Michal Ziv-ukelson

List of Publications by Year
in descending order

64 papers	1,249 citations	516710 16 h-index	395702 33 g-index
64 all docs	64 docs citations	64 times ranked	1233 citing authors

#	Article	IF	Citations
1	Alignment of metabolic pathways. Bioinformatics, 2005, 21, 3401-3408.	4.1	193
2	Composite effects of gene determinants on the translation speed and density of ribosomes. Genome Biology, 2011, 12, R110.	9.6	185
3	A Subquadratic Sequence Alignment Algorithm for Unrestricted Scoring Matrices. SIAM Journal on Computing, 2003, 32, 1654-1673.	1.0	122
4	Rich Parameterization Improves RNA Structure Prediction. Journal of Computational Biology, 2011, 18, 1525-1542.	1.6	80
5	Rich Parameterization Improves RNA Structure Prediction. Lecture Notes in Computer Science, 2011, , 546-562.	1.3	60
6	A Study of Accessible Motifs and RNA Folding Complexity. Journal of Computational Biology, 2007, 14, 856-872.	1.6	58
7	Sparse RNA folding: Time and space efficient algorithms. Journal of Discrete Algorithms, 2011, 9, 12-31.	0.7	45
8	The 3â€²-UTR mediates the cellular localization of an mRNA encoding a short plasma membrane protein. Rna, 2008, 14, 1352-1365.	3.5	44
9	On the Common Substring Alignment Problem. Journal of Algorithms, 2001, 41, 338-359.	0.9	41
10	The microRNA Transcriptome of Human Cytomegalovirus (HCMV). The Open Virology Journal, 2012, 6, 38-48.	1.8	36
11	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. PLoS Computational Biology, 2017, 13, e1005221.	3.2	31
12	Speeding Up HMM Decoding and Training by Exploiting Sequence Repetitions. Algorithmica, 2009, 54, 379-399.	1.3	27
13	Gene bi-targeting by viral and human miRNAs. BMC Bioinformatics, 2010, 11, 249.	2.6	27
14	A Faster Algorithm for RNA Co-folding. Lecture Notes in Computer Science, 2008, , 174-185.	1.3	20
15	MotifNet: a web-server for network motif analysis. Bioinformatics, 2017, 33, 1907-1909.	4.1	18
16	Sparse RNA Folding: Time and Space Efficient Algorithms. Lecture Notes in Computer Science, 2009, , 249-262.	1.3	17
17	Approximate Labelled Subtree Homeomorphism. Lecture Notes in Computer Science, 2004, , 59-73.	1.3	15
18	Discovery of multi-operon colinear syntenic blocks in microbial genomes. Bioinformatics, 2020, 36, i21-i29.	4.1	15

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19	Two algorithms for LCS Consecutive Suffix Alignment. Journal of Computer and System Sciences, 2007, 73, 1095-1117.	1.2	14
20	Reducing the worst case running times of a family of RNA and CFG problems, using Valiant's approach. Algorithms for Molecular Biology, 2011, 6, 20.	1.2	13
21	Sparse LCS Common Substring Alignment. Information Processing Letters, 2003, 88, 259-270.	0.6	12
22	Approximate labelled subtree homeomorphism. Journal of Discrete Algorithms, 2008, 6, 480-496.	0.7	12
23	Speeding Up HMM Decoding and Training by Exploiting Sequence Repetitions. Lecture Notes in Computer Science, 2007, , 4-15.	1.3	12
24	A High-Throughput Approach for Associating MicroRNAs with Their Activity Conditions. Journal of Computational Biology, 2006, 13, 245-266.	1.6	11
25	Seeded Tree Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 503-513.	3.0	11
26	CSBFinder: discovery of colinear syntenic blocks across thousands of prokaryotic genomes. Bioinformatics, 2019, 35, 1634-1643.	4.1	11
27	Seeded Tree Alignment and Planar Tanglegram Layout. Lecture Notes in Computer Science, 2007, , 98-110.	1.3	10
28	A Structure-Based Flexible Search Method for Motifs in RNA. Journal of Computational Biology, 2007, 14, 908-926.	1.6	9
29	A Faster Algorithm for Simultaneous Alignment and Folding of RNA. Journal of Computational Biology, 2010, 17, 1051-1065.	1.6	9
30	Two Algorithms for LCS Consecutive Suffix Alignment. Lecture Notes in Computer Science, 2004, , 173-193.	1.3	9
31	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. Bioinformatics, 2013, 29, i210-i216.	4.1	8
32	On the Complexity of Sparse Exon Assembly. Journal of Computational Biology, 2006, 13, 1013-1027.	1.6	7
33	RNAslider: a faster engine for consecutive windows folding and its application to the analysis of genomic folding asymmetry. BMC Bioinformatics, 2009, 10, 76.	2.6	6
34	Unrooted unordered homeomorphic subtree alignment of RNA trees. Algorithms for Molecular Biology, 2013, 8, 13.	1.2	6
35	Efficient edit distance with duplications and contractions. Algorithms for Molecular Biology, 2013, 8, 27.	1.2	6
36	A High-Throughput Approach for Associating microRNAs with Their Activity Conditions. Lecture Notes in Computer Science, 2005, , 133-151.	1.3	5

