

Ron Shamir

List of Publications by Year in descending order

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285
papers

20,185
citations

14614

66
h-index

12910

131
g-index

324
all docs

324
docs citations

324
times ranked

23700
citing authors

#	ARTICLE	IF	CITATIONS
1	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , 2012, 9, 796-804.	9.0	1,481
2	Modelling and analysis of gene regulatory networks. <i>Nature Reviews Molecular Cell Biology</i> , 2008, 9, 770-780.	16.1	1,002
3	Clustering Gene Expression Patterns. <i>Journal of Computational Biology</i> , 1999, 6, 281-297.	0.8	959
4	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , 2007, 3, 88.	3.2	918
5	Dynamic Changes in the Copy Number of Pluripotency and Cell Proliferation Genes in Human ESCs and iPSCs during Reprogramming and Time in Culture. <i>Cell Stem Cell</i> , 2011, 8, 106-118.	5.2	819
6	Discovering statistically significant biclusters in gene expression data. <i>Bioinformatics</i> , 2002, 18, S136-S144.	1.8	717
7	Quantification of protein half-lives in the budding yeast proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 13004-13009.	3.3	623
8	A clustering algorithm based on graph connectivity. <i>Information Processing Letters</i> , 2000, 76, 175-181.	0.4	397
9	Revealing modularity and organization in the yeast molecular network by integrated analysis of highly heterogeneous genomewide data. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 2981-2986.	3.3	344
10	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	9.4	341
11	A Fast Algorithm for Joint Reconstruction of Ancestral Amino Acid Sequences. <i>Molecular Biology and Evolution</i> , 2000, 17, 890-896.	3.5	329
12	CLICK and EXPANDER: a system for clustering and visualizing gene expression data. <i>Bioinformatics</i> , 2003, 19, 1787-1799.	1.8	327
13	Regulatory networks define phenotypic classes of human stem cell lines. <i>Nature</i> , 2008, 455, 401-405.	13.7	321
14	Multi-omic and multi-view clustering algorithms: review and cancer benchmark. <i>Nucleic Acids Research</i> , 2018, 46, 10546-10562.	6.5	316
15	EXPANDER—an integrative program suite for microarray data analysis. <i>BMC Bioinformatics</i> , 2005, 6, 232.	1.2	283
16	A global view of pleiotropy and phenotypically derived gene function in yeast. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0001.	3.2	282
17	Genome-Wide In Silico Identification of Transcriptional Regulators Controlling the Cell Cycle in Human Cells. <i>Genome Research</i> , 2003, 13, 773-780.	2.4	275
18	Cluster graph modification problems. <i>Discrete Applied Mathematics</i> , 2004, 144, 173-182.	0.5	274

