Alexander Zelikovsky

List of Publications by Year
in descending order

262 papers	5,136 citations	172207 29 h-index	149479 56 g-index
327 all docs	327 docs citations	327 times ranked	4282 citing authors

#	Article	IF	Citations
1	Eleven grand challenges in single-cell data science. Genome Biology, 2020, 21, 31.	3.8	742
2	An 11/6-approximation algorithm for the network steiner problem. Algorithmica, 1993, 9, 463-470.	1.0	284
3	Tighter Bounds for Graph Steiner Tree Approximation. SIAM Journal on Discrete Mathematics, 2005, 19, 122-134.	0.4	236
4	Estimation of alternative splicing isoform frequencies from RNA-Seq data. Algorithms for Molecular Biology, 2011, 6, 9.	0.3	155
5	New Approximation Algorithms for the Steiner Tree Problems. Journal of Combinatorial Optimization, 1997, 1, 47-65.	0.8	139
6	Systematic benchmarking of omics computational tools. Nature Communications, 2019, 10, 1393.	5.8	111
7	Power efficient monitoring management in sensor networks. , 0, , .		110
8	Network Lifetime and Power Assignment in ad hoc Wireless Networks. Lecture Notes in Computer Science, 2003, , 114-126.	1.0	105
9	Efficient error correction for next-generation sequencing of viral amplicons. BMC Bioinformatics, 2012, 13, S6.	1.2	95
10	A series of approximation algorithms for the acyclic directed steiner tree problem. Algorithmica, 1997, 18, 99-110.	1.0	93
11	Inferring viral quasispecies spectra from 454 pyrosequencing reads. BMC Bioinformatics, 2011, 12, S1.	1.2	89
12	Filling algorithms and analyses for layout density control. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 1999, 18, 445-462.	1.9	88
13	Selecting Forwarding Neighbors in Wireless Ad Hoc Networks. Mobile Networks and Applications, 2004, 9, 101-111.	2.2	84
14	Optimization of linear placements for wirelength minimization with free sites. , 1999, , .		81
15	Symmetric Connectivity with Minimum Power Consumption in Radio Networks. , 2002, , 119-130.		80
16	Power Efficient Range Assignment for Symmetric Connectivity in Static Ad Hoc Wireless Networks. Wireless Networks, 2006, 12, 287-299.	2.0	71
17	On wirelength estimations for row-based placement. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 1999, 18, 1265-1278.	1.9	65
18	The moving-target traveling salesman problem. Journal of Algorithms, 2003, 49, 153-174.	0.9	61

#	ARTICLE	IF	CITATIONS
19	An improved approximation scheme for the Group Steiner Problem. Networks, 2001, 37, 8-20.	1.6	56
20	QUENTIN: reconstruction of disease transmissions from viral quasispecies genomic data. Bioinformatics, 2018, 34, 163-170.	1.8	54
21	Epidemiological data analysis of viral quasispecies in the next-generation sequencing era. Briefings in Bioinformatics, 2021, 22, 96-108.	3.2	54
22	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. Journal of Computational Biology, 2007, 14, 927-949.	0.8	52
23	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51
24	Area fill synthesis for uniform layout density. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2002, 21, 1132-1147.	1.9	48
25	Maximum Lifetime of Sensor Networks with Adjustable Sensing Range. , 0, , .		48
26	Accurate viral population assembly from ultra-deep sequencing data. Bioinformatics, 2014, 30, i329-i337.	1.8	48
27	Bootstrap-based differential gene expression analysis for RNA-Seq data with and without replicates. BMC Genomics, 2014, 15, S2.	1.2	48
28	Practical iterated fill synthesis for CMP uniformity. , 2000, , .		45
29	Handbook of Approximation Algorithms and Metaheuristics. Computer Journal, 2010, 53, 1338-1339.	1.5	45
30	Power efficient range assignment in ad-hoc wireless networks. , 0, , .		44
31	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. Nature Communications, 2020, 11, 3126.	5.8	44
32	A faster approximation algorithm for the steiner tree problem in graphs. Information Processing Letters, 1993, 46, 79-83.	0.4	42
33	ScaffMatch: scaffolding algorithm based on maximum weight matching. Bioinformatics, 2015, 31, 2632-2638.	1.8	41
34	Fast bootstrapping-based estimation of confidence intervals of expression levels and differential expression from RNA-Seq data. Bioinformatics, 2017, 33, 3302-3304.	1.8	40
35	2SNP: scalable phasing based on 2-SNP haplotypes. Bioinformatics, 2006, 22, 371-373.	1.8	38
36	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. Nucleic Acids Research, 2021, 49, e102-e102.	6.5	36

