

# Alexander Zelikovsky

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

245  
papers

3,194  
citations

29  
h-index

50  
g-index

326  
ext. papers

4,128  
ext. citations

3.2  
avg, IF

5.25  
L-index

#	Paper	IF	Citations
245	Eleven grand challenges in single-cell data science. <i>Genome Biology</i> , <b>2020</b> , 21, 31	18.3	274
244	An 11/6-approximation algorithm for the network steiner problem. <i>Algorithmica</i> , <b>1993</b> , 9, 463-470	0.9	226
243	Tighter Bounds for Graph Steiner Tree Approximation. <i>SIAM Journal on Discrete Mathematics</i> , <b>2005</b> , 19, 122-134	0.7	187
242	Estimation of alternative splicing isoform frequencies from RNA-Seq data. <i>Algorithms for Molecular Biology</i> , <b>2011</b> , 6, 9	1.8	125
241	New Approximation Algorithms for the Steiner Tree Problems. <i>Journal of Combinatorial Optimization</i> , <b>1997</b> , 1, 47-65	0.9	95
240	Inferring viral quasispecies spectra from 454 pyrosequencing reads. <i>BMC Bioinformatics</i> , <b>2011</b> , 12 Suppl 6, S1	3.6	79
239	Efficient error correction for next-generation sequencing of viral amplicons. <i>BMC Bioinformatics</i> , <b>2012</b> , 13 Suppl 10, S6	3.6	73
238	Power efficient monitoring management in sensor networks		73
237	Network Lifetime and Power Assignment in ad hoc Wireless Networks. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 114-126	0.9	73
236	A series of approximation algorithms for the acyclic directed steiner tree problem. <i>Algorithmica</i> , <b>1997</b> , 18, 99-110	0.9	72
235	Filling algorithms and analyses for layout density control. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>1999</b> , 18, 445-462	2.5	68
234	Systematic benchmarking of omics computational tools. <i>Nature Communications</i> , <b>2019</b> , 10, 1393	17.4	62
233	Power Efficient Range Assignment for Symmetric Connectivity in Static Ad Hoc Wireless Networks. <i>Wireless Networks</i> , <b>2006</b> , 12, 287-299	2.5	61
232	Selecting Forwarding Neighbors in Wireless Ad Hoc Networks. <i>Mobile Networks and Applications</i> , <b>2004</b> , 9, 101-111	2.9	61
231	Symmetric Connectivity with Minimum Power Consumption in Radio Networks <b>2002</b> , 119-130		59
230	<b>1999</b> ,		55
229	The moving-target traveling salesman problem. <i>Journal of Algorithms</i> , <b>2003</b> , 49, 153-174		51

228	An improved approximation scheme for the Group Steiner Problem. <i>Networks</i> , <b>2001</b> , 37, 8-20	1.6	48
227	A novel method for signal transduction network inference from indirect experimental evidence. <i>Journal of Computational Biology</i> , <b>2007</b> , 14, 927-49	1.7	43
226	Accurate viral population assembly from ultra-deep sequencing data. <i>Bioinformatics</i> , <b>2014</b> , 30, i329-37	7.2	42
225	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>1999</b> , 18, 1265-1278	2.5	41
224	2SNP: scalable phasing based on 2-SNP haplotypes. <i>Bioinformatics</i> , <b>2006</b> , 22, 371-3	7.2	36
223	Area fill synthesis for uniform layout density. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2002</b> , 21, 1132-1147	2.5	36
222	QUENTIN: reconstruction of disease transmissions from viral quasispecies genomic data. <i>Bioinformatics</i> , <b>2018</b> , 34, 163-170	7.2	35
221	Bootstrap-based differential gene expression analysis for RNA-Seq data with and without replicates. <i>BMC Genomics</i> , <b>2014</b> , 15 Suppl 8, S2	4.5	35
220	Practical iterated fill synthesis for CMP uniformity <b>2000</b> ,		33
219	ScaffMatch: scaffolding algorithm based on maximum weight matching. <i>Bioinformatics</i> , <b>2015</b> , 31, 2632-87.2		31
218			31
217	A faster approximation algorithm for the steiner tree problem in graphs. <i>Information Processing Letters</i> , <b>1993</b> , 46, 79-83	0.8	31
216	Maximum Lifetime of Sensor Networks with Adjustable Sensing Range		28
215	Fast bootstrapping-based estimation of confidence intervals of expression levels and differential expression from RNA-Seq data. <i>Bioinformatics</i> , <b>2017</b> , 33, 3302-3304	7.2	27
214	MLR-tagging: informative SNP selection for unphased genotypes based on multiple linear regression. <i>Bioinformatics</i> , <b>2006</b> , 22, 2558-61	7.2	26
213	The Polymatroid Steiner Problems. <i>Journal of Combinatorial Optimization</i> , <b>2005</b> , 9, 281-294	0.9	22
212	Epidemiological data analysis of viral quasispecies in the next-generation sequencing era. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 96-108	13.4	22
211	A note on the MST heuristic for bounded edge-length Steiner trees with minimum number of Steiner points. <i>Information Processing Letters</i> , <b>2000</b> , 75, 165-167	0.8	21