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19	How prevalent is functional alternative splicing in the human genome?. Trends in Genetics, 2004, 20, 68-71.	2.9	267
20	Identification of functional modules using network topology and high-throughput data. BMC Systems Biology, 2007, 1, 8.	3.0	267
21	Conservation and evolvability in regulatory networks: The evolution of ribosomal regulation in yeast. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7203-7208.	3.3	244
22	Comprehensive MicroRNA Profiling Reveals a Unique Human Embryonic Stem Cell Signature Dominated by a Single Seed Sequence. Stem Cells, 2008, 26, 1506-1516.	1.4	202
23	Expander: from expression microarrays to networks and functions. Nature Protocols, 2010, 5, 303-322.	5.5	183
24	Transcription factor and microRNA motif discovery: The Amadeus platform and a compendium of metazoan target sets. Genome Research, 2008, 18, 1180-1189.	2.4	166
25	Dissection of Regulatory Networks that Are Altered in Disease via Differential Co-expression. PLoS Computational Biology, 2013, 9, e1002955.	1.5	164
26	Tractability of Parameterized Completion Problems on Chordal, Strongly Chordal, and Proper Interval Graphs. SIAM Journal on Computing, 1999, 28, 1906-1922.	0.8	161
27	Identification of Protein Complexes by Comparative Analysis of Yeast and Bacterial Protein Interaction Data. Journal of Computational Biology, 2005, 12, 835-846.	0.8	161
28	Graph Sandwich Problems. Journal of Algorithms, 1995, 19, 449-473.	0.9	152
29	A Faster and Simpler Algorithm for Sorting Signed Permutations by Reversals. SIAM Journal on Computing, 2000, 29, 880-892.	0.8	146
30	Complexity and algorithms for reasoning about time. Journal of the ACM, 1993, 40, 1108-1133.	1.8	143
31	Four Strikes Against Physical Mapping of DNA. Journal of Computational Biology, 1995, 2, 139-152.	0.8	141
32	NEMO: cancer subtyping by integration of partial multi-omic data. Bioinformatics, 2019, 35, 3348-3356.	1.8	141
33	Complexity classification of some edge modification problems. Discrete Applied Mathematics, 2001, 113, 109-128.	0.5	134
34	Recycler: an algorithm for detecting plasmids from <i>de novo</i> assembly graphs. Bioinformatics, 2017, 33, 475-482.	1.8	117
35	Accurate identification of alternatively spliced exons using support vector machine. Bioinformatics, 2005, 21, 897-901.	1.8	116
36	GERBIL: Genotype resolution and block identification using likelihood. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 158-162.	3.3	116

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37	The canine olfactory subgenome. <i>Genomics</i> , 2004, 83, 361-372.	1.3	114
38	DEGAS: De Novo Discovery of Dysregulated Pathways in Human Diseases. <i>PLoS ONE</i> , 2010, 5, e13367.	1.1	113
39	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , 2017, 89, 1676-1683.	1.5	112
40	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , 2009, 25, 1158-1164.	1.8	111
41	A Non-EST-Based Method for Exon-Skipping Prediction. <i>Genome Research</i> , 2004, 14, 1617-1623.	2.4	110
42	Tag SNP selection in genotype data for maximizing SNP prediction accuracy. <i>Bioinformatics</i> , 2005, 21, i195-i203.	1.8	109
43	Transcription factor family-specific $\langle scp \rangle$ DNA $\langle scp \rangle$ shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , 2017, 13, 910.	3.2	105
44	The degenerate primer design problem. <i>Bioinformatics</i> , 2002, 18, S172-S181.	1.8	102
45	Topology-Free Querying of Protein Interaction Networks. <i>Journal of Computational Biology</i> , 2010, 17, 237-252.	0.8	99
46	The Efficiency of the Simplex Method: A Survey. <i>Management Science</i> , 1987, 33, 301-334.	2.4	97
47	Transcription Factor/microRNA Axis Blocks Melanoma Invasion Program by miR-211 Targeting NUA1. <i>Journal of Investigative Dermatology</i> , 2014, 134, 441-451.	0.3	95
48	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 901-908.	3.6	93
49	Environmental Stresses Disrupt Telomere Length Homeostasis. <i>PLoS Genetics</i> , 2013, 9, e1003721.	1.5	89
50	A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data. <i>Nucleic Acids Research</i> , 2014, 42, e63-e63.	6.5	89
51	Enhancer methylation dynamics contribute to cancer plasticity and patient mortality. <i>Genome Research</i> , 2016, 26, 601-611.	2.4	88
52	Pathwidth, Bandwidth, and Completion Problems to Proper Interval Graphs with Small Cliques. <i>SIAM Journal on Computing</i> , 1996, 25, 540-561.	0.8	85
53	Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome. <i>Nucleic Acids Research</i> , 2014, 42, 9854-9861.	6.5	85
54	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , 2010, 38, e160-e160.	6.5	84

