

# Michal Ziv-ukelson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8837406/publications.pdf>

Version: 2024-02-01

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	Approximate search for known gene clusters in new genomes using PQ-trees. Algorithms for Molecular Biology, 2021, 16, 16.	1.2	2
2	Discovery of multi-operon colinear syntenic blocks in microbial genomes. Bioinformatics, 2020, 36, i21-i29.	4.1	15
3	A New Paradigm for Identifying Reconciliation-Scenario Altering Mutations Conferring Environmental Adaptation. Journal of Computational Biology, 2020, 27, 1561-1580.	1.6	0
4	Constrained Gene Block Discovery and Its Application to Prokaryotic Genomes. Journal of Computational Biology, 2019, 26, 745-766.	1.6	0
5	CSBFinder: discovery of colinear syntenic blocks across thousands of prokaryotic genomes. Bioinformatics, 2019, 35, 1634-1643.	4.1	11
6	On Almost Monge All Scores Matrices. Algorithmica, 2019, 81, 47-68.	1.3	0
7	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
8	MotifNet: a web-server for network motif analysis. Bioinformatics, 2017, 33, 1907-1909.	4.1	18
9	An Asymmetrically Balanced Organization of Kinases versus Phosphatases across Eukaryotes Determines Their Distinct Impacts. PLoS Computational Biology, 2017, 13, e1005221.	3.2	31
10	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
11	Learning Heuristics for Mining RNA Sequence-Structure Motifs. Genetic and Evolutionary Computation, 2016, , 21-38.	1.0	1
12	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
13	StemSearch: RNA search tool based on stem identification and indexing. Methods, 2014, 69, 326-334.	3.8	1
14	Algorithms for path-constrained sequence alignment. Journal of Discrete Algorithms, 2014, 24, 48-58.	0.7	1
15	The Worst Case Complexity of Maximum Parsimony. Journal of Computational Biology, 2014, 21, 799-808.	1.6	1
16	Efficient all path score computations on grid graphs. Theoretical Computer Science, 2014, 525, 138-149.	0.9	2
17	Unrooted unordered homeomorphic subtree alignment of RNA trees. Algorithms for Molecular Biology, 2013, 8, 13.	1.2	6
18	StemSearch: RNA search tool based on stem identification and indexing. , 2013, , .		0

#	ARTICLE	IF	CITATIONS
19	A context-sensitive framework for the analysis of human signalling pathways in molecular interaction networks. <i>Bioinformatics</i> , 2013, 29, i210-i216.	4.1	8
20	Efficient edit distance with duplications and contractions. <i>Algorithms for Molecular Biology</i> , 2013, 8, 27.	1.2	6
21	Efficient All Path Score Computations on Grid Graphs. <i>Lecture Notes in Computer Science</i> , 2013, , 211-222.	1.3	0
22	Finding quasi-modules of human and viral miRNAs: a case study of human cytomegalovirus (HCMV). <i>BMC Bioinformatics</i> , 2012, 13, 322.	2.6	3
23	The microRNA Transcriptome of Human Cytomegalovirus (HCMV). <i>The Open Virology Journal</i> , 2012, 6, 38-48.	1.8	36
24	RNA Tree Comparisons via Unrooted Unordered Alignments. <i>Lecture Notes in Computer Science</i> , 2012, , 135-148.	1.3	0
25	Composite effects of gene determinants on the translation speed and density of ribosomes. <i>Genome Biology</i> , 2011, 12, R110.	9.6	185
26	Rich Parameterization Improves RNA Structure Prediction. <i>Lecture Notes in Computer Science</i> , 2011, , 546-562.	1.3	60
27	Have your spaghetti and eat it too: evolutionary algorithmics and post-evolutionary analysis. <i>Genetic Programming and Evolvable Machines</i> , 2011, 12, 121-160.	2.2	2
28	Reducing the worst case running times of a family of RNA and CFG problems, using Valiant's approach. <i>Algorithms for Molecular Biology</i> , 2011, 6, 20.	1.2	13
29	Sparse RNA folding: Time and space efficient algorithms. <i>Journal of Discrete Algorithms</i> , 2011, 9, 12-31.	0.7	45
30	Rich Parameterization Improves RNA Structure Prediction. <i>Journal of Computational Biology</i> , 2011, 18, 1525-1542.	1.6	80
31	Regular Language Constrained Sequence Alignment Revisited. <i>Journal of Computational Biology</i> , 2011, 18, 771-781.	1.6	5
32	Edit Distance with Duplications and Contractions Revisited. <i>Lecture Notes in Computer Science</i> , 2011, , 441-454.	1.3	3
33	Gene bi-targeting by viral and human miRNAs. <i>BMC Bioinformatics</i> , 2010, 11, 249.	2.6	27
34	A Faster Algorithm for Simultaneous Alignment and Folding of RNA. <i>Journal of Computational Biology</i> , 2010, 17, 1051-1065.	1.6	9
35	Reducing the Worst Case Running Times of a Family of RNA and CFG Problems, Using Valiant's Approach. <i>Lecture Notes in Computer Science</i> , 2010, , 65-77.	1.3	5
36	SA-REPC " Sequence Alignment with Regular Expression Path Constraint. <i>Lecture Notes in Computer Science</i> , 2010, , 451-462.	1.3	1