210	Reconstruction of viral population structure from next-generation sequencing data using multicommodity flows. <i>BMC Bioinformatics</i> , <b>2013</b> , 14 Suppl 9, S2	3.6	19
209	HCV Quasispecies Assembly Using Network Flows <b>2008</b> , 159-170		19
208	Inference of genetic relatedness between viral quasispecies from sequencing data. <i>BMC Genomics</i> , <b>2017</b> , 18, 918	4.5	18
207	Provably good global buffering using an available buffer block plan		18
206	Informative SNP selection methods based on SNP prediction. <i>IEEE Transactions on Nanobioscience</i> , <b>2007</b> , 6, 60-7	3.4	17
205	Highly scalable algorithms for rectilinear and octilinear Steiner trees		17
204	MetNetAligner: a web service tool for metabolic network alignments. <i>Bioinformatics</i> , <b>2009</b> , 25, 1989-90	7.2	15
203	Provably good routing tree construction with multi-port terminals <b>1997</b> ,		15
202	On the skew-bounded minimum-buffer routing tree problem. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2003</b> , 22, 937-945	2.5	15
201	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, e102	20.1	15
200	Computational framework for next-generation sequencing of heterogeneous viral populations using combinatorial pooling. <i>Bioinformatics</i> , <b>2015</b> , 31, 682-90	7.2	14
199	Hierarchical dummy fill for process uniformity <b>2001</b> ,		14
198	Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing. <i>Nature Communications</i> , <b>2020</b> , 11, 3126	17.4	12
197	An integer programming approach to novel transcript reconstruction from paired-end RNA-Seq reads <b>2012</b> ,		12
196	Combinatorial search methods for multi-SNP disease association. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , <b>2006</b> , 2006, 5802-5		12
195	A practical transistor-level dual threshold voltage assignment methodology		12
194	Evaluation of placement techniques for DNA probe array layout <b>2003</b> ,		12
193	Minimum buffered routing with bounded capacitive load for slew rate and reliability control. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2003</b> , 22, 241-253	2.5	12

