 27, 1894-1900.	1.8	24
380	RNApredator: fast accessibility-based prediction of sRNA targets. Nucleic Acids Research, 2011, 39, W149-W154.	6.5	117
381	Combinatorial vector fields and the valley structure of fitness landscapes. Journal of Mathematical Biology, 2010, 61, 877-898.	0.8	7
382	Optimization of parameters for coverage of low molecular weight proteins. Analytical and Bioanalytical Chemistry, 2010, 398, 2867-2881.	1.9	43
383	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	0.8	32
384	Innovation in gene regulation: The case of chromatin computation. Journal of Theoretical Biology, 2010, 265, 27-44.	0.8	45
385	Reconstruction of pedigrees in clonal plant populations. Theoretical Population Biology, 2010, 78, 109-117.	0.5	9
386	G-stack modulated probe intensities on expression arrays - sequence corrections and signal calibration. BMC Bioinformatics, 2010, 11, 207.	1.2	20
387	Some novel intron positions in conserved Drosophila genes are caused by intron sliding or tandem duplication. BMC Evolutionary Biology, 2010, 10, 156.	3.2	17
388	Genomic organization of eukaryotic tRNAs. BMC Genomics, 2010, 11, 270.	1.2	91
389	Bcheck: a wrapper tool for detecting RNase P RNA genes. BMC Genomics, 2010, 11, 432.	1.2	23
390	Mitochondrial genome evolution in Ophiuroidea, Echinoidea, and Holothuroidea: Insights in phylogenetic relationships of Echinodermata. Molecular Phylogenetics and Evolution, 2010, 56, 201-211.	1.2	66
391	Polynomial algorithms for the Maximal Pairing Problem: efficient phylogenetic targeting on arbitrary trees. Algorithms for Molecular Biology, 2010, 5, 25.	0.3	5
392	Evolution of metabolic networks: a computational frame-work. Journal of Systems Chemistry, 2010, 1, 4.	1.7	15
393	The primary transcriptome of the major human pathogen Helicobacter pylori. Nature, 2010, 464, 250-255.	13.7	1,115
394	BarMap: RNA folding on dynamic energy landscapes. Rna, 2010, 16, 1308-1316.	1.6	53
395	Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 3622-3627.	3.3	65
396	<tt>RNAsnoop</tt>: efficient target prediction for H/ACA snoRNAs. Bioinformatics, 2010, 26, 610-616.	1.8	49

#	Article	IF	Citations
397	TEMPERATURE-DEPENDENT STRUCTURAL VARIABILITY OF RNAs: SPLICED LEADER RNAs AND THEIR EVOLUTIONARY HISTORY. Journal of Bioinformatics and Computational Biology, 2010, 08, 1-17.	0.3	8
398	Multi-Platform Next-Generation Sequencing of the Domestic Turkey (Meleagris gallopavo): Genome Assembly and Analysis. PLoS Biology, 2010, 8, e1000475.	2.6	348
399	A novel family of plasmid-transferred anti-sense ncRNAs. RNA Biology, 2010, 7, 120-124.	1.5	21
400	Target prediction and a statistical sampling algorithm for RNAâ€"RNA interaction. Bioinformatics, 2010, 26, 175-181.	1.8	57
401	Visualization of Graph Products. IEEE Transactions on Visualization and Computer Graphics, 2010, 16, 1082-1089.	2.9	11
402	Advances in Bioinformatics and Computational Biology. Lecture Notes in Computer Science, 2010, , .	1.0	2
403	Evolution of the Long Non-coding RNAs MALAT1 and MENÎ²Îµ. Lecture Notes in Computer Science, 2010, , 1-12.	1.0	18
404	Visual Network Analysis of Dynamic Metabolic Pathways. Lecture Notes in Computer Science, 2010, , 316-327.	1.0	9
405	Detection of Protein Domains in Eukaryotic Genome Sequences. Lecture Notes in Computer Science, 2010, , 71-74.	1.0	0
406	RNAz 2.0: improved noncoding RNA detection. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2010, , 69-79.	0.7	135
407	The tedious task of finding homologous noncoding RNA genes. Rna, 2009, 15, 2075-2082.	1.6	55
408	Customized strategies for discovering distant ncRNA homologs. Briefings in Functional Genomics & Proteomics, 2009, 8, 451-460.	3.8	17
409	Structural profiles of human miRNA families from pairwise clustering. Bioinformatics, 2009, 25, 291-294.	1.8	62
410	RNAZ 2.0:. , 2009, , 69-79.		68
411	A survey of nematode SmY RNAs. RNA Biology, 2009, 6, 5-8.	1.5	21
412	Comparative analysis of eukaryotic U3 snoRNA. RNA Biology, 2009, 6, 503-507.	1.5	24
413	Fast Mapping of Short Sequences with Mismatches, Insertions and Deletions Using Index Structures. PLoS Computational Biology, 2009, 5, e1000502.	1.5	487
414	Evolution of 7SK RNA and Its Protein Partners in Metazoa. Molecular Biology and Evolution, 2009, 26, 2821-2830.	3.5	76

