

# Daming Zhu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2105520/publications.pdf>

Version: 2024-02-01

80  
papers

403  
citations

933447

10  
h-index

888059

17  
g-index

86  
all docs

86  
docs citations

86  
times ranked

148  
citing authors

#	ARTICLE	IF	CITATIONS
1	Parameterized computational complexity of control problems in voting systems. Theoretical Computer Science, 2009, 410, 2746-2753. An $\langle \text{mml:math altimg="si1.gif" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="http://www.elsevier.com/x$	0.9	33
2	On the complexity of unsigned translocation distance. Theoretical Computer Science, 2006, 352, 322-328.	1.2	31
3	Faster algorithms for sorting by transpositions and sorting by block interchanges. ACM Transactions on Algorithms, 2007, 3, 25.	0.9	31
4	Minimum common string partition revisited. Journal of Combinatorial Optimization, 2012, 23, 519-527.	1.0	29
5	Parameterized complexity of control problems in Maximin election. Information Processing Letters, 2010, 110, 383-388.	1.3	27
6	An Improved Approximation Algorithm for Scaffold Filling to Maximize the Common Adjacencies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 905-913.	0.6	23
7	Algorithms for sorting unsigned linear genomes by the DCJ operations. Bioinformatics, 2011, 27, 311-316.	3.0	19
8	A 1.5-Approximation Algorithm for Two-Sided Scaffold Filling. Algorithmica, 2016, 74, 91-116.	4.1	15
9	Approximation algorithm for bottleneck Steiner tree problem in the Euclidean plane. Journal of Computer Science and Technology, 2004, 19, 791-794.	1.3	14
10	A $(1.5 + \hat{\mu})$ -Approximation Algorithm for Unsigned Translocation Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 56-66.	1.5	13
11	A 1.75-approximation algorithm for unsigned translocation distance. Journal of Computer and System Sciences, 2007, 73, 1045-1059.	3.0	12
12	An approximation algorithm for the Generalized $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si9.gif" display="inline" overflow="scroll" \rangle \langle \text{mml:mi} \rangle k \langle \text{mml:mi} \rangle \langle \text{mml:math} \rangle$ -Multicut problem. Discrete Applied Mathematics, 2012, 160, 1240-1247.	1.2	11
13	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	9
14	rzMLP-DTA: gMLP network with ReZero for sequence-based drug-target affinity prediction. , 2021, , .	0.9	8
15	A 14/11-approximation algorithm for sorting by short block-moves. Science China Information Sciences, 2011, 54, 279-292.	0.9	7
16	A $(1.408 + \hat{\mu})$ -Approximation Algorithm for Sorting Unsigned Genomes by Reciprocal Translocations. Lecture Notes in Computer Science, 2014, , 128-140.	4.3	6
17	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.	1.3	6
18	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

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19	A ( $\langle \text{mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML" altimg="si1.gif" display="inline" \rangle T_j \text{ETQq1}$ ) algorithm for sorting by short block-moves. Theoretical Computer Science, 2012, 439, 1-8.	0.784314 0.9	5
20	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
21	Characteristics and Prediction of RNA Structure. BioMed Research International, 2014, 2014, 1-10.	1.9	5
22	A spectrum graph-based protein sequence filtering algorithm for proteoform identification by top-down mass spectrometry. , 2017, 2017, 222-229.		5
23	DNA Encoding Method of Weight for Chinese Postman Problem. , 0, , .		4
24	Sorting Genomes by Reversals and Translocations. , 2009, , .		4
25	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
26	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
27	SVLR: Genome Structural Variant Detection Using Long-Read Sequencing Data. Journal of Computational Biology, 2021, 28, 774-788.	1.6	4
28	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
29	A Dynamic Programming Algorithm For (1,2)-Exemplar Breakpoint Distance. Journal of Computational Biology, 2015, 22, 666-676.	1.6	3
30	A factor- $(1.408 + \hat{\mu})$ approximation for sorting unsigned genomes by reciprocal translocations. Theoretical Computer Science, 2015, 607, 166-180.	0.9	3
31	A 2-approximation algorithm for the contig-based genomic scaffold filling problem. Journal of Bioinformatics and Computational Biology, 2018, 16, 1850022.	0.8	3
32	DTA-SiST: de novo transcriptome assembly by using simplified suffix trees. BMC Bioinformatics, 2019, 20, 698.	2.6	3
33	A 43-approximation algorithm for the Maximum Internal Spanning Tree Problem. Journal of Computer and System Sciences, 2021, 118, 131-140.	1.2	3
34	Hydrogen bonds meet self-attention: all you need for protein structure embedding. , 2021, , .		3
35	Sorting Unsigned Permutations by Weighted Reversals, Transpositions, and Transreversals. Journal of Computer Science and Technology, 2010, 25, 853-863.	1.5	2
36	On the Toggling-Branching Recurrence of Computability Logic. Journal of Computer Science and Technology, 2013, 28, 278-284.	1.5	2