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37	Unlocking capacities of genomics for the COVID-19 response and future pandemics. Nature Methods, 2022, 19, 374-380.	9.0	35
38	MLR-tagging: informative SNP selection for unphased genotypes based on multiple linear regression. Bioinformatics, 2006, 22, 2558-2561.	1.8	34
39	A note on the MST heuristic for bounded edge-length Steiner trees with minimum number of Steiner points. Information Processing Letters, 2000, 75, 165-167.	0.4	32
40	HCV Quasispecies Assembly Using Network Flows. , 2008, , 159-170.		29
41	Inference of genetic relatedness between viral quasispecies from sequencing data. BMC Genomics, 2017, 18, 918.	1.2	26
42	Benchmarking of computational error-correction methods for next-generation sequencing data. Genome Biology, 2020, 21, 71.	3.8	26
43	Provably good global buffering using an available buffer block plan. , 0, , .		25
44	Informative SNP Selection Methods Based on SNP Prediction. IEEE Transactions on Nanobioscience, 2007, 6, 60-67.	2.2	25
45	Optimal phase conflict removal for layout of dark field alternating phase shifting masks. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2000, 19, 175-187.	1.9	24
46	The Polymatroid Steiner Problems. Journal of Combinatorial Optimization, 2005, 9, 281-294.	0.8	24
47	Highly scalable algorithms for rectilinear and octilinear Steiner trees. , 0, , .		23
48	MetNetAligner: a web service tool for metabolic network alignments. Bioinformatics, 2009, 25, 1989-1990.	1.8	22
49	Fast yield driven fracture for variable shaped beam mask writing. , 2006, , .		21
50	Provably good routing tree construction with multi-port terminals. , 1997, , .		20
51	Evaluation of placement techniques for DNA probe array layout. , 2003, , .		20
52	Multi-project reticle floorplanning and wafer dicing. , 2004, , .		20
53	Reconstruction of viral population structure from next-generation sequencing data using multicommodity flows. BMC Bioinformatics, 2013, 14, S2.	1.2	20
54	Searching High-Order SNP Combinations for Complex Diseases Based on Energy Distribution Difference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 695-704.	1.9	20

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55	Hierarchical dummy fill for process uniformity. , 2001, , .		19
56	Minimum buffered routing with bounded capacitive load for slew rate and reliability control. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2003, 22, 241-253.	1.9	19
57	On the skew-bounded minimum-buffer routing tree problem. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2003, 22, 937-945.	1.9	19
58	Energy Efficiency of Load Balancing in MANET Routing Protocols. , 0, , .		19
59	Optimal phase conflict removal for layout of dark field alternating phase shifting masks. , 1999, , .		18
60	Yield- and cost-driven fracturing for variable shaped-beam mask writing. , 2004, , .		18
61	DEEPS: Deterministic Energy-Efficient Protocol for Sensor networks. , 0, , .		18
62	Combinatorial Search Methods for Multi-SNP Disease Association. , 2006, 2006, 5802-5.		18
63	New and exact filling algorithms for layout density control. , 1999, , .		17
64	Provably good global buffering by multi-terminal multicommodity flow approximation. , 2001, , .		17
65	Border Length Minimization in DNA Array Design*. Lecture Notes in Computer Science, 2002, , 435-448.	1.0	17
66	Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data. Lecture Notes in Computer Science, 2010, , 202-214.	1.0	17
67	A Practical Transistor-Level Dual Threshold Voltage Assignment Methodology. , 0, , .		16
68	Computational framework for next-generation sequencing of heterogeneous viral populations using combinatorial pooling. Bioinformatics, 2015, 31, 682-690.	1.8	16
69	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads. , 2012, , .		15
70	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. BMC Genomics, 2014, 15, S7.	1.2	15
71	Reconstructing viral quasispecies from NGS amplicon reads. In Silico Biology, 2011, 11, 237-49.	0.4	15
72	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. Journal of Computational Biology, 2017, 24, 558-570.	0.8	14