#	ARTICLE	IF	CITATIONS
415	FRANz: reconstruction of wild multi-generation pedigrees. Bioinformatics, 2009, 25, 2134-2139.	1.8	89
416	Measuring Transcription Factor–Binding Site Turnover: A Maximum Likelihood Approach Using Phylogenies. Genome Biology and Evolution, 2009, 1, 85-98.	1.1	17
417	Partition function and base pairing probabilities for RNA–RNA interaction prediction. Bioinformatics, 2009, 25, 2646-2654.	1.8	124
418	Solvent Exposure Imparts Similar Selective Pressures across a Range of Yeast Proteins. Molecular Biology and Evolution, 2009, 26, 1155-1161.	3.5	60
419	Conserved introns reveal novel transcripts in <i>Drosophila melanogaster</i>. Genome Research, 2009, 19, 1289-1300.	2.4	38
420	tRNAdb 2009: compilation of tRNA sequences and tRNA genes. Nucleic Acids Research, 2009, 37, D159-D162.	6.5	751
421	Evolution of Vault RNAs. Molecular Biology and Evolution, 2009, 26, 1975-1991.	3.5	130
422	Non-coding RNA annotation of the genome of Trichoplax adhaerens. Nucleic Acids Research, 2009, 37, 1602-1615.	6.5	56
423	Accurate and efficient reconstruction of deep phylogenies from structured RNAs. Nucleic Acids Research, 2009, 37, 6184-6193.	6.5	108
424	Evidence for human microRNA-offset RNAs in small RNA sequencing data. Bioinformatics, 2009, 25, 2298-2301.	1.8	120
425	Homology-based annotation of non-coding RNAs in the genomes of Schistosoma mansoni and Schistosoma japonicum. BMC Genomics, 2009, 10, 464.	1.2	51
426	Mutate now, die later. Evolutionary dynamics with delayed selection. Journal of Theoretical Biology, 2009, 260, 412-421.	0.8	1
427	Hox cluster duplication in the basal teleost Hiodon alosoides (Osteoglossomorpha). Theory in Biosciences, 2009, 128, 109-120.	0.6	18
428	Defining genes: a computational framework. Theory in Biosciences, 2009, 128, 165-170.	0.6	22
429	Local Algorithms for the Prime Factorization of Strong Product Graphs. Mathematics in Computer Science, 2009, 2, 653-682.	0.2	10
430	Sequence assembly. Computational Biology and Chemistry, 2009, 33, 121-136.	1.1	39
431	Discovering cis-regulatory modules by optimizing barbecues. Discrete Applied Mathematics, 2009, 157, 2458-2468.	0.5	0
432	A note on fundamental, non-fundamental, and robust cycle bases. Discrete Applied Mathematics, 2009, 157, 2432-2438.	0.5	8

#	Article	IF	Citations
433	Approximate graph products. European Journal of Combinatorics, 2009, 30, 1119-1133.	0.5	15
434	A Topological Approach to Chemical Organizations. Artificial Life, 2009, 15, 71-88.	1.0	15
435	A note on quasi-robust cycle bases. Ars Mathematica Contemporanea, 2009, 2, 231-240.	0.3	6
436	Automatic Classification of Embryonic Fruit Fly Gene Expression Patterns. Informatik Aktuell, 2009, , 415-419.	0.4	1
437	COMPUTATIONAL STUDIES OF NON-CODING RNAS â€" Session Introduction. , 2009, , 54-56.		0
438	Invertebrate 7SK snRNAs. Journal of Molecular Evolution, 2008, 66, 107-115.	0.8	37
439	Evolution of Spliceosomal snRNA Genes in Metazoan Animals. Journal of Molecular Evolution, 2008, 67, 594-607.	0.8	79
440	â€œGenesâ€. Theory in Biosciences, 2008, 127, 215-221.	0.6	12
441	PCR survey of <i>Xenoturbella bocki</i> Hox genes. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2008, 310B, 278-284.	0.6	26
442	The amphioxus <i>Hox</i> cluster: characterization, comparative genomics, and evolution. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2008, 310B, 465-477.	0.6	50
443	Evolution of mitochondrial gene orders in echinoderms. Molecular Phylogenetics and Evolution, 2008, 47, 855-864.	1.2	73
444	Funnels in energy landscapes. European Physical Journal B, 2008, 63, 387-391.	0.6	14
445	HLA-DRB1â—0401 and HLA-DRB1â—0408 Are Strongly Associated with the Development of Antibodies against Interferon-Î² Therapy in Multiple Sclerosis. American Journal of Human Genetics, 2008, 83, 219-227.	2.6	114
446	HLA-DRB10401 and HLA-DRB10408 Are Strongly Associated with the Development of Antibodies against Interferon-Î² Therapy in Multiple Sclerosis. American Journal of Human Genetics, 2008, 83, 541.	2.6	0
447	SynBlast: Assisting the analysis of conserved synteny information. BMC Bioinformatics, 2008, 9, 351.	1.2	12
448	RNAalifold: improved consensus structure prediction for RNA alignments. BMC Bioinformatics, 2008, 9, 474.	1.2	505
449	Noisy: Identification of problematic columns in multiple sequence alignments. Algorithms for Molecular Biology, 2008, 3, 7.	0.3	154
450	DUPLICATED RNA GENES IN TELEOST FISH GENOMES. Journal of Bioinformatics and Computational Biology, 2008, 06, 1157-1175.	0.3	10