192	New and exact filling algorithms for layout density control <b>1999</b> ,		12
191	Reconstructing viral quasispecies from NGS amplicon reads. <i>In Silico Biology</i> , <b>2011</b> , 11, 237-49	2	12
190	Accurate assembly of minority viral haplotypes from next-generation sequencing through efficient noise reduction		12
189	Moving-Target TSP and Related Problems. <i>Lecture Notes in Computer Science</i> , <b>1998</b> , 453-464	0.9	12
188	Benchmarking of computational error-correction methods for next-generation sequencing data. <i>Genome Biology</i> , <b>2020</b> , 21, 71	18.3	11
187	Searching High-Order SNP Combinations for Complex Diseases Based on Energy Distribution Difference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2015</b> , 12, 695-704	3	11
186	Optimal Testing of Digital Microfluidic Biochips. <i>INFORMS Journal on Computing</i> , <b>2011</b> , 23, 518-529	2.4	11
185	Association testing by haplotype-sharing methods applicable to whole-genome analysis. <i>BMC Proceedings</i> , <b>2007</b> , 1 Suppl 1, S129	2.3	11
184	Optimal phase conflict removal for layout of dark field alternating phase shifting masks. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2000</b> , 19, 175-187	2.5	11
183	Optimal phase conflict removal for layout of dark field alternating phase shifting masks <b>1999</b> ,		11
182	Estimation of Alternative Splicing isoform Frequencies from RNA-Seq Data. <i>Lecture Notes in Computer Science</i> , <b>2010</b> , 202-214	0.9	11
181	Global transmission network of SARS-CoV-2: from outbreak to pandemic <b>2020</b> ,		11
180	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Journal of Computational Biology</i> , <b>2017</b> , 24, 558-570	1.7	10
179	Transcriptome assembly and quantification from Ion Torrent RNA-Seq data. <i>BMC Genomics</i> , <b>2014</b> , 15 Suppl 5, S7	4.5	10
178	Formal Models of Gene Clusters <b>2007</b> , 175-202		10
177	Multi-project reticle floorplanning and wafer dicing <b>2004</b> ,		10
176	An 11/6-Approximation Algorithm for the Steiner Problem on Graphs. <i>Annals of Discrete Mathematics</i> , <b>1992</b> , 51, 351-354		10
175	Viral quasispecies reconstruction from amplicon 454 pyrosequencing reads <b>2011</b> ,		9

174	Yield- and cost-driven fracturing for variable shaped-beam mask writing <b>2004</b> ,		9
173	Antibody Response to Lyme Disease Spirochetes in the Context of VlsE-Mediated Immune Evasion. <i>Infection and Immunity</i> , <b>2017</b> , 85,	3.7	8
172	Fast and Efficient Bright-Field AAPSM Conflict Detection and Correction. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2007</b> , 26, 115-126	2.5	8
171	DEEPS: Deterministic Energy-Efficient Protocol for Sensor networks		8
170	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2006</b> , 25, 305-320	2.5	8
169	Fast yield driven fracture for variable shaped beam mask writing <b>2006</b> ,		8
168	A New Approximation Algorithm for Finding Heavy Planar Subgraphs. <i>Algorithmica</i> , <b>2003</b> , 36, 179-205	0.9	8
167	Improved Approximation Algorithms for the Quality of Service Multicast Tree Problem. <i>Algorithmica</i> , <b>2005</b> , 42, 109-120	0.9	8
166			8
165	Monte-Carlo algorithms for layout density control		8
164	Engineering a scalable placement heuristic for DNA probe arrays <b>2003</b> ,		8
163	Inferring metabolic pathway activity levels from RNA-Seq data. <i>BMC Genomics</i> , <b>2016</b> , 17 Suppl 5, 542	4.5	8
162	Combinatorial Methods for Disease Association Search and Susceptibility Prediction. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 286-297	0.9	8
161	Border Length Minimization in DNA Array Design*. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 435-448	0.9	8
160	GaussianCpG: a Gaussian model for detection of CpG island in human genome sequences. <i>BMC Genomics</i> , <b>2017</b> , 18, 392	4.5	7
159	Faster Approximation Algorithms for the Rectilinear Steiner Tree Problem. <i>Discrete and Computational Geometry</i> , <b>1997</b> , 18, 93-109	0.6	7
158	2SNP: scalable phasing method for trios and unrelated individuals. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2008</b> , 5, 313-8	3	7
157	Design and validation of methods searching for risk factors in genotype case-control studies. <i>Journal of Computational Biology</i> , <b>2008</b> , 15, 81-90	1.7	7

