

Daming Zhu

List of Publications by Year in descending order

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86
all docs

86
docs citations

86
times ranked

148
citing authors

#	ARTICLE	IF	CITATIONS
1	Algorithms and Hardness for Scaffold Filling to Maximize Increased Duo-Preservations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2071-2079.	3.0	1
2	mzMD: visualization-oriented MS data storage and retrieval. Bioinformatics, 2022, 38, 2333-2340.	4.1	0
3	Approximation algorithms for sorting by bounded singleton moves. Theoretical Computer Science, 2022, , .	0.9	0
4	MultiTrans: an algorithm for path extraction through mixed integer linear programming for transcriptome assembly. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	4
5	Sorting a Permutation by Best Short Swaps. Algorithmica, 2021, 83, 1953-1979.	1.3	2
6	On the solution bound of two-sided scaffold filling. Theoretical Computer Science, 2021, , .	0.9	1
7	A 43-approximation algorithm for the Maximum Internal Spanning Tree Problem. Journal of Computer and System Sciences, 2021, 118, 131-140.	1.2	3
8	SVLR: Genome Structural Variant Detection Using Long-Read Sequencing Data. Journal of Computational Biology, 2021, 28, 774-788.	1.6	4
9	Approximation algorithms for the maximum vertex coverage problem on bounded degree graphs. Theoretical Computer Science, 2021, 888, 22-30.	0.9	1
10	rzMLP-DTA: gMLP network with ReZero for sequence-based drug-target affinity prediction. , 2021, , .		7
11	Hydrogen bonds meet self-attention: all you need for protein structure embedding. , 2021, , .		3
12	TransCoord: Genome-guided Transcripts Assembly by Coordinating Candidate Paths into Two-phased Linear Programming. , 2021, , .		1
13	IsoTree: A New Framework for de novo Transcriptome Assembly from RNA-seq Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 938-948.	3.0	4
14	Improved detection algorithm for copy number variations based on hidden Markov model. Multimedia Tools and Applications, 2020, 79, 9237-9253.	3.9	1
15	Maximum Stacking Base Pairs: Hardness and Approximation by Nonlinear Linear Programming-Rounding. Journal of Computational Biology, 2020, 27, 200-211.	1.6	0
16	A 1.375-approximation algorithm for unsigned translocation sorting. Journal of Computer and System Sciences, 2020, 113, 163-178.	1.2	2
17	PASA: IDENTIFYING MORE CREDIBLE STRUCTURAL VARIANTS OF HEDOU12. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	1
18	Combinatorial Detection Algorithm for Copy Number Variations Using High-throughput Sequencing Reads. International Journal of Pattern Recognition and Artificial Intelligence, 2019, 33, 1950022.	1.2	0

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19	DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. BMC Bioinformatics, 2019, 20, 698.	2.6	3
20	An approximation algorithm for genome sorting by reversals to recover all adjacencies. Journal of Combinatorial Optimization, 2019, 37, 1170-1190.	1.3	0
21	An Approximation Algorithm for Sorting by Bounded Singleton Moves. Lecture Notes in Computer Science, 2019, , 580-590.	1.3	0
22	Predicting Model and Algorithm in RNA Folding Structure Including Pseudoknots. International Journal of Pattern Recognition and Artificial Intelligence, 2018, 32, 1851005.	1.2	1
23	Can a breakpoint graph be decomposed into none other than 2-cycles?. Theoretical Computer Science, 2018, 734, 38-45.	0.9	1
24	A graph-based filtering method for top-down mass spectral identification. BMC Genomics, 2018, 19, 666.	2.8	0
25	A 2-approximation algorithm for the contig-based genomic scaffold filling problem. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850022.	0.8	3
26	The Longest Common Exemplar Subsequence Problem. , 2018, , .		2
27	A spectrum graph-based protein sequence filtering algorithm for proteoform identification by top-down mass spectrometry. , 2017, 2017, 222-229.		5
28	A 1.4-Approximation Algorithm for Two-Sided Scaffold Filling. Lecture Notes in Computer Science, 2017, , 196-208.	1.3	2
29	A New Approximation Algorithm for Unsigned Translocation Sorting. Lecture Notes in Computer Science, 2016, , 269-280.	1.3	1
30	Mining structural variants of Heduo12 using paired-end reads. , 2016, , .		0
31	A 1.5-Approximation Algorithm for Two-Sided Scaffold Filling. Algorithmica, 2016, 74, 91-116.	1.3	14
32	A Dynamic Programming Algorithm For (1,2)-Exemplar Breakpoint Distance. Journal of Computational Biology, 2015, 22, 666-676.	1.6	3
33	A factor-($1.408 + \hat{\mu}$) approximation for sorting unsigned genomes by reciprocal translocations. Theoretical Computer Science, 2015, 607, 166-180.	0.9	3
34	Characteristics and Prediction of RNA Structure. BioMed Research International, 2014, 2014, 1-10.	1.9	5
35	Partition of a Binary Matrix into k $(\langle \text{mml:math xmlns:mml}=\text{"http://www.w3.org/1998/Math/MathML"} \text{id="M1"} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:mi} \rangle k \langle \text{mml:mi} \rangle \langle \text{mml:mrow} \rangle \langle \text{mml:math} \rangle (\langle \text{mml:math} \rangle T_j \text{ ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 1 12}$ Exclusive Row and Column Submatrices Is Difficult. Mathematical Problems in Engineering, 2014. 2014, 1-13.	1.1	0
36	A parameterized algorithm for (1,2)-exemplar breakpoint distance. , 2014, , .		0