#	Article	IF	Citations
451	Early Replicons: Origin and Evolution**Dedicated to Manfred Eigen, the pioneer of molecular evolution and intellectual father of quasispecies theory, on the occasion of his 80th birthday.. , 2008, , 1-41.		7
452	Folding Kinetics of Large RNAs. Journal of Molecular Biology, 2008, 379, 160-173.	2.0	77
453	NcDNAlign: Plausible multiple alignments of non-protein-coding genomic sequences. Genomics, 2008, 92, 65-74.	1.3	18
454	<tt>SnoReport</tt>: computational identification of snoRNAs with unknown targets. Bioinformatics, 2008, 24, 158-164.	1.8	116
455	Arthropod 7SK RNA. Molecular Biology and Evolution, 2008, 25, 1923-1930.	3.5	45
456	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
457	Structure and Function of the Smallest Vertebrate Telomerase RNA from Teleost Fish. Journal of Biological Chemistry, 2008, 283, 2049-2059.	1.6	78
458	Detection of small RNAs in Pseudomonas aeruginosa by RNomics and structure-based bioinformatic tools. Microbiology (United Kingdom), 2008, 154, 3175-3187.	0.7	99
459	Near Intron Positions Are Reliable Phylogenetic Markers: An Application to Holometabolous Insects. Molecular Biology and Evolution, 2008, 25, 821-830.	3.5	39
460	A STORY OF GROWING CONFUSION: GENES AND THEIR REGULATION. Biophysical Reviews and Letters, 2008, 03, 285-302.	0.9	2
461	Process flow for classification and clustering of fruit fly gene expression patterns. , 2008, 1, 721-724.		5
462	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
463	A STORY OF GROWING CONFUSION: GENES AND THEIR REGULATION. , 2008, , .		1
464	Visualization of Barrier Tree Sequences Revisited. Mathematics and Visualization, 2008, , 275-290.	0.4	1
465	Replicator Dynamics in Protocells. , 2008, , 317-336.		0
466	CREx: inferring genomic rearrangements based on common intervals. Bioinformatics, 2007, 23, 2957-2958.	1.8	276
467	Regulatory Signals in Genomic Sequences. , 2007, , 189-216.		1
468	Inferring Noncoding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. PLoS Computational Biology, 2007, 3, e65.	1.5	424

#	Article	IF	Citations
469	Interleukin-6–dependent survival of multiple myeloma cells involves the Stat3-mediated induction of microRNA-21 through a highly conserved enhancer. Blood, 2007, 110, 1330-1333.	0.6	597
470	Structured RNAs in the ENCODE selected regions of the human genome. Genome Research, 2007, 17, 852-864.	2.4	150
471	RNA Maps Reveal New RNA Classes and a Possible Function for Pervasive Transcription. Science, 2007, 316, 1484-1488.	6.0	2,250
472	U7 snRNAs: A Computational Survey. Genomics, Proteomics and Bioinformatics, 2007, 5, 187-195.	3.0	17
473	RNAstrand: reading direction of structured RNAs in multiple sequence alignments. Algorithms for Molecular Biology, 2007, 2, 6.	0.3	26
474	Modeling Conformational Flexibility and Evolution of Structure: RNA as an Example. Biological and Medical Physics Series, 2007, , 3-36.	0.3	1
475	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
476	PCR survey of hox genes in the goldfishCarassius auratus auratus. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 250-258.	0.6	24
477	Modeling amino acid substitution patterns in orthologous and paralogous genes. Molecular Phylogenetics and Evolution, 2007, 42, 298-307.	1.2	36
478	Comparative analysis of structured RNAs in S. cerevisiae indicates a multitude of different functions. BMC Biology, 2007, 5, 25.	1.7	32
479	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
480	Progressive multiple sequence alignments from triplets. BMC Bioinformatics, 2007, 8, 254.	1.2	19
481	RNase MRP and the RNA processing cascade in the eukaryotic ancestor. BMC Evolutionary Biology, 2007, 7, S13.	3.2	37
482	Detection of RNA structures in porcine EST data and related mammals. BMC Genomics, 2007, 8, 316.	1.2	11
483	Computational RNomics of Drosophilids. BMC Genomics, 2007, 8, 406.	1.2	38
484	Variations on RNA folding and alignment: lessons from Benasque. Journal of Mathematical Biology, 2007, 56, 129-144.	0.8	65
485	Towards theoretical formalisms. Theory in Biosciences, 2007, 126, 1-2.	0.6	0
486	Evolution of the vertebrate Y RNA cluster. Theory in Biosciences, 2007, 126, 9-14.	0.6	54

