Jacek BÅ‚aÅ¼ewicz

List of Publications by Year
in descending order

274 papers	7,649 citations	76326 40 h-index	76900 74 g-index
291 all docs	291 docs citations	291 times ranked	4642 citing authors

#	Article	IF	Citations
1	Learning vector quantization as an interpretable classifier for the detection of SARS-CoV-2 types based on their RNA sequences. Neural Computing and Applications, 2022, 34, 67-78.	5.6	6
2	Two-machine flow shop scheduling with a common due date to maximize total early work. European Journal of Operational Research, 2022, 300, 504-511.	5.7	6
3	RNA World Modeling: A Comparison of Two Complementary Approaches. Entropy, 2022, 24, 536.	2.2	1
4	RNAloops: a database of RNA multiloops. Bioinformatics, 2022, 38, 4200-4205.	4.1	8
5	Alternative algorithms for identical machines scheduling to maximize total early work with a common due date. Computers and Industrial Engineering, 2022, 171, 108386.	6.3	3
6	Mirror scheduling problems with early work and late work criteria. Journal of Scheduling, 2021, 24, 483-487.	1.9	9
7	Semi-online scheduling on two identical machines with a common due date to maximize total early work. Discrete Applied Mathematics, 2021, 290, 71-78.	0.9	17
8	Genome-scale de novo assembly using ALGA. Bioinformatics, 2021, 37, 1644-1651.	4.1	7
9	A Fast Algorithm for Knapsack Problem with Conflict Graph. Asia-Pacific Journal of Operational Research, 2021, 38, .	1.3	1
10	New Perspectives in Scheduling Theory. Journal of Scheduling, 2021, 24, 455-457.	1.9	1
11	Virxicon: a lexicon of viral sequences. Bioinformatics, 2021, 36, 5507-5513.	4.1	6
12	The correctness of large scale analysis of genomic data. Foundations of Computing and Decision Sciences, 2021, 46, 423-436.	1.2	0
13	Fully polynomial time approximation scheme to maximize early work on parallel machines with common due date. European Journal of Operational Research, 2020, 284, 67-74.	5.7	22
14	Multi-agent approach to sequence structure simulation in the RNA World hypothesis. PLoS ONE, 2020, 15, e0238253.	2.5	2
15	Exact and heuristic algorithms for scheduling on two identical machines with early work maximization. Computers and Industrial Engineering, 2020, 144, 106449.	6.3	14
16	Searching for the Origins of Life â€“ Detecting RNA Life Signatures Using Learning Vector Quantization. Advances in Intelligent Systems and Computing, 2020, , 324-333.	0.6	0
17	Recent Results on Computational Molecular Modeling of The Origins of Life. Foundations of Computing and Decision Sciences, 2020, 45, 35-46.	1.2	0
18	RNAvista: a webserver to assess RNA secondary structures with non-canonical base pairs. Bioinformatics, 2019, 35, 152-155.	4.1	11

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19	Online Scheduling. , 2019, , 577-608.		0
20	Open Shop Scheduling. , 2019, , 321-343.		0
21	Prebiotic Soup Components Trapped in Montmorillonite Nanoclay Form New Molecules: Car-Parrinello Ab Initio Simulations. Life, 2019, 9, 46.	2.4	6
22	Flow Shop Scheduling. , 2019, , 271-320.		0
23	Scheduling under Resource Constraints. , 2019, , 475-525.		4
24	Scheduling Imprecise Computations. , 2019, , 527-576.		2
25	Handbook on Scheduling. , 2019, , .		41
26	Detecting life signatures with RNA sequence similarity measures. Journal of Theoretical Biology, 2019, 463, 110-120.	1.7	5
27	Clarification of lower bounds of two-machine flow-shop scheduling to minimize total late work. Engineering Optimization, 2019, 51, 1279-1280.	2.6	6
28	Two-machine flow-shop scheduling to minimize total late work: revisited. Engineering Optimization, 2019, 51, 1268-1278.	2.6	12
29	PUM1 and PUM2 exhibit different modes of regulation for SIAH1 that involve cooperativity with NANOS paralogues. Cellular and Molecular Life Sciences, 2019, 76, 147-161.	5.4	16
30	Cloud Brokering with Bundles: Multi-objective Optimization of Services Selection. Foundations of Computing and Decision Sciences, 2019, 44, 407-426.	1.2	1
31	VirDB: Crowdsourced Database for Evaluation of Dynamical Viral Infection Models. Current Bioinformatics, 2019, 14, 740-748.	1.5	0
32	RNApdbee 2.0: multifunctional tool for RNA structure annotation. Nucleic Acids Research, 2018, 46, W30-W35.	14.5	81
33	Graph algorithms for DNA sequencing â€“ origins, current models and the future. European Journal of Operational Research, 2018, 264, 799-812.	5.7	16
34	GRASShopPERâ€”An algorithm for de novo assembly based on GPU alignments. PLoS ONE, 2018, 13, e0202355.	2.5	3
35	New challenges in scheduling theory. Journal of Scheduling, 2018, 21, 581-582.	1.9	0
36	NPM1 alternative transcripts are upregulated in acute myeloid and lymphoblastic leukemia and their expression level affects patient outcome. Journal of Translational Medicine, 2018, 16, 232.	4.4	15