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37	Characteristics of equipartition for RNA structure. BMC Proceedings, 2014, 8, S3.	1.6	0
38	A $(1.408+\hat{\mu})$ -Approximation Algorithm for Sorting Unsigned Genomes by Reciprocal Translocations. Lecture Notes in Computer Science, 2014, , 128-140.	1.3	6
39	On the Toggling-Branching Recurrence of Computability Logic. Journal of Computer Science and Technology, 2013, 28, 278-284.	1.5	2
40	An Improved Approximation Algorithm for Scaffold Filling to Maximize the Common Adjacencies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 905-913.	3.0	19
41	An Exact Algorithm for the Zero Exemplar Breakpoint Distance Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1469-1477.	3.0	5
42	Parameterized complexity of control by voter selection in Maximin, Copeland, Borda, Bucklin, and Approval election systems. Theoretical Computer Science, 2013, 498, 115-123.	0.9	8
43	Sorting genomes by generalized translocations. Theoretical Computer Science, 2013, 491, 127-135.	0.9	1
44	A Dynamic Programming Algorithm for Unsigned (1,2)-Exemplar Breakpoint Distance Problem with Span Constraint. , 2013, , .		1
45	The Duplication-Loss Problem: Novel Algorithms Based on k-NNI Local Search. , 2013, , .		0
46	De Novo Peptide Sequencing Based on Vertex Contraction Algorithm. , 2012, , .		0
47	Improved approximation algorithm of RNA structure prediction with pseudoknots. , 2012, , .		0
48	Minimum common string partition revisited. Journal of Combinatorial Optimization, 2012, 23, 519-527.	1.3	27
49	An approximation algorithm for the Generalized k -Multicut problem. Discrete Applied Mathematics, 2012, 160, 1240-1247.	0.9	9
50	A T_j algorithm for sorting by short block-moves. Theoretical Computer Science, 2012, 439, 1-8.	0.9	5
51	A new approximation algorithm for cut-and-paste sorting of unsigned circular permutations. Journal of Computer and System Sciences, 2012, 78, 1099-1114.	1.2	3
52	New Heuristic Algorithm of RNA Secondary Structure Prediction with Pseudoknots. , 2011, , .		1
53	A $14/11$ -approximation algorithm for sorting by short block-moves. Science China Information Sciences, 2011, 54, 279-292.	4.3	6
54	Algorithms for sorting unsigned linear genomes by the DCJ operations. Bioinformatics, 2011, 27, 311-316.	4.1	15

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55	Sorting Unsigned Permutations by Weighted Reversals, Transpositions, and Transreversals. Journal of Computer Science and Technology, 2010, 25, 853-863.	1.5	2
56	Parameterized complexity of control problems in Maximin election. Information Processing Letters, 2010, 110, 383-388.	0.6	23
57	A faster algorithm for gene-duplication problem based on rSPR local search. , 2010, , .		0
58	Notice of Retraction: An algorithm for gene-loss problem based on rNNI local search. , 2010, , .		0
59	Parameterized Complexity of Inverse Scope Problems in Metabolic Networks. , 2009, , .		0
60	A translocation, insertion and deletion distance formula for sorting genomes. , 2009, , .		0
61	A Practical Exponential-Time Algorithm on Sorting by Short Block-Moves. , 2009, , .		0
62	Parameterized Complexity of Finding Elementary Modes in Metabolic Networks. , 2009, , .		0
63	Sorting Genomes by Reversals and Translocations. , 2009, , .		4
64	Translocation-Deletions Distance Formula for Sorting Genomes. , 2009, , .		1
65	A $(1+e)$ -Approximation Algorithm for Sorting by Short Block-Moves. , 2009, , .		1
66	Parameterized computational complexity of control problems in voting systems. Theoretical Computer Science, 2009, 410, 2746-2753.	0.9	33
67	A Bicriteria Approximation Algorithm for Generalized k -Multicut in Trees. , 2009, , .		1
68	On Constrained Facility Location Problems. Journal of Computer Science and Technology, 2008, 23, 740-748.	1.5	1
69	A polynomial algorithm to compute the minimum degree spanning trees of directed acyclic graphs with applications to the broadcast problem. Discrete Mathematics, 2008, 308, 3951-3959.	0.7	5
70	A $(1.5 + \hat{\mu})$ -Approximation Algorithm for Unsigned Translocation Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 56-66.	3.0	12
71	Randomized algorithm with constant approximation for k -means based on the least cluster size. , 2008, , .		1
72	New Evolutionary Subset: Application to Symbiotic Evolutionary Algorithm for Job-Shop Scheduling Problem. , 2008, , .		1

#	ARTICLE	IF	CITATIONS
73	Faster algorithms for sorting by transpositions and sorting by block interchanges. ACM Transactions on Algorithms, 2007, 3, 25.	1.0	29
74	A 1.75-approximation algorithm for unsigned translocation distance. Journal of Computer and System Sciences, 2007, 73, 1045-1059.	1.2	11
75	On the complexity of unsigned translocation distance. Theoretical Computer Science, 2006, 352, 322-328.	0.9	31
76	An $\langle \text{mml:math altimg="si1.gif" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="http://www.elsevier.com/x} \rangle$ algorithm for signed translocation problem. , 2005, , .	1.2	31
77	AN $O(n^2)$ ALGORITHM FOR SIGNED TRANSLOCATION PROBLEM. , 2005, , .		2
78	Approximation algorithm for bottleneck Steiner tree problem in the Euclidean plane. Journal of Computer Science and Technology, 2004, 19, 791-794.	1.5	13
79	Hardness and methods to solve CLIQUE. Journal of Computer Science and Technology, 2001, 16, 388-391.	1.5	1
80	DNA Encoding Method of Weight for Chinese Postman Problem. , 0, , .		4