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73	From Alpha to Zeta: Identifying Variants and Subtypes of SARS-CoV-2 Via Clustering. Journal of Computational Biology, 2021, 28, 1113-1129.	0.8	14
74	Tag SNP Selection Based on Multivariate Linear Regression. Lecture Notes in Computer Science, 2006, , 750-757.	1.0	14
75	Bright-Field AAPSM Conflict Detection and Correction. , 0, , .		13
76	Fast and Efficient Bright-Field AAPSM Conflict Detection and Correction. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2007, 26, 115-126.	1.9	13
77	Design and Validation of Methods Searching for Risk Factors in Genotype Case-Control Studies. Journal of Computational Biology, 2008, 15, 81-90.	0.8	13
78	Optimal Testing of Digital Microfluidic Biochips. INFORMS Journal on Computing, 2011, 23, 518-529.	1.0	13
79	GaussianCpG: a Gaussian model for detection of CpG island in human genome sequences. BMC Genomics, 2017, 18, 392.	1.2	13
80	Sensory Nerves Impede the Formation of Tertiary Lymphoid Structures and Development of Protective Antimelanoma Immune Responses. Cancer Immunology Research, 2022, 10, 1141-1154.	1.6	13
81	A New Approximation Algorithm for Finding Heavy Planar Subgraphs. Algorithmica, 2003, 36, 179-205.	1.0	12
82	Association testing by haplotype-sharing methods applicable to whole-genome analysis. BMC Proceedings, 2007, 1, S129.	1.8	12
83	Antibody Response to Lyme Disease Spirochetes in the Context of VlsE-Mediated Immune Evasion. Infection and Immunity, 2017, 85, .	1.0	12
84	Using earth mover's distance for viral outbreak investigations. BMC Genomics, 2020, 21, 582.	1.2	12
85	Engineering a scalable placement heuristic for DNA probe arrays. , 2003, , .		12
86	An 11/6-Approximation Algorithm for the Steiner Problem on Graphs. Annals of Discrete Mathematics, 1992, 51, 351-354.	1.4	11
87	Faster Approximation Algorithms for the Rectilinear Steiner Tree Problem. Discrete and Computational Geometry, 1997, 18, 93-109.	0.4	11
88	Node caching enhancement of reactive ad hoc routing protocols. , 0, , .		11
89	Viral quasispecies reconstruction from amplicon 454 pyrosequencing reads. , 2011, , .		11
90	Inferring metabolic pathway activity levels from RNA-Seq data. BMC Genomics, 2016, 17, 542.	1.2	11