#	ARTICLE	IF	CITATIONS
37	The Longest Common Exemplar Subsequence Problem. , 2018, , .		2
38	Sorting a Permutation by Best Short Swaps. <i>Algorithmica</i> , 2021, 83, 1953-1979.	1.3	2
39	A 1.4-Approximation Algorithm for Two-Sided Scaffold Filling. <i>Lecture Notes in Computer Science</i> , 2017, , 196-208.	1.3	2
40	AN $O(n^2)$ ALGORITHM FOR SIGNED TRANSLOCATION PROBLEM. , 2005, , .		2
41	A 1.375-approximation algorithm for unsigned translocation sorting. <i>Journal of Computer and System Sciences</i> , 2020, 113, 163-178.	1.2	2
42	Hardness and methods to solve CLIQUE. <i>Journal of Computer Science and Technology</i> , 2001, 16, 388-391.	1.5	1
43	On Constrained Facility Location Problems. <i>Journal of Computer Science and Technology</i> , 2008, 23, 740-748.	1.5	1
44	Randomized algorithm with constant approximation for k-means based on the least cluster size. , 2008, , .		1
45	New Evolutionary Subset: Application to Symbiotic Evolutionary Algorithm for Job-Shop Scheduling Problem. , 2008, , .		1
46	Translocation-Deletions Distance Formula for Sorting Genomes. , 2009, , .		1
47	A $(1+\epsilon)$ -Approximation Algorithm for Sorting by Short Block-Moves. , 2009, , .		1
48	A Bicriteria Approximation Algorithm for Generalized k-Multicut in Trees. , 2009, , .		1
49	New Heuristic Algorithm of RNA Secondary Structure Prediction with Pseudoknots. , 2011, , .		1
50	Sorting genomes by generalized translocations. <i>Theoretical Computer Science</i> , 2013, 491, 127-135.	0.9	1
51	A Dynamic Programming Algorithm for Unsigned (1,2)-Exemplar Breakpoint Distance Problem with Span Constraint. , 2013, , .		1
52	A New Approximation Algorithm for Unsigned Translocation Sorting. <i>Lecture Notes in Computer Science</i> , 2016, , 269-280.	1.3	1
53	Predicting Model and Algorithm in RNA Folding Structure Including Pseudoknots. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2018, 32, 1851005.	1.2	1
54	Can a breakpoint graph be decomposed into none other than 2-cycles?. <i>Theoretical Computer Science</i> , 2018, 734, 38-45.	0.9	1

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55	PASA: IDENTIFYING MORE CREDIBLE STRUCTURAL VARIANTS OF HEDOU12. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	1
56	Improved detection algorithm for copy number variations based on hidden Markov model. Multimedia Tools and Applications, 2020, 79, 9237-9253.	3.9	1
57	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
58	On the solution bound of two-sided scaffold filling. Theoretical Computer Science, 2021, , .	0.9	1
59	Approximation algorithms for the maximum vertex coverage problem on bounded degree graphs. Theoretical Computer Science, 2021, 888, 22-30.	0.9	1
60	TransCoord: Genome-guided Transcripts Assembly by Coordinating Candidate Paths into Two-phased Linear Programming. , 2021, , .		1
61	Parameterized Complexity of Inverse Scope Problems in Metabolic Networks. , 2009, , .		0
62	A translocation, insertion and deletion distance formula for sorting genomes. , 2009, , .		0
63	A Practical Exponential-Time Algorithm on Sorting by Short Block-Moves. , 2009, , .		0
64	Parameterized Complexity of Finding Elementary Modes in Metabolic Networks. , 2009, , .		0
65	A faster algorithm for gene-duplication problem based on rSPR local search. , 2010, , .		0
66	Notice of Retraction: An algorithm for gene-loss problem based on rNNI local search. , 2010, , .		0
67	De Novo Peptide Sequencing Based on Vertex Contraction Algorithm. , 2012, , .		0
68	Improved approximation algorithm of RNA structure prediction with pseudoknots. , 2012, , .		0
69	The Duplication-Loss Problem: Novel Algorithms Based on k-NNI Local Search. , 2013, , . Partition of a Binary Matrix into		0
70	Exclusive Row and Column Submatrices Is Difficult. Mathematical Problems in Engineering, 2014, 2014, 1-13.	1.1	0
71	A parameterized algorithm for (1,2)-exemplar breakpoint distance. , 2014, , .		0
72	Characteristics of equipartition for RNA structure. BMC Proceedings, 2014, 8, S3.	1.6	0

#	ARTICLE	IF	CITATIONS
73	Mining structural variants of Heduo12 using paired-end reads. , 2016, , .		0
74	A graph-based filtering method for top-down mass spectral identification. BMC Genomics, 2018, 19, 666.	2.8	0
75	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
76	An approximation algorithm for genome sorting by reversals to recover all adjacencies. Journal of Combinatorial Optimization, 2019, 37, 1170-1190.	1.3	0
77	Maximum Stacking Base Pairs: Hardness and Approximation by Nonlinear Linear Programming-Rounding. Journal of Computational Biology, 2020, 27, 200-211.	1.6	0
78	An Approximation Algorithm for Sorting by Bounded Singleton Moves. Lecture Notes in Computer Science, 2019, , 580-590.	1.3	0
79	mzMD: visualization-oriented MS data storage and retrieval. Bioinformatics, 2022, 38, 2333-2340.	4.1	0
80	Approximation algorithms for sorting by bounded singleton moves. Theoretical Computer Science, 2022, , .	0.9	0