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37	Regular Language Constrained Sequence Alignment Revisited. Journal of Computational Biology, 2011, 18, 771-781.	1.6	5
38	Reducing the Worst Case Running Times of a Family of RNA and CFG Problems, Using Valiant's Approach. Lecture Notes in Computer Science, 2010, , 65-77.	1.3	5
39	Fast algorithms for computing tree LCS. Theoretical Computer Science, 2009, 410, 4303-4314.	0.9	4
40	Sparse LCS Common Substring Alignment. Lecture Notes in Computer Science, 2003, , 225-236.	1.3	4
41	On the Repeat-Annotated Phylogenetic Tree Reconstruction Problem. Journal of Computational Biology, 2006, 13, 1397-1418.	1.6	3
42	Finding quasi-modules of human and viral miRNAs: a case study of human cytomegalovirus (HCMV). BMC Bioinformatics, 2012, 13, 322.	2.6	3
43	Edit Distance with Duplications and Contractions Revisited. Lecture Notes in Computer Science, 2011, , 441-454.	1.3	3
44	Have your spaghetti and eat it too: evolutionary algorithmics and post-evolutionary analysis. Genetic Programming and Evolvable Machines, 2011, 12, 121-160.	2.2	2
45	Efficient all path score computations on grid graphs. Theoretical Computer Science, 2014, 525, 138-149.	0.9	2
46	Algorithms for Regular Tree Grammar Network Search and Their Application to Mining Human–viral Infection Patterns. Journal of Computational Biology, 2016, 23, 165-179.	1.6	2
47	Approximate search for known gene clusters in new genomes using PQ-trees. Algorithms for Molecular Biology, 2021, 16, 16.	1.2	2
48	Fast Algorithms for Computing Tree LCS. , 2008, , 230-243.		2
49	On the Complexity of Sparse Exon Assembly. Lecture Notes in Computer Science, 2005, , 201-218.	1.3	1
50	StemSearch: RNA search tool based on stem identification and indexing. Methods, 2014, 69, 326-334.	3.8	1
51	Algorithms for path-constrained sequence alignment. Journal of Discrete Algorithms, 2014, 24, 48-58.	0.7	1
52	The Worst Case Complexity of Maximum Parsimony. Journal of Computational Biology, 2014, 21, 799-808.	1.6	1
53	A Biclique Approach to Reference-Anchored Gene Blocks and Its Applications to Genomic Islands. Journal of Computational Biology, 2018, 25, 214-235.	1.6	1
54	Learning Heuristics for Mining RNA Sequence-Structure Motifs. Genetic and Evolutionary Computation, 2016, , 21-38.	1.0	1

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55	SA-REPC â€" Sequence Alignment with Regular Expression Path Constraint. Lecture Notes in Computer Science, 2010, , 451-462.	1.3	1
56	StemSearch: RNA search tool based on stem identification and indexing. , 2013, , .		0
57	Constrained Gene Block Discovery and Its Application to Prokaryotic Genomes. Journal of Computational Biology, 2019, 26, 745-766.	1.6	0
58	On Almost Monge All Scores Matrices. Algorithmica, 2019, 81, 47-68.	1.3	0
59	A New Paradigm for Identifying Reconciliation-Scenario Altering Mutations Conferring Environmental Adaptation. Journal of Computational Biology, 2020, 27, 1561-1580.	1.6	0
60	Dynamic De-Novo Prediction of microRNAs Associated with Cell Conditions: A Search Pruned by Expression. Lecture Notes in Computer Science, 2005, , 13-26.	1.3	0
61	RNA Tree Comparisons via Unrooted Unordered Alignments. Lecture Notes in Computer Science, 2012, , 135-148.	1.3	0
62	Efficient All Path Score Computations on Grid Graphs. Lecture Notes in Computer Science, 2013, , 211-222.	1.3	0
63	A dictionary matching algorithm fast on the average for terms of varying length. Lecture Notes in Computer Science, 1998, , 34-54.	1.3	0
64	Algorithms for Regular Tree Grammar Network Search and Their Application to Mining Human-Viral Infection Patterns. Lecture Notes in Computer Science, 2015, , 53-65.	1.3	0