#	ARTICLE	IF	CITATIONS
37	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
38	Speeding Up HMM Decoding and Training by Exploiting Sequence Repetitions. Algorithmica, 2009, 54, 379-399.	1.3	27
39	Fast algorithms for computing tree LCS. Theoretical Computer Science, 2009, 410, 4303-4314.	0.9	4
40	Sparse RNA Folding: Time and Space Efficient Algorithms. Lecture Notes in Computer Science, 2009, , 249-262.	1.3	17
41	Approximate labelled subtree homeomorphism. Journal of Discrete Algorithms, 2008, 6, 480-496.	0.7	12
42	Seeded Tree Alignment. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 503-513.	3.0	11
43	The 3' UTR mediates the cellular localization of an mRNA encoding a short plasma membrane protein. Rna, 2008, 14, 1352-1365.	3.5	44
44	A Faster Algorithm for RNA Co-folding. Lecture Notes in Computer Science, 2008, , 174-185.	1.3	20
45	Fast Algorithms for Computing Tree LCS. , 2008, , 230-243.		2
46	A Structure-Based Flexible Search Method for Motifs in RNA. Journal of Computational Biology, 2007, 14, 908-926.	1.6	9
47	A Study of Accessible Motifs and RNA Folding Complexity. Journal of Computational Biology, 2007, 14, 856-872.	1.6	58
48	Two algorithms for LCS Consecutive Suffix Alignment. Journal of Computer and System Sciences, 2007, 73, 1095-1117.	1.2	14
49	Speeding Up HMM Decoding and Training by Exploiting Sequence Repetitions. Lecture Notes in Computer Science, 2007, , 4-15.	1.3	12
50	Seeded Tree Alignment and Planar Tanglegram Layout. Lecture Notes in Computer Science, 2007, , 98-110.	1.3	10
51	On the Repeat-Annotated Phylogenetic Tree Reconstruction Problem. Journal of Computational Biology, 2006, 13, 1397-1418.	1.6	3
52	A High-Throughput Approach for Associating MicroRNAs with Their Activity Conditions. Journal of Computational Biology, 2006, 13, 245-266.	1.6	11
53	On the Complexity of Sparse Exon Assembly. Journal of Computational Biology, 2006, 13, 1013-1027.	1.6	7
54	A High-Throughput Approach for Associating microRNAs with Their Activity Conditions. Lecture Notes in Computer Science, 2005, , 133-151.	1.3	5

#	ARTICLE	IF	CITATIONS
55	On the Complexity of Sparse Exon Assembly. Lecture Notes in Computer Science, 2005, , 201-218.	1.3	1
56	Alignment of metabolic pathways. Bioinformatics, 2005, 21, 3401-3408.	4.1	193
57	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
58	Approximate Labelled Subtree Homeomorphism. Lecture Notes in Computer Science, 2004, , 59-73.	1.3	15
59	Two Algorithms for LCS Consecutive Suffix Alignment. Lecture Notes in Computer Science, 2004, , 173-193.	1.3	9
60	Sparse LCS Common Substring Alignment. Information Processing Letters, 2003, 88, 259-270.	0.6	12
61	A Subquadratic Sequence Alignment Algorithm for Unrestricted Scoring Matrices. SIAM Journal on Computing, 2003, 32, 1654-1673.	1.0	122
62	Sparse LCS Common Substring Alignment. Lecture Notes in Computer Science, 2003, , 225-236.	1.3	4
63	On the Common Substring Alignment Problem. Journal of Algorithms, 2001, 41, 338-359.	0.9	41
64	A dictionary matching algorithm fast on the average for terms of varying length. Lecture Notes in Computer Science, 1998, , 34-54.	1.3	0