#	Article	IF	Citations
487	The mitochondrial DNA of Xenoturbella bocki: genomic architecture and phylogenetic analysis. Theory in Biosciences, 2007, 126, 35-42.	0.6	47
488	A stochastic model for the evolution of transcription factor binding site abundance. Journal of Theoretical Biology, 2007, 247, 544-553.	0.8	8
489	Evolutionary Genomics of Hox Gene Clusters. , 2007, , 68-90.		1
490	Saddles and Barrier in Landscapes of Generalized Search Operators. Lecture Notes in Computer Science, 2007, , 194-212.	1.0	10
491	Laplacian Eigenvectors of Graphs. Lecture Notes in Mathematics, 2007, , .	0.1	112
492	Homology Search with Fragmented Nucleic Acid Sequence Patterns. Lecture Notes in Computer Science, 2007, , 335-345.	1.0	13
493	Multiple sequence alignment with user-defined anchor points. Algorithms for Molecular Biology, 2006, 1, 6.	0.3	52
494	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
495	New journal: Algorithms for Molecular Biology. Algorithms for Molecular Biology, 2006, 1, 1.	0.3	44
496	Statistics of cycles in large networks. Physical Review E, 2006, 73, 025101.	0.8	18
497	Visualization of Barrier Tree Sequences. IEEE Transactions on Visualization and Computer Graphics, 2006, 12, 781-788.	2.9	13
498	Fragrep: An Efficient Search Tool for Fragmented Patterns in Genomic Sequences. Genomics, Proteomics and Bioinformatics, 2006, 4, 56-60.	3.0	21
499	Evolution of MicroRNAs. , 2006, 342, 335-350.		32
500	Thermodynamics of RNA-RNA binding. Bioinformatics, 2006, 22, 1177-1182.	1.8	338
501	Genotype-Phenotype Maps. Biological Theory, 2006, 1, 268-279.	0.8	31
502	Evolving towards the hypercycle: A spatial model of molecular evolution. Physica D: Nonlinear Phenomena, 2006, 217, 134-141.	1.3	16
503	Alignments of mitochondrial genome arrangements: Applications to metazoan phylogeny. Journal of Theoretical Biology, 2006, 240, 511-520.	0.8	49
504	Algebraic comparison of metabolic networks, phylogenetic inference, and metabolic innovation. BMC Bioinformatics, 2006, 7, 67.	1.2	33

#	Article	IF	Citations
505	The expansion of the metazoan microRNA repertoire. BMC Genomics, 2006, 7, 25.	1.2	304
506	Prediction of structured non-coding RNAs in the genomes of the nematodesCaenorhabditis elegans andCaenorhabditis briggsae. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2006, 306B, 379-392.	0.6	39
507	Evolution of the vertebrate parahox clusters. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2006, 306B, 481-487.	0.6	12
508	Effect of pH on growth, cell volume, and production of freshwater ciliates, and implications for their distribution. Limnology and Oceanography, 2006, 51, 1708-1715.	1.6	67
509	Exploring the lower part of discrete polymer model energy landscapes. Europhysics Letters, 2006, 74, 726-732.	0.7	19
510	Memory efficient folding algorithms for circular RNA secondary structures. Bioinformatics, 2006, 22, 1172-1176.	1.8	183
511	The â€œFish-Specificâ€•Hox Cluster Duplication Is Coincident with the Origin of Teleosts. Molecular Biology and Evolution, 2006, 23, 121-136.	3.5	170
512	Hairpins in a Haystack: recognizing microRNA precursors in comparative genomics data. Bioinformatics, 2006, 22, e197-e202.	1.8	180
513	miRNAMap: genomic maps of microRNA genes and their target genes in mammalian genomes. Nucleic Acids Research, 2006, 34, D135-D139.	6.5	199
514	Local RNA base pairing probabilities in large sequences. Bioinformatics, 2006, 22, 614-615.	1.8	217
515	A prime factor theorem for a generalized direct product. Discussiones Mathematicae - Graph Theory, 2006, 26, 135.	0.2	6
516	Modeling RNA Folding. , 2006, , 227-245.		0
517	RNA Folding in silico. , 2005, , 177-190.		1
518	Evolutionary patterns of non-coding RNAs. Theory in Biosciences, 2005, 123, 301-369.	0.6	64
519	MATH/CHEM/COMP 2004 Contributions. Theory in Biosciences, 2005, 123, 263-264.	0.6	0
520	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
521	Multiple sequence alignments of partially coding nucleic acid sequences. BMC Bioinformatics, 2005, 6, 160.	1.2	25
522	Comparative promoter region analysis powered by CORG. BMC Genomics, 2005, 6, 24.	1.2	28

