Nadia Pisanti

List of Publications by Year
in descending order

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	Elastic-Degenerate String Matching via Fast Matrix Multiplication. SIAM Journal on Computing, 2022, 51, 549-576.	1.0	3
2	Beyond the BEST Theorem: Fast Assessment of Eulerian Trails. Lecture Notes in Computer Science, 2021, , 162-175.	1.3	2
3	Approximate pattern matching on elastic-degenerate text. Theoretical Computer Science, 2020, 812, 109-122.	0.9	9
4	Variable-order reference-free variant discovery with the Burrows-Wheeler Transform. BMC Bioinformatics, 2020, 21, 260.	2.6	9
5	Comparing Degenerate Strings. Fundamenta Informaticae, 2020, 175, 41-58.	0.4	4
6	Longest property-preserved common factor: A new string-processing framework. Theoretical Computer Science, 2020, 812, 244-251.	0.9	2
7	Editorial: Special Issue on International Workshop on Combinatorial Algorithms (IWOCA 2019). Theory of Computing Systems, 2020, 64, 1155-1157.	1.1	0
8	Comparing Degenerate Strings. , 2020, , .		0
9	SNPs detection by eBWT positional clustering. Algorithms for Molecular Biology, 2019, 14, 3.	1.2	20
10	Motif trie: An efficient text index for pattern discovery with don't cares. Theoretical Computer Science, 2018, 710, 74-87.	0.9	6
11	Longest Property-Preserved Common Factor. Lecture Notes in Computer Science, 2018, , 42-49.	1.3	3
12	Circular sequence comparison: algorithms and applications. Algorithms for Molecular Biology, 2016, 11, 12.	1.2	17
13	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
14	PWHATSHAP: efficient haplotyping for future generation sequencing. BMC Bioinformatics, 2016, 17, 342.	2.6	11
15	HapCol: accurate and memory-efficient haplotype assembly from long reads. Bioinformatics, 2016, 32, 1610-1617.	4.1	40
16	Circular Sequence Comparison with q-grams. Lecture Notes in Computer Science, 2015, , 203-216.	1.3	3
17	WhatsHap: Weighted Haplotype Assembly for Future-Generation Sequencing Reads. Journal of Computational Biology, 2015, 22, 498-509.	1.6	337
18	Rime : Repeat identification. Discrete Applied Mathematics, 2014, 163, 275-286.	0.9	2

#	Article	IF	Citations
19	Mobilomics in Saccharomyces cerevisiae strains. BMC Bioinformatics, 2013, 14, 102.	2.6	9
20	Efficient Bubble Enumeration in Directed Graphs. Lecture Notes in Computer Science, 2012, , 118-129.	1.3	13
21	MADMX: A Strategy for Maximal Dense Motif Extraction. Journal of Computational Biology, 2011, 18, 535-545.	1.6	14
22	Removing Artifacts of Approximated Motifs. Lecture Notes in Computer Science, 2011, , 153-167.	1.3	1
23	Identifying SNPs without a Reference Genome by Comparing Raw Reads. Lecture Notes in Computer Science, 2010, , 147-158.	1.3	35
24	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
25	MADMX: A Novel Strategy for Maximal Dense Motif Extraction. Lecture Notes in Computer Science, 2009, , 362-374.	1.3	5
26	Mining Biological Sequences with Masks. , 2009, , .		1
27	Masking patterns in sequences: A new class of motif discovery with don't cares. Theoretical Computer Science, 2009, 410, 4327-4340.	0.9	4
28	Suffix tree characterization of maximal motifs in biological sequences. Theoretical Computer Science, 2009, 410, 4391-4401.	0.9	18
29	Lossless filter for multiple repeats with bounded edit distance. Algorithms for Molecular Biology, 2009, 4, 3.	1.2	13
30	Lossless filter for multiple repetitions with Hamming distance. Journal of Discrete Algorithms, 2008, 6, 497-509.	0.7	12
31	Suffix Tree Characterization of Maximal Motifs in Biological Sequences. Communications in Computer and Information Science, 2008, , 456-465.	0.5	2
32	RISOTTO: Fast Extraction of Motifs with Mismatches. Lecture Notes in Computer Science, 2006, , 757-768.	1.3	51
33	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
34	A FIRST APPROACH TO FINDING COMMON MOTIFS WITH GAPS. International Journal of Foundations of Computer Science, 2005, 16, 1145-1154.	1.1	23
35	Incremental Inference of Relational Motifs with a Degenerate Alphabet. Lecture Notes in Computer Science, 2005, , 229-240.	1.3	3
36	Room allocation: a polynomial subcase of the quadratic assignment problem. Discrete Applied Mathematics, 2004, 144, 263-269.	0.9	9

#	ARTICLE	IF	CITATIONS
37	PaTre: A Method for Paralogy Trees Construction. Journal of Computational Biology, 2003, 10, 791-802.	1.6	1