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37	An integrated model for the transshipment yard scheduling problem. Journal of Scheduling, 2017, 20, 57-65.	1.9	13
38	Understanding Life: A Bioinformatics Perspective. European Review, 2017, 25, 231-245.	0.7	7
39	Tabu Search for the RNA Partial Degradation Problem. International Journal of Applied Mathematics and Computer Science, 2017, 27, 401-415.	1.5	1
40	Complexity of late work minimization in flow shop systems and a particle swarm optimization algorithm for learning effect. Computers and Industrial Engineering, 2017, 111, 176-182.	6.3	27
41	Modeling of the catalytic core of Arabidopsis thaliana Dicer-like 4 protein and its complex with double-stranded RNA. Computational Biology and Chemistry, 2017, 66, 44-56.	2.3	12
42	Simulating the origins of life: The dual role of RNA replicases as an obstacle to evolution. PLoS ONE, 2017, 12, e0180827.	2.5	9
43	Computational prediction of nonenzymatic RNA degradation patterns. Acta Biochimica Polonica, 2017, 63, 745-751.	0.5	4
44	Novel dual discounting functions for the Internet shopping optimization problem: new algorithms. Journal of Scheduling, 2016, 19, 245-255.	1.9	15
45	Computer Representations of Bioinformatics Models. Current Bioinformatics, 2016, 11, 551-560.	1.5	11
46	AmiRNA Designer - new method of artificial miRNA design.. Acta Biochimica Polonica, 2016, 63, 71-77.	0.5	17
47	Hypercycle. PLoS Computational Biology, 2016, 12, e1004853.	3.2	29
48	Exact and heuristic approaches to solve the Internet shopping optimization problem with delivery costs. International Journal of Applied Mathematics and Computer Science, 2016, 26, 391-406.	1.5	10
49	New challenges in scheduling theory. Journal of Scheduling, 2016, 19, 617-618.	1.9	0
50	Recent Advances in Operations Research in Computational Biology, Bioinformatics and Medicine. RAIRO - Operations Research, 2016, 50, 327-330.	1.8	0
51	Automated RNA 3D Structure Prediction with RNAComposer. Methods in Molecular Biology, 2016, 1490, 199-215.	0.9	118
52	G-MAPSEQ â€“ a new method for mapping reads to a reference genome. Foundations of Computing and Decision Sciences, 2016, 41, 123-142.	1.2	4
53	Structural alignment of protein descriptors â€“ a combinatorial model. BMC Bioinformatics, 2016, 17, 383.	2.6	4
54	DomGen-Graph based method for protein domain delineation. RAIRO - Operations Research, 2016, 50, 363-374.	1.8	1

