

Nadia Pisanti

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9055765/publications.pdf>

Version: 2024-02-01

37
papers

1,035
citations

759233

12
h-index

580821

25
g-index

41
all docs

41
docs citations

41
times ranked

1407
citing authors

#	ARTICLE	IF	CITATIONS
1	W<sc>hats</sc>H<sc>ap</sc>: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. Journal of Computational Biology, 2015, 22, 498-509.	1.6	337
2	RISOTTO: Fast Extraction of Motifs with Mismatches. Lecture Notes in Computer Science, 2006, , 757-768.	1.3	51
3	Bases of Motifs for Generating Repeated Patterns with Wild Cards. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2005, 2, 40-50.	3.0	50
4	H<sc>ap</sc>C<sc>ol</sc>: accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617.	4.1	40
5	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
6	On the Minimum Error Correction Problem for Haplotype Assembly in Diploid and Polyploid Genomes. Journal of Computational Biology, 2016, 23, 718-736.	1.6	29
7	A FIRST APPROACH TO FINDING COMMON MOTIFS WITH GAPS. International Journal of Foundations of Computer Science, 2005, 16, 1145-1154.	1.1	23
8	SNPs detection by eBWT positional clustering. Algorithms for Molecular Biology, 2019, 14, 3.	1.2	20
9	Suffix tree characterization of maximal motifs in biological sequences. Theoretical Computer Science, 2009, 410, 4391-4401.	0.9	18
10	Circular sequence comparison: algorithms and applications. Algorithms for Molecular Biology, 2016, 11, 12.	1.2	17
11	MADMX: A Strategy for Maximal Dense Motif Extraction. Journal of Computational Biology, 2011, 18, 535-545.	1.6	14
12	Lossless filter for multiple repeats with bounded edit distance. Algorithms for Molecular Biology, 2009, 4, 3.	1.2	13
13	Efficient Bubble Enumeration in Directed Graphs. Lecture Notes in Computer Science, 2012, , 118-129.	1.3	13
14	Lossless filter for multiple repetitions with Hamming distance. Journal of Discrete Algorithms, 2008, 6, 497-509.	0.7	12
15	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	2.6	11
16	Room allocation: a polynomial subcase of the quadratic assignment problem. Discrete Applied Mathematics, 2004, 144, 263-269.	0.9	9
17	Mobilomics in Saccharomyces cerevisiae strains. BMC Bioinformatics, 2013, 14, 102.	2.6	9
18	Approximate pattern matching on elastic-degenerate text. Theoretical Computer Science, 2020, 812, 109-122.	0.9	9

#	ARTICLE	IF	CITATIONS
19	Variable-order reference-free variant discovery with the Burrows-Wheeler Transform. BMC Bioinformatics, 2020, 21, 260.	2.6	9
20	Motif trie: An efficient text index for pattern discovery with don't cares. Theoretical Computer Science, 2018, 710, 74-87.	0.9	6
21	A Relational Extension of the Notion of Motifs: Application to the Common 3D Protein Substructures Searching Problem. Journal of Computational Biology, 2009, 16, 1635-1660.	1.6	5
22	MADMX: A Novel Strategy for Maximal Dense Motif Extraction. Lecture Notes in Computer Science, 2009, , 362-374.	1.3	5
23	Masking patterns in sequences: A new class of motif discovery with don't cares. Theoretical Computer Science, 2009, 410, 4327-4340.	0.9	4
24	Comparing Degenerate Strings. Fundamenta Informaticae, 2020, 175, 41-58.	0.4	4
25	Circular Sequence Comparison with q-grams. Lecture Notes in Computer Science, 2015, , 203-216.	1.3	3
26	Incremental Inference of Relational Motifs with a Degenerate Alphabet. Lecture Notes in Computer Science, 2005, , 229-240.	1.3	3
27	Longest Property-Preserved Common Factor. Lecture Notes in Computer Science, 2018, , 42-49.	1.3	3
28	Elastic-Degenerate String Matching via Fast Matrix Multiplication. SIAM Journal on Computing, 2022, 51, 549-576.	1.0	3
29	Suffix Tree Characterization of Maximal Motifs in Biological Sequences. Communications in Computer and Information Science, 2008, , 456-465.	0.5	2
30	Rime : Repeat identification. Discrete Applied Mathematics, 2014, 163, 275-286.	0.9	2
31	Longest property-preserved common factor: A new string-processing framework. Theoretical Computer Science, 2020, 812, 244-251.	0.9	2
32	Beyond the BEST Theorem: Fast Assessment of Eulerian Trails. Lecture Notes in Computer Science, 2021, , 162-175.	1.3	2
33	PaTre: A Method for Paralogy Trees Construction. Journal of Computational Biology, 2003, 10, 791-802.	1.6	1
34	Mining Biological Sequences with Masks. , 2009, , .		1
35	Removing Artifacts of Approximated Motifs. Lecture Notes in Computer Science, 2011, , 153-167.	1.3	1
36	Editorial: Special Issue on International Workshop on Combinatorial Algorithms (IWOCA 2019). Theory of Computing Systems, 2020, 64, 1155-1157.	1.1	0

#	ARTICLE	IF	CITATIONS
37	Comparing Degenerate Strings. , 2020, , .		0