#	Article	IF	Citations
523	Minimum path bases and relevant paths. Networks, 2005, 46, 119-123.	1.6	0
524	Evolution of microRNAs located withinHox gene clusters. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2005, 304B, 75-85.	0.6	139
525	Molecular Evolution of Duplicated Ray Finned Fish HoxA Clusters: Increased Synonymous Substitution Rate and Asymmetrical Co-divergence of Coding and Non-coding Sequences. Journal of Molecular Evolution, 2005, 60, 665-676.	0.8	36
526	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
527	Non-coding RNAs in Ciona intestinalis. Bioinformatics, 2005, 21, ii77-ii78.	1.8	39
528	Multiple sequence alignment with user-defined constraints at GOBICS. Bioinformatics, 2005, 21, 1271-1273.	1.8	34
529	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
530	NEUTRAL NETWORKS OF INTERACTING RNA SECONDARY STRUCTURES. International Journal of Modeling, Simulation, and Scientific Computing, 2005, 08, 275-283.	0.9	4
531	The effect of RNA secondary structures on RNA-ligand binding and the modifier RNA mechanism: a quantitative model. Gene, 2005, 345, 3-12.	1.0	49
532	Inferring Non-Coding RNA Families and Classes by Means of Genome-Scale Structure-Based Clustering. PLoS Computational Biology, 2005, preprint, e65.	1.5	26
533	CelloS: A Multi-level Approach to Evolutionary Dynamics. Lecture Notes in Computer Science, 2005, , 500-509.	1.0	1
534	Efficient computation of RNA folding dynamics. Journal of Physics A, 2004, 37, 4731-4741.	1.6	99
535	Divergence of Conserved Non-Coding Sequences: Rate Estimates and Relative Rate Tests. Molecular Biology and Evolution, 2004, 21, 2116-2121.	3.5	24
536	Potential toxicity of chrysophytes affiliated with Poterioochromonas and related 'Spumella-like' flagellates. Journal of Plankton Research, 2004, 26, 1507-1514.	0.8	44
537	Conserved RNA secondary structures in Flaviviridae genomes. Journal of General Virology, 2004, 85, 1113-1124.	1.3	165
538	Living and Nonliving Matter. Science, 2004, 305, 41-44.	6.0	3
539	Alignment of RNA base pairing probability matrices. Bioinformatics, 2004, 20, 2222-2227.	1.8	205
540	The Topology of Evolutionary Biology. Natural Computing Series, 2004, , 267-286.	2.2	21

#	Article	IF	Citations
541	Prediction of locally stable RNA secondary structures for genome-wide surveys. Bioinformatics, 2004, 20, 186-190.	1.8	145
542	Proto-Organism Kinetics: Evolutionary Dynamics of Lipid Aggregates with Genes and Metabolism. Origins of Life and Evolution of Biospheres, 2004, 34, 171-180.	0.8	32
543	Graph Laplacians, nodal domains, and hyperplane arrangements. Linear Algebra and Its Applications, 2004, 390, 155-174.	0.4	22
544	The Shark HoxN Cluster Is Homologous to the Human HoxD Cluster. Journal of Molecular Evolution, 2004, 58, 212-217.	0.8	22
545	Exclusion of repetitive DNA elements from gnathostomeHox clusters. The Journal of Experimental Zoology, 2004, 302B, 165-173.	1.4	35
546	Surveying phylogenetic footprints in large gene clusters: applications to Hox cluster duplications. Molecular Phylogenetics and Evolution, 2004, 31, 581-604.	1.2	45
547	Evidence for independent Hox gene duplications in the hagfish lineage: a PCR-based gene inventory of Eptatretus stoutii. Molecular Phylogenetics and Evolution, 2004, 32, 686-694.	1.2	82
548	Aggregation of Variables and System Decomposition: Applications to Fitness Landscape Analysis. Theory in Biosciences, 2004, 123, 33-68.	0.6	16
549	Editorial. Theory in Biosciences, 2004, 123, 1-2.	0.6	1
550	The duplication of the Hox gene clusters in teleost fishes*1. Theory in Biosciences, 2004, 123, 89-110.	0.6	40
551	Simon?Ando decomposability and fitness landscapes. Theory in Biosciences, 2004, 123, 139-180.	0.6	11
552	Gene phylogenies and protein–protein interactions: possible artifacts resulting from shared protein interaction partners. Journal of Theoretical Biology, 2004, 231, 197-202.	0.8	9
553	Prediction of consensus RNA secondary structures including pseudoknots. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 66-77.	1.9	51
554	Interactions in Oligonucleotide Hybrid Duplexes on Microarrays. Journal of Physical Chemistry B, 2004, 108, 18015-18025.	1.2	25
555	Conserved RNA secondary structures in viral genomes: a survey. Bioinformatics, 2004, 20, 1495-1499.	1.8	43
556	Sensitivity of Microarray Oligonucleotide Probes:Â Variability and Effect of Base Composition. Journal of Physical Chemistry B, 2004, 108, 18003-18014.	1.2	46
557	The Footprint Sorting Problem€. Journal of Chemical Information and Computer Sciences, 2004, 44, 332-338.	2.8	10
558	Counterexamples in Chemical Ring Perception€. Journal of Chemical Information and Computer Sciences, 2004, 44, 323-331.	2.8	32