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55	Scheduling on parallel identical machines with late work criterion: Offline and online cases. Journal of Scheduling, 2016, 19, 729-736.	1.9	48
56	Simultaneous detection of mutations and copy number variation of NPM1 in the acute myeloid leukemia using multiplex ligation-dependent probe amplification. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2016, 786, 14-26.	1.0	10
57	Good Laboratory Practice for optimization research. Journal of the Operational Research Society, 2016, 67, 676-689.	3.4	63
58	Algorithms solving the Internet shopping optimization problem with price discounts. Bulletin of the Polish Academy of Sciences: Technical Sciences, 2016, 64, 505-516.	0.8	5
59	New in silico approach to assessing RNA secondary structures with non-canonical base pairs. BMC Bioinformatics, 2015, 16, 276.	2.6	31
60	Cloud Brokering: Current Practices and Upcoming Challenges. IEEE Cloud Computing, 2015, 2, 40-47.	3.9	38
61	RNAssessâ€”a web server for quality assessment of RNA 3D structures. Nucleic Acids Research, 2015, 43, W502-W506.	14.5	24
62	SphereGrinder - reference structure-based tool for quality assessment of protein structural models. , 2015, , .		17
63	Building the library of RNA 3D nucleotide conformations using the clustering approach. International Journal of Applied Mathematics and Computer Science, 2015, 25, 689-700.	1.5	6
64	Automated 3D RNA Structure Prediction Using the RNAComposer Method for Riboswitches1. Methods in Enzymology, 2015, 553, 3-34.	1.0	34
65	A study of scheduling problems with preemptions on multi-core computers with GPU accelerators. Discrete Applied Mathematics, 2015, 196, 72-82.	0.9	1
66	Optimal pathway reconstruction on 3D NMR maps. Discrete Applied Mathematics, 2015, 182, 134-149.	0.9	7
67	New perspectives in scheduling theory. Journal of Scheduling, 2015, 18, 333-334.	1.9	7
68	New challenges in scheduling theory. RAIRO - Operations Research, 2015, 49, 335-337.	1.8	0
69	Reference Alignment Based Methods for Quality Evaluation of Multiple Sequence Alignment - A Survey. Current Bioinformatics, 2014, 9, 44-56.	1.5	2
70	Message from the BusinessClouds 2014 Workshop Chairs. , 2014, , .		0
71	Sorting signal targeting mRNA into hepatic extracellular vesicles. RNA Biology, 2014, 11, 836-844.	3.1	42
72	The Orderly Colored Longest Path Problem â€“ a survey of applications and new algorithms. RAIRO - Operations Research, 2014, 48, 25-51.	1.8	15

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73	RNApdbeeâ€”a webserver to derive secondary structures from pdb files of knotted and unknotted RNAs. Nucleic Acids Research, 2014, 42, W368-W372.	14.5	61
74	Internet shopping with price sensitive discounts. 4or, 2014, 12, 35-48.	1.6	21
75	Recent advances in computational biology, bioinformatics, medicine, and healthcare by modern OR. Central European Journal of Operations Research, 2014, 22, 427-430.	1.8	6
76	Unified encoding for hyper-heuristics with application to bioinformatics. Central European Journal of Operations Research, 2014, 22, 567-589.	1.8	11
77	Multi-agent model of hepatitis C virus infection. Artificial Intelligence in Medicine, 2014, 60, 123-131.	6.5	17
78	How to Efficiently Solve Internet Shopping Optimization Problem with Price Sensitive Discounts?. , 2014, , .		2
79	Guest editorial: â€œNew trends in schedulingâ€. Journal of Scheduling, 2013, 16, 347-348.	1.9	0
80	A hyper-heuristic approach to sequencing by hybridization of DNA sequences. Annals of Operations Research, 2013, 207, 27-41.	4.1	16
81	MLP accompanied beam search for the resonance assignment problem. Journal of Heuristics, 2013, 19, 443-464.	1.4	6
82	-MSA â€” A GPU-based, fast and accurate algorithm for multiple sequence alignment. Journal of Parallel and Distributed Computing, 2013, 73, 32-41.	4.1	44
83	RNAlyzerâ€”novel approach for quality analysis of RNA structural models. Nucleic Acids Research, 2013, 41, 5978-5990.	14.5	22
84	ModeLang: A New Approach for Experts-Friendly Viral Infections Modeling. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-8.	1.3	11
85	Turning data into folds using RNAComposer. , 2013, , .		0
86	G-DNA â€“ a highly efficient multi-GPU/MPI tool for aligning nucleotide reads. Bulletin of the Polish Academy of Sciences: Technical Sciences, 2013, 61, 989-992.	0.8	6
87	Dna Sequence Assembly Involving an Acyclic Graph Model. Foundations of Computing and Decision Sciences, 2013, 38, 25-34.	1.2	5
88	Ties between Graph Theory and Biology. Discrete Mathematics and Its Applications, 2013, , 1559-1579.	0.1	0
89	Automated 3D structure composition for large RNAs. Nucleic Acids Research, 2012, 40, e112-e112.	14.5	564
90	New algorithms for coupled tasks scheduling â€“ a survey. RAIRO - Operations Research, 2012, 46, 335-353.	1.8	16

