

Marta Kasprzak

List of Publications by Year in descending order

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35
papers

385
citations

687220

13
h-index

794469

19
g-index

36
all docs

36
docs citations

36
times ranked

182
citing authors

#	ARTICLE	IF	CITATIONS
1	Complexity of DNA sequencing by hybridization. Theoretical Computer Science, 2003, 290, 1459-1473.	0.5	49
2	Hybrid Genetic Algorithm for DNA Sequencing with Errors. Journal of Heuristics, 2002, 8, 495-502.	1.1	38
3	A heuristic managing errors for DNA sequencing. Bioinformatics, 2002, 18, 652-660.	1.8	36
4	DNA Sequencing – Tabu and Scatter Search Combined. INFORMS Journal on Computing, 2004, 16, 232-240.	1.0	24
5	Selected combinatorial problems of computational biology. European Journal of Operational Research, 2005, 161, 585-597.	3.5	22
6	Whole genome assembly from 454 sequencing output via modified DNA graph concept. Computational Biology and Chemistry, 2009, 33, 224-230.	1.1	18
7	Sequencing by hybridization with isothermic oligonucleotide libraries. Discrete Applied Mathematics, 2004, 145, 40-51.	0.5	16
8	An Integrated Approach (CLuster Analysis Integration Method) to Combine Expression Data and Protein – Protein Interaction Networks in Agrigenomics: Application on <i>Arabidopsis thaliana</i> . OMICS A Journal of Integrative Biology, 2014, 18, 155-165.	1.0	16
9	Graph algorithms for DNA sequencing – origins, current models and the future. European Journal of Operational Research, 2018, 264, 799-812.	3.5	16
10	Tabu search algorithm for DNA sequencing by hybridization with isothermic libraries. Computational Biology and Chemistry, 2004, 28, 11-19.	1.1	14
11	On the recognition of de Bruijn graphs and their induced subgraphs. Discrete Mathematics, 2002, 245, 81-92.	0.4	13
12	Evolutionary Approaches to DNA Sequencing with Errors. Annals of Operations Research, 2005, 138, 67-78.	2.6	13
13	Computational complexity of isothermic DNA sequencing by hybridization. Discrete Applied Mathematics, 2006, 154, 718-729.	0.5	13
14	Dealing with repetitions in sequencing by hybridization. Computational Biology and Chemistry, 2006, 30, 313-320.	1.1	11
15	Simplified Partial Digest Problem: Enumerative and Dynamic Programming Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 668-680.	1.9	10
16	Finding Hamiltonian circuits in quasi-adjoint graphs. Discrete Applied Mathematics, 2008, 156, 2573-2580.	0.5	10
17	Combinatorial optimization in DNA mapping – a computational thread of the Simplified Partial Digest Problem. RAIRO - Operations Research, 2005, 39, 227-241.	1.0	9
18	RNA Partial Degradation Problem: Motivation, Complexity, Algorithm. Journal of Computational Biology, 2011, 18, 821-834.	0.8	8

#	ARTICLE	IF	CITATIONS
19	Genome-scale <i>de novo</i> assembly using ALGA. <i>Bioinformatics</i> , 2021, 37, 1644-1651.	1.8	7
20	Classification of deBruijn-based labeled digraphs. <i>Discrete Applied Mathematics</i> , 2018, 234, 86-92.	0.5	6
21	Reduced-by-matching Graphs: Toward Simplifying Hamiltonian Circuit Problem. <i>Fundamenta Informaticae</i> , 2012, 118, 225-244.	0.3	5
22	Complexity Issues in Computational Biology. <i>Fundamenta Informaticae</i> , 2012, 118, 385-401.	0.3	5
23	Dna Sequence Assembly Involving an Acyclic Graph Model. <i>Foundations of Computing and Decision Sciences</i> , 2013, 38, 25-34.	0.5	5
24	A polynomial time equivalence between DNA sequencing and the exact perfect matching problem. <i>Discrete Optimization</i> , 2007, 4, 154-162.	0.6	4
25	The simplified partial digest problem: Approximation and a graph-theoretic model. <i>European Journal of Operational Research</i> , 2011, 208, 142-152.	3.5	4
26	Structural alignment of protein descriptors – a combinatorial model. <i>BMC Bioinformatics</i> , 2016, 17, 383.	1.2	4
27	GRASShopPER – An algorithm for de novo assembly based on GPU alignments. <i>PLoS ONE</i> , 2018, 13, e0202355.	1.1	3
28	On the approximability of the Simplified Partial Digest Problem. <i>Discrete Applied Mathematics</i> , 2009, 157, 3586-3592.	0.5	2
29	High-order statistical compressor for long-term storage of DNA sequencing data. <i>RAIRO - Operations Research</i> , 2016, 50, 351-361.	1.0	2
30	A new algorithm for genome assembly from short reads. , 2008, , .		1
31	Tabu Search for the RNA Partial Degradation Problem. <i>International Journal of Applied Mathematics and Computer Science</i> , 2017, 27, 401-415.	1.5	1
32	Parallel Implementation of the Novel Approach to Genome Assembly. , 2008, , .		0
33	Labeled Graphs in Life Sciences – Two Important Applications. <i>Mechanisms and Machine Science</i> , 2022, , 201-217.	0.3	0
34	Highly Efficient Parallel Approach to the Next-Generation DNA Sequencing. <i>Lecture Notes in Computer Science</i> , 2012, , 262-271.	1.0	0
35	Ties between Graph Theory and Biology. <i>Discrete Mathematics and Its Applications</i> , 2013, , 1559-1579.	0.1	0