156	A Survey of Seeding for Sequence Alignment <b>2007</b> , 117-142		7
155	Linear reduction method for predictive and informative tag SNP selection. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2005</b> , 1, 249-60	0.9	7
154	Transactions on Computational Systems Biology II. <i>Lecture Notes in Computer Science</i> , <b>2005</b> ,	0.9	7
153	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , <b>2021</b> , 22, 249	18.3	7
152	HapIso: An Accurate Method for the Haplotype- Specific Isoforms Reconstruction From Long Single-Molecule Reads. <i>IEEE Transactions on Nanobioscience</i> , <b>2017</b> , 16, 108-115	3.4	6
151	<b>2016</b> ,		6
150	Fast Alignments of Metabolic Networks <b>2008</b> ,		6
149	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2002</b> , 21, 263-274	2.5	6
148	Minimum-buffered routing of non-critical nets for slew rate and reliability control		6
147	New multilevel and hierarchical algorithms for layout density control <b>1999</b> ,		6
146	From Alpha to Zeta: Identifying Variants and Subtypes of SARS-CoV-2 Via Clustering. <i>Journal of Computational Biology</i> , <b>2021</b> , 28, 1113-1129	1.7	6
145	Identification of Surface Epitopes Associated with Protection against Highly Immune-Evasive VlsE-Expressing Lyme Disease Spirochetes. <i>Infection and Immunity</i> , <b>2018</b> , 86,	3.7	5
144	Inference of clonal selection in cancer populations using single-cell sequencing data. <i>Bioinformatics</i> , <b>2019</b> , 35, i398-i407	7.2	5
143	Identification of cancer-specific motifs in mimotope profiles of serum antibody repertoire. <i>BMC Bioinformatics</i> , <b>2017</b> , 18, 244	3.6	5
142	ILP-based maximum likelihood genome scaffolding. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 9, S9	3.6	5
141	Scalable heuristics for design of DNA probe arrays. <i>Journal of Computational Biology</i> , <b>2004</b> , 11, 429-47	1.7	5
140	Energy-efficient continuous and event-driven monitoring		5
139	Provably good global buffering by multi-terminal multicommodity flow approximation <b>2001</b> ,		5

138	New graph bipartizations for double-exposure, bright field alternating phase-shift mask layout		5
137	SyD: A Middleware Testbed for Collaborative Applications over Small Heterogeneous Devices and Data Stores. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 352-371	0.9	5
136	Profiling immunoglobulin repertoires across multiple human tissues by RNA Sequencing		5
135	Using earth mover's distance for viral outbreak investigations. <i>BMC Genomics</i> , <b>2020</b> , 21, 582	4.5	5
134	Influence of symbiont-produced bioactive natural products on holobiont fitness in the marine bryozoan, <i>Bugula neritina</i> via protein kinase C (PKC). <i>Marine Biology</i> , <b>2016</b> , 163, 1	2.5	5
133	Repeat-aware evaluation of scaffolding tools. <i>Bioinformatics</i> , <b>2018</b> , 34, 2530-2537	7.2	4
132	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks. <i>International Journal of Networking and Computing</i> , <b>2013</b> , 3, 55-74	0.2	4
131	Collaborative Topology Control for Lifetime Maximization <b>2011</b> ,		4
130	Scalable genome scaffolding using integer linear programming <b>2012</b> ,		4
129	<b>2007</b> ,		4
128	Compressible area fill synthesis. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2005</b> , 24, 1169-1187	2.5	4
127	Design flow enhancements for DNA arrays		4
126	Approaching the $5/4$ approximation for rectilinear Steiner trees. <i>Lecture Notes in Computer Science</i> , <b>1994</b> , 60-71	0.9	4
125	Improved transcriptome quantification and reconstruction from RNA-Seq reads using partial annotations. <i>In Silico Biology</i> , <b>2011</b> , 11, 251-61	2	4
124	Tag SNP Selection Based on Multivariate Linear Regression. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 750-757	0.9	4
123	Linear Reduction for Haplotype Inference. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 242-253	0.9	4
122	Mean Square Residue Biclustering with Missing Data and Row Inversions. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 28-39	0.9	4
121	Quantitative differences between intra-host HCV populations from persons with recently established and persistent infections. <i>Virus Evolution</i> , <b>2021</b> , 7, veaa103	3.7	4