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91	Reduced-by-matching Graphs: Toward Simplifying Hamiltonian Circuit Problem. Fundamenta Informaticae, 2012, 118, 225-244.	0.4	5
92	G-PAS 2.0 â€“ an improved version of protein alignment tool with an efficient backtracking routine on multiple GPUs. Bulletin of the Polish Academy of Sciences: Technical Sciences, 2012, 60, 491-494.	0.8	5
93	Poseidon: An information retrieval and extraction system for metagenomic marine science. Ecological Informatics, 2012, 12, 10-15.	5.2	7
94	GeVaDSs â€“ decision support system for novel Genetic Vaccine development process. BMC Bioinformatics, 2012, 13, 91.	2.6	4
95	Complexity Issues in Computational Biology. Fundamenta Informaticae, 2012, 118, 385-401.	0.4	5
96	Editorial: new branches, old roots. Journal of Scheduling, 2012, 15, 399-401.	1.9	0
97	A simulated annealing hyper-heuristic methodology for flexible decision support. 4or, 2012, 10, 43-66.	1.6	57
98	Highly Efficient Parallel Approach to the Next-Generation DNA Sequencing. Lecture Notes in Computer Science, 2012, , 262-271.	1.3	0
99	RNA Partial Degradation Problem: Motivation, Complexity, Algorithm. Journal of Computational Biology, 2011, 18, 821-834.	1.6	8
100	Berth and quay crane allocation: a moldable task scheduling model. Journal of the Operational Research Society, 2011, 62, 1189-1197.	3.4	44
101	Combinatorial optimization issues in scheduling. Journal of Scheduling, 2011, 14, 221-223.	1.9	10
102	Some aspects of the anemia of chronic disorders modeled and analyzed by petri net based approach. Bioprocess and Biosystems Engineering, 2011, 34, 581-595.	3.4	19
103	Adaptive memory programming: local search parallel algorithms for phylogenetic tree construction. Annals of Operations Research, 2011, 183, 75-94.	4.1	1
104	Protein alignment algorithms with an efficient backtracking routine on multiple GPUs. BMC Bioinformatics, 2011, 12, 181.	2.6	51
105	On the complexity of the independent set problem in triangle graphs. Discrete Mathematics, 2011, 311, 1670-1680.	0.7	10
106	The simplified partial digest problem: Approximation and a graph-theoretic model. European Journal of Operational Research, 2011, 208, 142-152.	5.7	4
107	A Parallel Branch-and-Bound Approach to the Rectangular Guillotine Strip Cutting Problem. INFORMS Journal on Computing, 2011, 23, 15-25.	1.7	7
108	E-Commerce Evaluation â€“ Multi-Item Internet Shopping. Optimization and Heuristic Algorithms. Operations Research Proceedings: Papers of the Annual Meeting = VortrÃge Der Jahrestagung / DGOR, 2011, , 149-154.	0.1	11

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109	Internet shopping optimization problem. International Journal of Applied Mathematics and Computer Science, 2010, 20, 385-390.	1.5	24
110	Some operations research methods for analyzing protein sequences and structures. Annals of Operations Research, 2010, 175, 9-35.	4.1	12
111	Hepatitis C virus quasispecies in chronically infected children subjected to interferonâ€“ribavirin therapy. Archives of Virology, 2010, 155, 1977-1987.	2.1	18
112	Scheduling of coupled tasks with unit processing times. Journal of Scheduling, 2010, 13, 453-461.	1.9	23
113	Operations Research Models for Computational Biology, Bioinformatics and Medicine. Mathematical Modelling and Algorithms, 2010, 9, 209-211.	0.5	1
114	RNA FRABASE 2.0: an advanced web-accessible database with the capacity to search the three-dimensional fragments within RNA structures. BMC Bioinformatics, 2010, 11, 231.	2.6	130
115	Towards Prediction of HCV Therapy Efficiency. Computational and Mathematical Methods in Medicine, 2010, 11, 185-199.	1.3	9
116	Genetic and Tabu search algorithms for peptide assembly problem. RAIRO - Operations Research, 2010, 44, 153-166.	1.8	2
117	New insights into the human body iron metabolism analyzed by a Petri net based approach. BioSystems, 2009, 96, 104-113.	2.0	9
118	Whole genome assembly from 454 sequencing output via modified DNA graph concept. Computational Biology and Chemistry, 2009, 33, 224-230.	2.3	18
119	Modeling the process of human body iron homeostasis using a variant of timed Petri nets. Discrete Applied Mathematics, 2009, 157, 2221-2231.	0.9	7
120	On the approximability of the Simplified Partial Digest Problem. Discrete Applied Mathematics, 2009, 157, 3586-3592.	0.9	2
121	An assignment walk through 3D NMR spectrum. , 2009, , .		8
122	327 TWO TYPES OF VIRAL QUASISPECIES IDENTIFIED IN CHILDREN SUFFERING FROM CHRONIC HEPATITIS C. Journal of Hepatology, 2009, 50, S127.	3.7	1
123	The Knapsack-Lightening problem and its application to scheduling HRT tasks. Bulletin of the Polish Academy of Sciences: Technical Sciences, 2009, 57, .	0.8	0
124	Translational and structural analysis of the shortest legume ENOD40 gene in Lupinus luteus.. Acta Biochimica Polonica, 2009, 56, .	0.5	8
125	Some remarks on evaluating the quality of the multiple sequence alignment based on the BAliBASE benchmark. International Journal of Applied Mathematics and Computer Science, 2009, 19, 675-678.	1.5	5
126	Metaheuristic approaches for the two-machine flow-shop problem with weighted late work criterion and common due date. Computers and Operations Research, 2008, 35, 574-599.	4.0	40