#	Article	IF	Citations
559	Structural and evolutionary analysis of the transcribed sequence of Boudicca, a Schistosoma mansoni retrotransposon. Gene, 2004, 329, 103-114.	1.0	6
560	Molecular Evolution of a MicroRNA Cluster. Journal of Molecular Biology, 2004, 339, 327-335.	2.0	554
561	EVOLUTION: Transitions from Nonliving to Living Matter. Science, 2004, 303, 963-965.	6.0	339
562	Comparative Genomics, cis-Regulatory Elements, and Gene Duplication. Methods in Cell Biology, 2004, 77, 545-561.	0.5	7
563	Discrete Models of Biopolymers. , 2004, , 187-221.		0
564	Computational Biology. , 2004, , 451-501.		0
565	On the evolution of primitive genetic codes. Origins of Life and Evolution of Biospheres, 2003, 33, 491-514.	0.8	20
566	Barrier Trees on Poset-Valued Landscapes. Genetic Programming and Evolvable Machines, 2003, 4, 7-20.	1.5	19
567	Independent Hox-cluster duplications in lampreys. The Journal of Experimental Zoology, 2003, 299B, 18-25.	1.4	102
568	Minimum cycle bases of Halin graphs. Journal of Graph Theory, 2003, 43, 150-155.	0.5	19
569	Quasi-Independence, Homology and the Unity of Type: A Topological Theory of Characters. Journal of Theoretical Biology, 2003, 220, 505-527.	0.8	66
570	Centers of complex networks. Journal of Theoretical Biology, 2003, 223, 45-53.	0.8	317
571	MOLECULAR REPLICATOR DYNAMICS. International Journal of Modeling, Simulation, and Scientific Computing, 2003, 06, 47-77.	0.9	37
572	A Graph-Based Toy Model of Chemistry. Journal of Chemical Information and Computer Sciences, 2003, 43, 1085-1093.	2.8	82
573	Bichir HoxA Cluster Sequence Reveals Surprising Trends in Ray-Finned Fish Genomic Evolution. Genome Research, 2003, 14, 11-17.	2.4	89
574	Phase transition and landscape statistics of the number partitioning problem. Physical Review E, 2003, 67, 056701.	0.8	17
575	Generic Properties of Chemical Networks: Artificial Chemistry Based on Graph Rewriting. Lecture Notes in Computer Science, 2003, , 10-19.	1.0	16
576	Shapes of tree representations of spin-glass landscapes. Journal of Physics A, 2003, 36, 3671-3681.	1.6	13

#	Article	IF	Citations
577	Landscapes and Effective Fitness. Comments on Theoretical Biology, 2003, 8, 389-431.	0.6	37
578	Circuit bases of strongly connected digraphs. Discussiones Mathematicae - Graph Theory, 2003, 23, 241.	0.2	19
579	Glassy States in a Shaken Sandbox. , 2003, , 141-151.		1
580	Combinatorial Landscapes. SIAM Review, 2002, 44, 3-54.	4.2	201
581	Recombination Spaces, Metrics, and Pretopologies. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	21
582	Barrier Trees of Degenerate Landscapes. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	130
583	Fractal geometry of spin-glass models. Journal of Physics A, 2002, 35, 1509-1516.	1.6	13
584	Evolution in Systems of Ligation-Based Replicators. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	1
585	Fitness landscapes. , 2002, , 183-204.		106
586	Generalized Topological Spaces in Evolutionary Theory and Combinatorial Chemistry. Journal of Chemical Information and Computer Sciences, 2002, 42, 577-585.	2.8	73
587	Secondary Structure Prediction for Aligned RNA Sequences. Journal of Molecular Biology, 2002, 319, 1059-1066.	2.0	545
588	Shaking a box of sand. Europhysics Letters, 2002, 57, 46-52.	0.7	21
589	Fast Fourier Transform for Fitness Landscapes. Applied and Computational Harmonic Analysis, 2002, 12, 57-76.	1.1	31
590	Networks in molecular evolution. Complexity, 2002, 8, 34-42.	0.9	17
591	Landscapes on spaces of trees. Applied Mathematics and Computation, 2002, 131, 439-459.	1.4	14
592	RELEVANT CYCLES IN CHEMICAL REACTION NETWORKS. International Journal of Modeling, Simulation, and Scientific Computing, 2001, 04, 207-226.	0.9	61
593	New Chronological Frame for the Young Neolithic Baden Culture in Central Europe (4th Millennium) Tj ETQq1 1 0.784314 rgBT /Overl	0.8	13
594	Design of multistable RNA molecules. Rna, 2001, 7, 254-265.	1.6	138