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91	Inference of clonal selection in cancer populations using single-cell sequencing data. Bioinformatics, 2019, 35, i398-i407.	1.8	11
92	Combinatorial Methods for Disease Association Search and Susceptibility Prediction. Lecture Notes in Computer Science, 2006, , 286-297.	1.0	11
93	Scalable Heuristics for Design of DNA Probe Arrays. Journal of Computational Biology, 2004, 11, 429-447.	0.8	10
94	Linear Reduction for Haplotype Inference. Lecture Notes in Computer Science, 2004, , 242-253.	1.0	10
95	New multilevel and hierarchical algorithms for layout density control. , 1999, , .		9
96	Provably good global buffering by generalized multiterminal multicommodity flow approximation. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2002, 21, 263-274.	1.9	9
97	Linear reduction method for predictive and informative tag SNP selection. International Journal of Bioinformatics Research and Applications, 2005, 1, 249.	0.1	9
98	Improved Approximation Algorithms for the Quality of Service Multicast Tree Problem. Algorithmica, 2005, 42, 109-120.	1.0	9
99	Computer-Aided Optimization of DNA Array Design and Manufacturing. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2006, 25, 305-320.	1.9	9
100	Fast Alignments of Metabolic Networks. , 2008, , .		9
101	2SNP: Scalable Phasing Method for Trios and Unrelated Individuals. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 313-318.	1.9	9
102	Clustering Based Identification of SARS-CoV-2 Subtypes. Lecture Notes in Computer Science, 2021, , 127-141.	1.0	9
103	Quantitative differences between intra-host HCV populations from persons with recently established and persistent infections. Virus Evolution, 2021, 7, veaa103.	2.2	9
104	Approaching the 5/4 â€" approximation for rectilinear Steiner trees. Lecture Notes in Computer Science, 1994, , 60-71.	1.0	8
105	Monte-Carlo algorithms for layout density control. , 0, , .		8
106	Minimum-buffered routing of non-critical nets for slew rate and reliability control. , 0, , .		8
107	Energy-efficient continuous and event-driven monitoring. , 0, , .		8
108	Compressible area fill synthesis. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2005, 24, 1169-1187.	1.9	8

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109	A Combinatorial Method for Predicting Genetic Susceptibility to Complex Diseases. , 2005, 2006, 224-7.		8
110	Genotype susceptibility and integrated risk factors for complex diseases. , 0, , .		8
111	Risk Factor Searching Heuristics for SNP Case-Control Studies. , 2007, , .		8
112	Influence of symbiont-produced bioactive natural products on holobiont fitness in the marine bryozoan, Bugula neritina via protein kinase C (PKC). Marine Biology, 2016, 163, 1.	0.7	8
113	Identification of Surface Epitopes Associated with Protection against Highly Immune-Evasive VlsE-Expressing Lyme Disease Spirochetes. Infection and Immunity, 2018, 86, .	1.0	8
114	Computational Approaches to Detect Illicit Drug Ads and Find Vendor Communities Within Social Media Platforms. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 180-191.	1.9	8
115	New graph bipartizations for double-exposure, bright field alternating phase-shift mask layout. , 0, , .		7
116	Yield-driven multi-project reticle design and wafer dicing. , 2005, 5992, 1247.		7
117	Algorithms for Multiplex PCR Primer Set Selection with Amplification Length Constraints. , 2007, , 241-258.		7
118	Practical Approximation Algorithms for Zero- and Bounded-Skew Trees. SIAM Journal on Discrete Mathematics, 2001, 15, 97-111.	0.4	6
119	Homomorphisms of Multisource Trees into Networks with Applications to Metabolic Pathways. , 2007, , .		6
120	Advances in Hidden Markov Models for Sequence Annotation. , 2007, , 55-91.		6
121	Scalable genome scaffolding using integer linear programming. , 2012, , .		6
122	ILP-based maximum likelihood genome scaffolding. BMC Bioinformatics, 2014, 15, S9.	1.2	6
123	HapIso: An Accurate Method for the Haplotype- Specific Isoforms Reconstruction From Long Single-Molecule Reads. IEEE Transactions on Nanobioscience, 2017, 16, 108-115.	2.2	6
124	Identification of cancer-specific motifs in mimotope profiles of serum antibody repertoire. BMC Bioinformatics, 2017, 18, 244.	1.2	6
125	Repeat-aware evaluation of scaffolding tools. Bioinformatics, 2018, 34, 2530-2537.	1.8	6
126	New Zealand White Rabbits Effectively Clear Borrelia burgdorferi B31 despite the Bacteriumâ€™s Functional<i>vlsE</i>Antigenic Variation System. Infection and Immunity, 2019, 87, .	1.0	6

