

StÃ©phane Vialette

List of Publications by Year in descending order

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Version: 2024-02-01

40
papers

588
citations

687363

13
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610901

24
g-index

42
all docs

42
docs citations

42
times ranked

404
citing authors

#	ARTICLE	IF	CITATIONS
1	On recognising words that are squares for the shuffle product. Theoretical Computer Science, 2023, 956, 111156.	0.9	2
2	Efficient, robust and effective rank aggregation for massive biological datasets. Future Generation Computer Systems, 2021, 124, 406-421.	7.5	4
3	Recognizing binary shuffle squares is NP-hard. Theoretical Computer Science, 2020, 806, 116-132.	0.9	3
4	The Clever Shopper Problem. Theory of Computing Systems, 2020, 64, 17-34.	1.1	0
5	Sorting with forbidden intermediates. Discrete Applied Mathematics, 2020, 279, 49-68.	0.9	0
6	Algorithmic and algebraic aspects of unshuffling permutations. Theoretical Computer Science, 2018, 729, 20-41.	0.9	1
7	The S-labeling problem: An algorithmic tour. Discrete Applied Mathematics, 2018, 246, 49-61.	0.9	2
8	Solving the tree containment problem in linear time for nearly stable phylogenetic networks. Discrete Applied Mathematics, 2018, 246, 62-79.	0.9	13
9	The Clever Shopper Problem. Lecture Notes in Computer Science, 2018, , 53-64.	1.3	1
10	Spot Weight Adaptation for Moving Target in Spot Scanning Proton Therapy. Frontiers in Oncology, 2015, 5, 119.	2.8	1
11	Some algorithmic results for [2]-sumset covers. Information Processing Letters, 2015, 115, 1-5.	0.6	1
12	Locating a Tree in a Phylogenetic Network in Quadratic Time. Lecture Notes in Computer Science, 2015, , 96-107.	1.3	15
13	Finding approximate and constrained motifs in graphs. Theoretical Computer Science, 2013, 483, 10-21.	0.9	12
14	On the combinatorics of suffix arrays. Information Processing Letters, 2013, 113, 915-920.	0.6	12
15	MINIMUM MOSAIC INFERENCE OF A SET OF RECOMBINANTS. International Journal of Foundations of Computer Science, 2013, 24, 51-66.	1.1	3
16	A Faster Algorithm for Finding Minimum Tucker Submatrices. Theory of Computing Systems, 2012, 51, 270-281.	1.1	4
17	Approximation of RNA multiple structural alignment. Journal of Discrete Algorithms, 2011, 9, 365-376.	0.7	0
18	Complexity issues in vertex-colored graph pattern matching. Journal of Discrete Algorithms, 2011, 9, 82-99.	0.7	27

#	ARTICLE	IF	CITATIONS
19	Upper and lower bounds for finding connected motifs in vertex-colored graphs. <i>Journal of Computer and System Sciences</i> , 2011, 77, 799-811.	1.2	60
20	A Polynomial-Time Algorithm for Finding a Minimal Conflicting Set Containing a Given Row. <i>Lecture Notes in Computer Science</i> , 2011, , 373-384.	1.3	4
21	Finding common structured patterns in linear graphs. <i>Theoretical Computer Science</i> , 2010, 411, 2475-2486.	0.9	1
22	Querying Graphs in Protein-Protein Interactions Networks Using Feedback Vertex Set. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 628-635.	3.0	25
23	Complexity issues in color-preserving graph embeddings. <i>Theoretical Computer Science</i> , 2010, 411, 716-729.	0.9	0
24	Finding occurrences of protein complexes in protein-protein interaction graphs. <i>Journal of Discrete Algorithms</i> , 2009, 7, 90-101.	0.7	2
25	On the S-Labeling problem. <i>Electronic Notes in Discrete Mathematics</i> , 2009, 34, 273-277.	0.4	3
26	RECOMB-Comparative Genomics Special Issue. <i>Journal of Computational Biology</i> , 2009, 16, 1285-1286.	1.6	0
27	On the Approximability of Comparing Genomes with Duplicates. <i>Journal of Graph Algorithms and Applications</i> , 2009, 13, 19-53.	0.4	54
28	Bounded list injective homomorphism for comparative analysis of protein-protein interaction graphs. <i>Journal of Discrete Algorithms</i> , 2008, 6, 178-191.	0.7	4
29	Fixed-parameter algorithms for protein similarity search under mRNA structure constraints. <i>Journal of Discrete Algorithms</i> , 2008, 6, 618-626.	0.7	8
30	Approximating the 2-interval pattern problem. <i>Theoretical Computer Science</i> , 2008, 395, 283-297.	0.9	15
31	The Minimum Substring Cover problem. <i>Information and Computation</i> , 2008, 206, 1303-1312.	0.7	11
32	Efficient Tools for Computing the Number of Breakpoints and the Number of Adjacencies between Two Genomes with Duplicate Genes. <i>Journal of Computational Biology</i> , 2008, 15, 1093-1115.	1.6	25
33	A Pseudo-Boolean Framework for Computing Rearrangement Distances between Genomes with Duplicates. <i>Journal of Computational Biology</i> , 2007, 14, 379-393.	1.6	18
34	Exemplar Longest Common Subsequence. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 535-543.	3.0	30
35	Comparing Genomes with Duplications: A Computational Complexity Point of View. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 523-534.	3.0	31
36	Extracting constrained 2-interval subsets in 2-interval sets. <i>Theoretical Computer Science</i> , 2007, 385, 241-263.	0.9	14

#	ARTICLE	IF	CITATIONS
37	Packing of $(0, \hat{\epsilon}\%1)$ -matrices. RAIRO - Theoretical Informatics and Applications, 2006, 40, 519-535.	0.5	5
38	What Makes the Arc-Preserving Subsequence Problem Hard?. Lecture Notes in Computer Science, 2005, , 1-36.	1.3	7
39	On the computational complexity of 2-interval pattern matching problems. Theoretical Computer Science, 2004, 312, 223-249.	0.9	69
40	In <i>Saccharomyces cerevisiae</i> , ATP2 mRNA sorting to the vicinity of mitochondria is essential for respiratory function. EMBO Journal, 2002, 21, 6893-6904.	7.8	98