#	Article	IF	Citations
595	Discrete nodal domain theorems. Linear Algebra and Its Applications, 2001, 336, 51-60.	0.4	97
596	Neutrality in fitness landscapes. Applied Mathematics and Computation, 2001, 117, 321-350.	1.4	89
597	Exploring Protein Sequence Space Using Knowledge-based Potentials. Journal of Theoretical Biology, 2001, 212, 35-46.	0.8	49
598	The Topology of the Possible: Formal Spaces Underlying Patterns of Evolutionary Change. Journal of Theoretical Biology, 2001, 213, 241-274.	0.8	265
599	Conserved RNA secondary structures in Picornaviridae genomes. Nucleic Acids Research, 2001, 29, 5079-5089.	6.5	84
600	GLASSY STATES IN A SHAKEN SANDBOX. International Journal of Modeling, Simulation, and Scientific Computing, 2001, 04, 429-439.	0.9	7
601	Population Dependent Fourier Decomposition of Fitness Landscapes over Recombination Spaces: Evolvability of Complex Characters. Bulletin of Mathematical Biology, 2000, 62, 399-428.	0.9	34
602	Dynamics of Autocatalytic Replicator Networks Based on Higher-order Ligation Reactions. Bulletin of Mathematical Biology, 2000, 62, 1061-1086.	0.9	28
603	Three different premature stop codons lead to skipping of exon 7 in neurofibromatosis type I patients. Human Mutation, 2000, 16, 90-91.	1.1	17
604	RNA Shape Space Topology. Artificial Life, 2000, 6, 3-23.	1.0	19
605	Prediction of RNA Base Pairing Probabilities on Massively Parallel Computers. Journal of Computational Biology, 2000, 7, 171-182.	0.8	27
606	Landscape statistics of the low-autocorrelation binary string problem. Journal of Physics A, 2000, 33, 8635-8647.	1.6	23
607	Error propagation in the hypercycle. Physical Review E, 2000, 61, 2996-3002.	0.8	22
608	Interchangeability of Relevant Cycles in Graphs. Electronic Journal of Combinatorics, 2000, 7, .	0.2	8
609	Nature and evolution of early replicons. , 1999, , 1-24.		17
610	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
611	Metastable states in short-ranged p-spin glasses. Journal of Physics A, 1999, 32, 8793-8802.	1.6	13
612	Automatic detection of conserved base pairing patterns in RNA virus genomes. Computers & Chemistry, 1999, 23, 401-414.	1.2	53

#	Article	IF	Citations
613	Autocatalytic replication in a CSTR and constant organization. Journal of Mathematical Biology, 1999, 38, 422-434.	0.8	9
614	Random field models for fitness landscapes. Journal of Mathematical Biology, 1999, 38, 435-478.	0.8	60
615	Fitness landscapes arising from the sequence-structure maps of biopolymers. Computational and Theoretical Chemistry, 1999, 463, 7-19.	1.5	19
616	RNA Structures with Pseudo-knots: Graph-theoretical, Combinatorial, and Statistical Properties. Bulletin of Mathematical Biology, 1999, 61, 437-467.	0.9	81
617	Viral RNA and evolved mutational robustness. , 1999, 285, 119-127.		68
618	The Evolution of Diversity in Replicator Networks. Journal of Theoretical Biology, 1998, 195, 329-338.	0.8	27
619	The dynamics of locally adaptive parties under spatial voting. Journal of Economic Dynamics and Control, 1998, 23, 171-189.	0.9	8
620	Combinatorics of RNA secondary structures. Discrete Applied Mathematics, 1998, 88, 207-237.	0.5	120
621	Amplitude Spectra of Fitness Landscapes. International Journal of Modeling, Simulation, and Scientific Computing, 1998, 01, 39-66.	0.9	41
622	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. Nucleic Acids Research, 1998, 26, 3825-3836.	6.5	115
623	Spontaneous and Engineered Deletions in the 3â€² Noncoding Region of Tick-Borne Encephalitis Virus: Construction of Highly Attenuated Mutants of a Flavivirus. Journal of Virology, 1998, 72, 2132-2140.	1.5	187
624	Minimal Cycle Bases of Outerplanar Graphs. Electronic Journal of Combinatorics, 1998, 5, .	0.2	32
625	Generic Properties of the Sequence-Structure Relations of Biopolymers. , 1998, , 149-156.		0
626	Algebraic Theory of Recombination Spaces. Evolutionary Computation, 1997, 5, 241-275.	2.3	68
627	RNA structures and folding: from conventional to new issues in structure predictions. Current Opinion in Structural Biology, 1997, 7, 229-235.	2.6	58
628	Autocatalytic networks with intermediates I: Irreversible reactions. Mathematical Biosciences, 1997, 140, 33-74.	0.9	9
629	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
630	Generic properties of combinatory maps: Neutral networks of RNA secondary structures. Bulletin of Mathematical Biology, 1997, 59, 339-397.	0.9	189