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127	Finding Hamiltonian circuits in quasi-adjoint graphs. Discrete Applied Mathematics, 2008, 156, 2573-2580.	0.9	10
128	A new algorithm for genome assembly from short reads. , 2008, , .		1
129	Branch and bound algorithm for nonenzymatic RNA degradation. , 2008, , .		0
130	Parallel Implementation of the Novel Approach to Genome Assembly. , 2008, , .		0
131	Web and Grid Technologies in Bioinformatics, Computational and Systems Biology: A Review. Current Bioinformatics, 2008, 3, 10-31.	1.5	11
132	Simplified Partial Digest Problem: Enumerative and Dynamic Programming Algorithms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 668-680.	3.0	10
133	An analysis of the Petri net based model of the human body iron homeostasis process. Computational Biology and Chemistry, 2007, 31, 1-10.	2.3	60
134	A polynomial time equivalence between DNA sequencing and the exact perfect matching problem. Discrete Optimization, 2007, 4, 154-162.	0.9	4
135	ProCKSI: a decision support system for Protein (Structure) Comparison, Knowledge, Similarity and Information. BMC Bioinformatics, 2007, 8, 416.	2.6	48
136	Petri net based model of the body iron homeostasis. Journal of Biomedical Informatics, 2007, 40, 476-485.	4.3	23
137	Selected papers from the Dagstuhl workshop. Journal of Scheduling, 2007, 10, 85-86.	1.9	0
138	A note on the two machine job shop with the weighted late work criterion. Journal of Scheduling, 2007, 10, 87-95.	1.9	25
139	Preemptable malleable task scheduling problem. IEEE Transactions on Computers, 2006, 55, 486-490.	3.4	44
140	DNA Sequencing by Hybridization via Genetic Search. Operations Research, 2006, 54, 1185-1192.	1.9	16
141	Computational complexity of isothermic DNA sequencing by hybridization. Discrete Applied Mathematics, 2006, 154, 718-729.	0.9	13
142	Dealing with repetitions in sequencing by hybridization. Computational Biology and Chemistry, 2006, 30, 313-320.	2.3	11
143	Some operations research methods for analyzing protein sequences and structures. 4or, 2006, 4, 91-123.	1.6	11
144	Coordination number prediction using learning classifier systems. , 2006, , .		16