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127	On Approximation of the Power-p and Bottleneck Steiner Trees. Combinatorial Optimization, 2000, , 117-135.	0.7	6
128	1.25-Approximation Algorithm for Steiner Tree Problem with Distances 1 and 2. Lecture Notes in Computer Science, 2009, , 86-97.	1.0	6
129	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. In Silico Biology, 2011, 11, 251-61.	0.4	6
130	Design flow enhancements for DNA arrays. , 0, , .		5
131	Linear reduction methods for tag SNP selection. , 2004, 2004, 2840-3.		5
132	Collaborative Topology Control for Lifetime Maximization. , 2011, , .		5
133	Maximum Series-Parallel Subgraph. Algorithmica, 2012, 63, 137-157.	1.0	5
134	kGEM: An EM-based algorithm for local reconstruction of viral quasispecies. , 2013, , .		5
135	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks. International Journal of Networking and Computing, 2013, 3, 55-74.	0.3	5
136	Delineating Surface Epitopes of Lyme Disease Pathogen Targeted by Highly Protective Antibodies of New Zealand White Rabbits. Infection and Immunity, 2019, 87, .	1.0	5
137	Faster approximation algorithms for the rectilinear steiner tree problem. Lecture Notes in Computer Science, 1993, , 533-542.	1.0	5
138	SyD: A Middleware Testbed for Collaborative Applications over Small Heterogeneous Devices and Data Stores. Lecture Notes in Computer Science, 2004, , 352-371.	1.0	5
139	Improved Approximation Algorithms for the Quality of Service Steiner Tree Problem. Lecture Notes in Computer Science, 2003, , 401-411.	1.0	4
140	Multiple Linear Regression for Index SNP Selection on Unphased Genotypes. , 2006, 2006, 5759-62.		4
141	Fill for Shallow Trench Isolation CMP. IEEE/ACM International Conference on Computer-Aided Design, Digest of Technical Papers, 2006, , .	0.0	4
142	Fast estimation of genetic relatedness between members of heterogeneous populations of closely related genomic variants. BMC Bioinformatics, 2018, 19, 360.	1.2	4
143	The T-join Problem in Sparse Graphs: Applications to Phase Assignment Problem in VLSI Mask Layout. Lecture Notes in Computer Science, 1999, , 25-36.	1.0	4
144	Mean Square Residue Biclustering with Missing Data and Row Inversions. Lecture Notes in Computer Science, 2009, , 28-39.	1.0	4

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145	Analysis of heterogeneous genomic samples using image normalization and machine learning. BMC Genomics, 2020, 21, 405.	1.2	4
146	Inference of mutability landscapes of tumors from single cell sequencing data. PLoS Computational Biology, 2020, 16, e1008454.	1.5	4
147	New approximation algorithms for routing with multiport terminals. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2000, 19, 1118-1128.	1.9	3
148	<title>Monte-Carlo methods for chemical-mechanical planarization on multiple-layer and dual-material models</title>. , 2002, , .		3
149	Primal-dual algorithms for QoS multimedia multicast. , 0, , .		3
150	Phasing and Missing Data Recovery in Family Trios. Lecture Notes in Computer Science, 2005, , 1011-1019.	1.0	3
151	Hybrid SVM kernels for protein secondary structure prediction. , 0, , .		3
152	Computational Approaches to Predict Protein-Protein and Domain-Domain Interactions. , 2007, , 465-491.		3
153	Enhanced Design Flow and Optimizations for Multiproject Wafers. IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems, 2007, 26, 301-311.	1.9	3
154	Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies. , 2007, , .		3
155	Efficient Alignments of Metabolic Networks with Bounded Treewidth. , 2010, , .		3
156	RNA-Seq based discovery and reconstruction of unannotated transcripts in partially annotated genomes. , 2011, , .		3
157	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data. , 2014, , .		3
158	ScaffMatch: Scaffolding Algorithm Based on Maximum Weight Matching. Lecture Notes in Computer Science, 2015, , 222-223.	1.0	3
159	Assessment of HCV infection stage as recent or chronic using multi-parameter analysis and machine learning. , 2017, , .		3
160	Automated quality control for a molecular surveillance system. BMC Bioinformatics, 2018, 19, 358.	1.2	3
161	A study of optimal cost-skew tradeoff and remaining suboptimality in interconnect tree constructions. , 2018, , .		3
162	QoS Multimedia Multicast Routing. Chapman & Hall/CRC Computer and Information Science Series, 2007, , 71-1-71-16.	0.4	3