#	Article	IF	Citations
631	Correlation length, isotropy and meta-stable states. Physica D: Nonlinear Phenomena, 1997, 107, 240-254.	1.3	29
632	Generic properties of combinatory maps: Neutral networks of RNA secondary structures. Bulletin of Mathematical Biology, 1997, 59, 339-397.	0.9	72
633	Permanence of sparse catalytic networks. Mathematical Biosciences, 1996, 131, 111-133.	0.9	10
634	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
635	Autocatalytic networks with translation. Bulletin of Mathematical Biology, 1996, 58, 877-905.	0.9	3
636	Hamming chromatography. Molecular Diversity, 1996, 1, 187-192.	2.1	1
637	Algorithm independent properties of RNA secondary structure predictions. European Biophysics Journal, 1996, 25, 115-130.	1.2	79
638	Canonical approximation of fitness landscapes. , 1996, 2, 53-58.		12
639	Approximate Scaling Properties of RNA Free Energy Landscapes. Journal of Theoretical Biology, 1996, 181, 299-310.	0.8	11
640	Autocatalytic networks with translation. Bulletin of Mathematical Biology, 1996, 58, 877-905.	0.9	3
641	Analysis of RNA sequence structure maps by exhaustive enumeration I. Neutral networks. Monatshefte FÃ¼r Chemie, 1996, 127, 355-374.	0.9	112
642	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
643	Landscapes and their correlation functions. Journal of Mathematical Chemistry, 1996, 20, 1-45.	0.7	214
644	Bio-molecular shapes and algebraic structures. Computers & Chemistry, 1996, 20, 85-94.	1.2	29
645	Base Pairing Probabilities in a Complete HIV-1 RNA. Journal of Computational Biology, 1996, 3, 253-274.	0.8	28
646	Local minima in the graph bipartitioning problem. Europhysics Letters, 1996, 34, 85-90.	0.7	8
647	Random walks and orthogonal functions associated with highly symmetric graphs. Discrete Mathematics, 1995, 145, 229-237.	0.4	8
648	Dynamics of small autocatalytic reaction networksâ€”II. Replication, mutation and catalysis. Bulletin of Mathematical Biology, 1995, 57, 21-61.	0.9	23

#	Article	IF	Citations
649	Towards a theory of landscapes. , 1995, , 78-163.		59
650	Immune networks modeled by replicator equations. Journal of Mathematical Biology, 1994, 33, 111-137.	0.8	15
651	Statistics of RNA melting kinetics. European Biophysics Journal, 1994, 23, 29-38.	1.2	45
652	Fast folding and comparison of RNA secondary structures. Monatshefte FÃ¼r Chemie, 1994, 125, 167-188.	0.9	1,862
653	Landscapes: Complex optimization problems and biopolymer structures. Computers & Chemistry, 1994, 18, 295-324.	1.2	70
654	The influence of mutation on autocatalytic reaction networks. Mathematical Biosciences, 1994, 122, 127-160.	0.9	14
655	Random structures and evolution of biopolymers. Zeitschrift Fur Elektrotechnik Und Elektrochemie, 1994, 98, 1128-1128.	0.9	0
656	Linear operators on correlated landscapes. Journal De Physique, I, 1994, 4, 681-696.	1.2	12
657	Why Some Fitness Landscapes are Fractal. Journal of Theoretical Biology, 1993, 163, 255-275.	0.8	52
658	Error Thresholds on Correlated Fitness Landscapes. Journal of Theoretical Biology, 1993, 164, 359-372.	0.8	44
659	Anisotropy in Fitness Landscapes. Journal of Theoretical Biology, 1993, 165, 373-388.	0.8	24
660	Statistics of RNA secondary structures. Biopolymers, 1993, 33, 1389-1404.	1.2	265
661	RNA multi-structure landscapes. European Biophysics Journal, 1993, 22, 13-24.	1.2	65
662	Random catalytic reaction networks. Physica D: Nonlinear Phenomena, 1993, 63, 378-392.	1.3	66
663	The probability of permanence. Mathematical Biosciences, 1993, 113, 25-50.	0.9	19
664	RNA folding and combinatory landscapes. Physical Review E, 1993, 47, 2083-2099.	0.8	202
665	Correlation structure of the landscape of the graph-bipartitioning problem. Journal of Physics A, 1992, 25, 3103-3110.	1.6	27
666	Mutation in autocatalytic reaction networks. Journal of Mathematical Biology, 1992, 30, 597.	0.8	1

#	Article	IF	Citations
667	Mutation in autocatalytic reaction networks. Journal of Mathematical Biology, 1992, 30, 597-631.	0.8	77
668	The landscape of the traveling salesman problem. Physics Letters, Section A: General, Atomic and Solid State Physics, 1992, 161, 337-344.	0.9	120
669	Complementary replication. Mathematical Biosciences, 1991, 107, 83-109.	0.9	13
670	Dynamics of autocatalytic reaction networks IV: Inhomogeneous replicator networks. BioSystems, 1991, 26, 1-19.	0.9	18
671	Small autocatalytic reaction networksâ€"III. Monotone growth functions. Bulletin of Mathematical Biology, 1991, 53, 469-485.	0.9	0
672	Full characterization of a strange attractor. Physica D: Nonlinear Phenomena, 1991, 48, 65-90.	1.3	65
673	Small autocatalytic reaction networksâ€"III. Monotone growth functions. Bulletin of Mathematical Biology, 1991, 53, 469-485.	0.9	9
674	Statistics of landscapes based on free energies, replication and degradation rate constants of RNA secondary structures. Monatshefte FÃ¼r Chemie, 1991, 122, 795-819.	0.9	36
675	Dynamics of small autocatalytic reaction networksâ€"I. bifurcations, permanence and exclusion. Bulletin of Mathematical Biology, 1990, 52, 485-508.	0.9	8
676	Visualization of Lattice-Based Protein Folding Simulations. , 0, , .		2
677	RNA Secondary Structures. , 0, , 439-489.		6
678	Computational RNomics: Genome-wide detection of structured non-coding RNAs and their evolutionary patterns. , 0, 2005, .		2
679	Evolution of MicroRNAs. , 0, , 334-350.		0