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145	From HP Lattice Models to Real Proteins: Coordination Number Prediction Using Learning Classifier Systems. Lecture Notes in Computer Science, 2006, , 208-220.	1.3	11
146	PREDICTION OF RESIDUE EXPOSURE AND CONTACT NUMBER FOR SIMPLIFIED HP LATTICE MODEL PROTEINS USING LEARNING CLASSIFIER SYSTEMS. , 2006, , .		3
147	Human fertility protein PUMILIO2 interacts in vitro with testis mRNA encoding Cdc42 effector 3 (CEP3). Reproductive Biology, 2006, 6, 103-13.	1.9	6
148	The two-machine flow-shop problem with weighted late work criterion and common due date. European Journal of Operational Research, 2005, 165, 408-415.	5.7	52
149	Multistage isothermic sequencing by hybridization. Computational Biology and Chemistry, 2005, 29, 69-77.	2.3	3
150	An improved approximation algorithm for the single machine total completion time scheduling problem with availability constraints. European Journal of Operational Research, 2005, 161, 3-10.	5.7	109
151	Selected combinatorial problems of computational biology. European Journal of Operational Research, 2005, 161, 585-597.	5.7	22
152	Recent advances in scheduling in computer and manufacturing systems. European Journal of Operational Research, 2005, 164, 573-574.	5.7	11
153	Application of tabu search strategy for finding low energy structure of protein. Artificial Intelligence in Medicine, 2005, 35, 135-145.	6.5	23
154	A novel representation of graph structures in web mining and data analysis. Omega, 2005, 33, 65-71.	5.9	10
155	Predicting secondary structures of proteins. IEEE Engineering in Medicine and Biology Magazine, 2005, 24, 88-94.	0.8	8
156	A comparison of solution procedures for two-machine flow shop scheduling with late work criterion. Computers and Industrial Engineering, 2005, 49, 611-624.	6.3	33
157	Evolutionary Approaches to DNA Sequencing with Errors. Annals of Operations Research, 2005, 138, 67-78.	4.1	13
158	Metaheuristics for Late Work Minimization in Two-Machine Flow Shop with Common Due Date. Lecture Notes in Computer Science, 2005, , 222-234.	1.3	4
159	Homologous Crossovers among Molecules of Brome Mosaic Bromovirus RNA1 or RNA2 Segments In Vivo. Journal of Virology, 2005, 79, 5732-5742.	3.4	45
160	RNA tertiary structure determination: NOE pathways construction by tabu search. Bioinformatics, 2005, 21, 2356-2361.	4.1	18
161	Tabu Search Method for Determining Sequences of Amino Acids in Long Polypeptides. Lecture Notes in Computer Science, 2005, , 22-32.	1.3	2
162	NMR Analysis of RNA Bulged Structures: Tabu Search Application in NOE Signal Assignment. , 2005, , .		1

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163	Combinatorial optimization in DNA mapping â€" a computational thread of the Simplified Partial Digest Problem. RAIRO - Operations Research, 2005, 39, 227-241.	1.8	9
164	Parallel tabu search approaches for two-dimensional cutting. Parallel Processing Letters, 2004, 14, 23-32.	0.6	16
165	Scheduling Malleable Tasks on Parallel Processors to Minimize the Makespan. Annals of Operations Research, 2004, 129, 65-80.	4.1	58
166	Open shop scheduling problems with late work criteria. Discrete Applied Mathematics, 2004, 134, 1-24.	0.9	50
167	Sequencing by hybridization with isothermic oligonucleotide libraries. Discrete Applied Mathematics, 2004, 145, 40-51.	0.9	16
168	Tabu search algorithm for DNA sequencing by hybridization with isothermic libraries. Computational Biology and Chemistry, 2004, 28, 11-19.	2.3	14
169	An Algorithm for an Automatic NOE Pathways Analysis of 2D NMR Spectra of RNA Duplexes. Journal of Computational Biology, 2004, 11, 163-179.	1.6	15
170	Parallel DNA sequence assembly. , 2004, , .		2
171	DNA Sequencingâ€"Tabu and Scatter Search Combined. INFORMS Journal on Computing, 2004, 16, 232-240.	1.7	24
172	A TABU SEARCH STRATEGY FOR FINDING LOW ENERGY STRUCTURES OF PROTEINS IN HP-MODEL*. Computational Methods in Science and Technology, 2004, 10, 7-19.	0.3	15
173	Parallel Algorithms for Evolutionary History Reconstruction. Lecture Notes in Computer Science, 2004, , 1138-1145.	1.3	0
174	Complexity of DNA sequencing by hybridization. Theoretical Computer Science, 2003, 290, 1459-1473.	0.9	49
175	Scheduling multiprocessor tasks on parallel processors with limited availability. European Journal of Operational Research, 2003, 149, 377-389.	5.7	22
176	New Algorithm for the Simplified Partial Digest Problem. Lecture Notes in Computer Science, 2003, , 95-110.	1.3	1
177	DNA Based Algorithms for Some Scheduling Problems. Lecture Notes in Computer Science, 2003, , 673-683.	1.3	1
178	Scheduling production tasks in a two-stage FMS. International Journal of Production Research, 2002, 40, 4341-4352.	7.5	3
179	A heuristic managing errors for DNA sequencing. Bioinformatics, 2002, 18, 652-660.	4.1	36
180	Scheduling multiprocessor tasks on two parallel processors. RAIRO - Operations Research, 2002, 36, 37-51.	1.8	9