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163	Minimum Steiner Tree Construction*. , 2008, , .		3
164	Toward an easy programming environment for implementing mobile applications: a fleet application case study using SyD middleware. , 0, , .		2
165	Area fill generation with inherent data volume reduction. , 0, , .		2
166	Consolidating software tools for DNA microarray design and manufacturing. , 2004, 2006, 172-5.		2
167	Family trio phasing and missing data recovery. International Journal of Bioinformatics Research and Applications, 2005, 1, 221.	0.1	2
168	Haplotype tagging using support vector machines. , 0, , .		2
169	Topological Indices in Combinatorial Chemistry. , 2007, , 417-438.		2
170	Classification Accuracy Based Microarray Missing Value Imputation. , 2007, , 303-327.		2
171	Scheduling Bursts Using Interval Graphs in Optical Burst Switching Networks. , 2009, , .		2
172	SILP3: Maximum likelihood approach to scaffolding. , 2014, , .		2
173	Detection of genetic relatedness between viral samples using EM-based clustering of next-generation sequencing data. , 2014, , .		2
174	GaussianCpG: A Gaussian model for detection of human CpG island. , 2015, , .		2
175	Predicting Opioid Epidemic by Using Twitter Data. Lecture Notes in Computer Science, 2018, , 314-318.	1.0	2
176	Pipeline for Analyzing Activity of Metabolic Pathways in Planktonic Communities Using Metatranscriptomic Data. Journal of Computational Biology, 2021, 28, 842-855.	0.8	2
177	Bottleneck Steiner Tree Problems. , 2008, , 311-313.		2
178	Modeling the Spread of HIV and HCV Infections Based on Identification and Characterization of High-Risk Communities Using Social Media. Lecture Notes in Computer Science, 2017, , 425-430.	1.0	2
179	Scalable Reconstruction of SARS-CoV-2 Phylogeny with Recurrent Mutations. Journal of Computational Biology, 2021, 28, 1130-1141.	0.8	2
180	Practical Approximation Algorithms for Separable Packing Linear Programs. Lecture Notes in Computer Science, 2001, , 325-337.	1.0	2

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181	Auctions with Buyer Preferences. IFIP Advances in Information and Communication Technology, 2002, , 223-238.	0.5	2
182	Phasing of 2-SNP Genotypes Based on Non-random Mating Model. Lecture Notes in Computer Science, 2006, , 767-774.	1.0	2
183	Maximum Likelihood Estimation of Incomplete Genomic Spectrum from HTS Data. Lecture Notes in Computer Science, 2011, , 213-224.	1.0	2
184	Improved approximation bounds for the group Steiner problem. , 0, , .		1
185	Evaluation of the new OASIS format for layout fill compression. , 0, , .		1
186	Multi-project reticle design and wafer dicing under uncertain demand. , 2006, , .		1
187	Meta-Analysis of Microarray Data. , 2007, , 329-352.		1
188	Analytical and Algorithmic Methods for Haplotype Frequency Inference: What do they Tell Us?. , 2007, , 373-394.		1
189	Dynamic Programming Algorithms for Biological Sequence and Structure Comparison. , 2007, , 7-28.		1
190	Sorting- and FFT-Based Techniques in the Discovery of Biopatterns. , 2007, , 93-115.		1
191	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks. , 2012, , .		1
192	TRIP: a method for novel transcript reconstruction from paired-end RNA-seq reads. BMC Bioinformatics, 2012, 13, .	1.2	1
193	Optimizing pooling strategies for the massive next-generation sequencing of viral samples. , 2013, , .		1
194	Monte-Carlo Regression algorithm for isoform frequency estimation from RNA-Seq data. , 2013, , .		1
195	Deterministic regression algorithm for transcriptome frequency estimation. , 2014, , .		1
196	Metabolic Analysis of Metatranscriptomic Data from Planktonic Communities. Lecture Notes in Computer Science, 2017, , 396-402.	1.0	1
197	Detecting Illicit Drug Ads in Google+ Using Machine Learning. Lecture Notes in Computer Science, 2019, , 171-179.	1.0	1
198	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. Lecture Notes in Computer Science, 2016, , 164-175.	1.0	1