120	New Zealand White Rabbits Effectively Clear <i>Borrelia burgdorferi</i> B31 despite the Bacterium's Functional Antigenic Variation System. <i>Infection and Immunity</i> , <b>2019</b> , 87,	3.7	3
119	Maximum Series-Parallel Subgraph. <i>Algorithmica</i> , <b>2012</b> , 63, 137-157	0.9	3
118	Practical Approximation Algorithms for Zero- and Bounded-Skew Trees. <i>SIAM Journal on Discrete Mathematics</i> , <b>2001</b> , 15, 97-111	0.7	3
117	Scaffolding Algorithms <b>2016</b> , 105-131		3
116	Microbiome Analysis: State of the Art and Future Trends <b>2016</b> , 401-424		3
115	Clustering Based Identification of SARS-CoV-2 Subtypes. <i>Lecture Notes in Computer Science</i> , <b>2021</b> , 127-141	1.9	3
114	Fast estimation of genetic relatedness between members of heterogeneous populations of closely related genomic variants. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 360	3.6	3
113	Delineating Surface Epitopes of Lyme Disease Pathogen Targeted by Highly Protective Antibodies of New Zealand White Rabbits. <i>Infection and Immunity</i> , <b>2019</b> , 87,	3.7	2
112	Computational Approaches to Detect Illicit Drug Ads and Find Vendor Communities Within Social Media Platforms. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> ,	3	2
111	Predicting Opioid Epidemic by Using Twitter Data. <i>Lecture Notes in Computer Science</i> , <b>2018</b> , 314-318	0.9	2
110	Assessment of HCV infection stage as recent or chronic using multi-parameter analysis and machine learning <b>2017</b> ,		2
109	Detection of genetic relatedness between viral samples using EM-based clustering of next-generation sequencing data <b>2014</b> ,		2
108	kGEM: An EM-based algorithm for local reconstruction of viral quasispecies <b>2013</b> ,		2
107	Efficient Alignments of Metabolic Networks with Bounded Treewidth <b>2010</b> ,		2
106	Hybrid SVM kernels for protein secondary structure prediction		2
105	Multiple linear regression for index SNP selection on unphased genotypes. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , <b>2006</b> , 2006, 5759-62		2
104	Fill for Shallow Trench Isolation CMP. <i>IEEE/ACM International Conference on Computer-Aided Design, Digest of Technical Papers</i> , <b>2006</b> ,		2
103	Advances in Hidden Markov Models for Sequence Annotation <b>2007</b> , 55-91		2

102	The Comparison of Phylogenetic Networks: Algorithms and Complexity <b>2007</b> , 143-173		2
101	. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2007</b> , 26, 301-311	2.5	2
100	Phasing and Missing Data Recovery in Family Trios. <i>Lecture Notes in Computer Science</i> , <b>2005</b> , 1011-1019	0.9	2
99	Improved Approximation Algorithms for the Quality of Service Steiner Tree Problem. <i>Lecture Notes in Computer Science</i> , <b>2003</b> , 401-411	0.9	2
98	Toward an easy programming environment for implementing mobile applications: a fleet application case study using SyD middleware		2
97			2
96	Monte-Carlo methods for chemical-mechanical planarization on multiple-layer and dual-material models <b>2002</b> ,		2
95	New approximation algorithms for routing with multiport terminals. <i>IEEE Transactions on Computer-Aided Design of Integrated Circuits and Systems</i> , <b>2000</b> , 19, 1118-1128	2.5	2
94	Spanning closed trail and hamiltonian cycle in grid graphs. <i>Lecture Notes in Computer Science</i> , <b>1995</b> , 342-351		2
93	Analysis of heterogeneous genomic samples using image normalization and machine learning. <i>BMC Genomics</i> , <b>2020</b> , 21, 405	4.5	2
92	Inference of mutability landscapes of tumors from single cell sequencing data. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008454	5	2
91	Using Earth Mover's Distance for Viral Outbreak Investigations		2
90	Error Correction of NGS Reads from Viral Populations <b>2016</b> , 329-353		2
89	Automated quality control for a molecular surveillance system. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 358	3.6	2
88	Applications of the Linear Matroid Parity Algorithm to Approximating Steiner Trees. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 70-79	0.9	2
87	The T-join Problem in Sparse Graphs: Applications to Phase Assignment Problem in VLSI Mask Layout. <i>Lecture Notes in Computer Science</i> , <b>1999</b> , 25-36	0.9	2
86	On Approximation of the Power-p and Bottleneck Steiner Trees. <i>Combinatorial Optimization</i> , <b>2000</b> , 117-135		2
85	Metabolic Analysis of Metatranscriptomic Data from Planktonic Communities. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 396-402	0.9	1