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181	Scheduling jobs in open shops with limited machine availability. RAIRO - Operations Research, 2002, 36, 149-156.	1.8	3
182	The complexity of two group scheduling problems. Journal of Scheduling, 2002, 5, 477-485.	1.9	17
183	Two-machine flow shops with limited machine availability. European Journal of Operational Research, 2002, 136, 528-540.	5.7	105
184	Linear and quadratic algorithms for scheduling chains and opposite chains. European Journal of Operational Research, 2002, 137, 248-264.	5.7	5
185	Review of properties of different precedence graphs for scheduling problems. European Journal of Operational Research, 2002, 142, 435-443.	5.7	16
186	On the recognition of de Bruijn graphs and their induced subgraphs. Discrete Mathematics, 2002, 245, 81-92.	0.7	13
187	Hybrid Genetic Algorithm for DNA Sequencing with Errors. Journal of Heuristics, 2002, 8, 495-502.	1.4	38
188	DNA Sequencing, Eulerian Graphs, and the Exact Perfect Matching Problem. Lecture Notes in Computer Science, 2002, , 13-24.	1.3	4
189	A New Parallel Approach for Multi-dimensional Packing Problems. Lecture Notes in Computer Science, 2002, , 194-201.	1.3	1
190	Tabu Search for Two-Dimensional Irregular Cutting. Operations Research/ Computer Science Interfaces Series, 2002, , 101-128.	0.3	3
191	A note on the complexity of scheduling coupled tasks on a single processor. Journal of the Brazilian Computer Society, 2001, 7, 23-26.	1.3	5
192	Production planning and scheduling in flexible assembly systems. Tadeusz Sawik, Springer, Berlin. ISBN 3-540-64998-0. Journal of Scheduling, 2001, 4, 66-67.	1.9	0
193	Heuristic algorithms for the two-machine flowshop with limited machine availability. Omega, 2001, 29, 599-608.	5.9	57
194	Construction of DNA restriction maps based on a simplified experiment. Bioinformatics, 2001, 17, 398-404.	4.1	25
195	Scheduling Computer and Manufacturing Processes. , 2001, , .		147
196	Extension of Disjunctive Graph Model for Job Shop Scheduling Problem. Operations Research Proceedings: Papers of the Annual Meeting = VortrÃge Der Jahrestagung / DGOR, 2001, , 359-365.	0.1	0
197	Communication Delays and Multiprocessor Tasks. , 2001, , 205-246.		0
198	Scheduling on Parallel Processors. , 2001, , 137-203.		0

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199	Scheduling in Job Shops. , 2001, , 273-315.		0
200	Scheduling under Resource Constraints. , 2001, , 317-365.		1
201	New trends on scheduling in parallel and distributed systems. Parallel Computing, 2000, 26, 1061-1063.	2.1	0
202	Scheduling preemptable tasks on parallel processors with limited availability. Parallel Computing, 2000, 26, 1195-1211.	2.1	32
203	Tabu search for DNA sequencing with false negatives and false positives. European Journal of Operational Research, 2000, 125, 257-265.	5.7	43
204	The disjunctive graph machine representation of the job shop scheduling problem. European Journal of Operational Research, 2000, 127, 317-331.	5.7	69
205	Total Late Work Criteria for Shop Scheduling Problems. , 2000, , 354-359.		10
206	Management of Resources in Parallel Systems. , 2000, , 263-341.		5
207	DNA Sequencing With Positive and Negative Errors. Journal of Computational Biology, 1999, 6, 113-123.	1.6	55
208	Scheduling a divisible task in a two-dimensional toroidal mesh. Discrete Applied Mathematics, 1999, 94, 35-50.	0.9	40
209	On some properties of DNA graphs. Discrete Applied Mathematics, 1999, 98, 1-19.	0.9	48
210	Divisible task scheduling â€“ Concept and verification. Parallel Computing, 1999, 25, 87-98.	2.1	80
211	Resource Constrained Chain Scheduling of UET Jobs on Two Machines. Operations Research, 1998, 46, 742-746.	1.9	1
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