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199	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. Lecture Notes in Computer Science, 2007, , 407-419.	1.0	1
200	Genotype Tagging with Limited Overfitting. Lecture Notes in Computer Science, 2009, , 1-12.	1.0	1
201	The associative-skew clock routing problem. , 0, , .		0
202	Message from the SAWN 2006 Workshop Co-chairs. , 2006, , .		0
203	A Novel Strategy of Coalition Evolvement Based on Interest. , 2007, , .		0
204	Efficient Algorithms for Structural Recall in Databases. , 2007, , 439-463.		0
205	Educating Biologists in the 21st Century: Bioinformatics Scientists versus Bioinformatics Technicians. , 2007, , 1-5.		0
206	Efficient Combinatorial Algorithms for DNA Sequence Processing. , 2007, , 223-239.		0
207	Recent Developments in Alignment and Motif Finding for Sequences and Networks. , 2007, , 259-276.		0
208	Algorithms for Oligonucleotide Microarray Layout. , 2007, , 277-301.		0
209	Graph Theoretical Approaches to Delineate Dynamics of Biological Processes. , 2007, , 29-54.		0
210	Message from the Conference and the Workshop Chairs. , 2007, , .		0
211	Introduction to the Special Section on Computational Nanobioscience. IEEE Transactions on Nanobioscience, 2007, 6, 1-3.	2.2	0
212	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 513-514.	1.9	0
213	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 321-322.	1.9	0
214	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 178-179.	1.9	0
215	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 577-578.	1.9	0
216	WS-GraphMatching. , 2010, , .		0

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217	Fixed-Parameter Tractable Combinatorial Algorithms for Metabolic Networks Alignments. , 2010, , .		0
218	Invited: Metabolic network alignments. , 2011, , .		0
219	Poster: Haplotype discovery from high-throughput sequencing data. , 2011, , .		0
220	Poster: Scaffolding draft genomes using paired sequencing data. , 2011, , .		0
221	Poster: ViSpA: Viral spectrum assembling method. , 2011, , .		0
222	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 865-866.	1.9	0
223	Poster: Accurate scaffolding of large genomes using integer programming and Non-Serial Dynamic Programming. , 2012, , .		0
224	Messages from the Chairs. , 2012, , .		0
225	Guest Editors' Introduction to the Special Section on Bioinformatics Research and Applications. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1002-1003.	1.9	0
226	Workshop: Novel transcript reconstruction from paired-end RNA-Seq reads using fragment length distribution. , 2012, , .		0
227	Workshop: Bioinformatics methods for reconstruction of Infectious Bronchitis Virus quasispecies from next generation sequencing data. , 2012, , .		0
228	Workshop: A maximum likelihood method for quasispecies spectrum assembly. , 2012, , .		0
229	Guest Editors' Introduction. BMC Bioinformatics, 2012, 13, S1.	1.2	0
230	Message from Workshop Chairs. , 2013, , .		0
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