84	ScaffMatch: Scaffolding Algorithm Based on Maximum Weight Matching. <i>Lecture Notes in Computer Science</i> , <b>2015</b> , 222-223	0.9	1
83	GaussianCpG: A Gaussian model for detection of human CpG island <b>2015</b> ,		1
82	Deterministic regression algorithm for transcriptome frequency estimation <b>2014</b> ,		1
81	VGA: A method for viral quasispecies assembly from ultra-deep sequencing data <b>2014</b> ,		1
80	Distributed Algorithms for TDMA Link Scheduling in Sensor Networks <b>2012</b> ,		1
79	Monte-Carlo Regression algorithm for isoform frequency estimation from RNA-Seq data <b>2013</b> ,		1
78	Discrete Methods for Association Search and Status Prediction in Genotype Case-Control Studies <b>2007</b> ,		1
77	Topological Indices in Combinatorial Chemistry <b>2007</b> , 417-438		1
76	Computational Approaches to Predict ProteinProtein and DomainDomain Interactions <b>2007</b> , 465-491		1
75	Classification Accuracy Based Microarray Missing Value Imputation <b>2007</b> , 303-327		1
74	Dynamic Programming Algorithms for Biological Sequence and Structure Comparison <b>2007</b> , 7-28		1
73	Sorting- and FFT-Based Techniques in the Discovery of Biopatterns <b>2007</b> , 93-115		1
72	Integer Linear Programming Techniques for Discovering Approximate Gene Clusters <b>2007</b> , 203-221		1
71	Haplotype tagging using support vector machines		1
70	Consolidating software tools for DNA microarray design and manufacturing. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , <b>2004</b> , 2006, 172-5		1
69	Linear reduction methods for tag SNP selection. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society</i> , <b>2004</b> , 2004, 2840-3		1
68	Area fill generation with inherent data volume reduction		1
67	Family trio phasing and missing data recovery. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2005</b> , 1, 221-9	0.9	1

66	Practical Approximation Algorithms for Separable Packing Linear Programs. <i>Lecture Notes in Computer Science</i> , <b>2001</b> , 325-337	0.9	1
65	Auctions with Buyer Preferences. <i>IFIP Advances in Information and Communication Technology</i> , <b>2002</b> , 223-238	0.5	1
64	Phasing of 2-SNP Genotypes Based on Non-random Mating Model. <i>Lecture Notes in Computer Science</i> , <b>2006</b> , 767-774	0.9	1
63	A Novel Method for Signal Transduction Network Inference from Indirect Experimental Evidence. <i>Lecture Notes in Computer Science</i> , <b>2007</b> , 407-419	0.9	1
62	Detecting Illicit Drug Ads in Google+ Using Machine Learning. <i>Lecture Notes in Computer Science</i> , <b>2019</b> , 171-179	0.9	1
61	Long Single-Molecule Reads Can Resolve the Complexity of the Influenza Virus Composed of Rare, Closely Related Mutant Variants. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 164-175	0.9	1
60	Modeling the Spread of HIV and HCV Infections Based on Identification and Characterization of High-Risk Communities Using Social Media. <i>Lecture Notes in Computer Science</i> , <b>2017</b> , 425-430	0.9	1
59	1.25-Approximation Algorithm for Steiner Tree Problem with Distances 1 and 2. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 86-97	0.9	1
58	HapIso: An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads		1
57	Inference of clonal selection in cancer populations using single-cell sequencing data		1
56	Genotype Tagging with Limited Overfitting. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 1-12	0.9	1
55	Introduction to the Analysis of Environmental Sequence Information Using Metapathways <b>2016</b> , 25-56		1
54	Bisulfite-Conversion-Based Methods for DNA Methylation Sequencing Data Analysis <b>2016</b> , 227-243		1
53	Transcriptome Quantification and Differential Expression from NGS Data <b>2016</b> , 301-327		1
52	Reconstruction of Infectious Bronchitis Virus Quasispecies from NGS Data <b>2016</b> , 383-400		1
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