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55	On the Complexity of DNA Physical Mapping. <i>Advances in Applied Mathematics</i> , 1994, 15, 251-261.	0.4	82
56	Transcriptional modulation induced by ionizing radiation: p53 remains a central player. <i>Molecular Oncology</i> , 2011, 5, 336-348.	2.1	82
57	Faster Subtree Isomorphism. <i>Journal of Algorithms</i> , 1999, 33, 267-280.	0.9	81
58	Reduced changes in protein compared to mRNA levels across non-proliferating tissues. <i>BMC Genomics</i> , 2017, 18, 305.	1.2	77
59	An Algorithm for Clustering cDNA Fingerprints. <i>Genomics</i> , 2000, 66, 249-256.	1.3	76
60	Computing Has Changed Biology – Biology Education Must Catch Up. <i>Science</i> , 2009, 325, 541-542.	6.0	76
61	Expression and methylation patterns partition luminal-A breast tumors into distinct prognostic subgroups. <i>Breast Cancer Research</i> , 2016, 18, 74.	2.2	75
62	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , 2011, 39, D793-D799.	6.5	74
63	Integration of Transcriptomics, Proteomics, and MicroRNA Analyses Reveals Novel MicroRNA Regulation of Targets in the Mammalian Inner Ear. <i>PLoS ONE</i> , 2011, 6, e18195.	1.1	74
64	Dissection of a DNA-damage-induced transcriptional network using a combination of microarrays, RNA interference and computational promoter analysis. <i>Genome Biology</i> , 2005, 6, R43.	13.9	71
65	The Degenerate Primer Design Problem: Theory and Applications. <i>Journal of Computational Biology</i> , 2005, 12, 431-456.	0.8	70
66	Strongly Polynomial Algorithms for the High Multiplicity Scheduling Problem. <i>Operations Research</i> , 1991, 39, 648-653.	1.2	69
67	Scoring clustering solutions by their biological relevance. <i>Bioinformatics</i> , 2003, 19, 2381-2389.	1.8	69
68	Parallel induction of ATM-dependent pro- and antiapoptotic signals in response to ionizing radiation in murine lymphoid tissue. <i>Oncogene</i> , 2006, 25, 1584-1592.	2.6	69
69	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , 2008, 4, 209.	3.2	69
70	A genome-wide analysis in <i>Saccharomyces cerevisiae</i> demonstrates the influence of chromatin modifiers on transcription. <i>Nature Genetics</i> , 2007, 39, 303-309.	9.4	68
71	PlasClass improves plasmid sequence classification. <i>PLoS Computational Biology</i> , 2020, 16, e1007781.	1.5	67
72	ElemNT: a computational tool for detecting core promoter elements. <i>Transcription</i> , 2015, 6, 41-50.	1.7	66

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73	SPIKE – a database, visualization and analysis tool of cellular signaling pathways. BMC Bioinformatics, 2008, 9, 110.	1.2	65
74	A catalog of stability-associated sequence elements in 3' UTRs of yeast mRNAs. Genome Biology, 2005, 6, R86.	13.9	63
75	A Probabilistic Methodology for Integrating Knowledge and Experiments on Biological Networks. Journal of Computational Biology, 2006, 13, 165-181.	0.8	63
76	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. Genome Biology, 2018, 19, 56.	3.8	63
77	Improving the performance of minimizers and winnowing schemes. Bioinformatics, 2017, 33, i110-i117.	1.8	62
78	Pediatric onset Crohn's colitis is characterized by genotype-dependent age-related susceptibility. Inflammatory Bowel Diseases, 2007, 13, 1509-1515.	0.9	58
79	A large-scale perspective on stress-induced alterations in resting-state networks. Scientific Reports, 2016, 6, 21503.	1.6	56
80	A Fully Dynamic Algorithm for Recognizing and Representing Proper Interval Graphs. SIAM Journal on Computing, 2001, 31, 289-305.	0.8	55
81	A Block-Free Hidden Markov Model for Genotypes and Its Application to Disease Association. Journal of Computational Biology, 2005, 12, 1243-1260.	0.8	55
82	Incomplete Directed Perfect Phylogeny. SIAM Journal on Computing, 2004, 33, 590-607.	0.8	54
83	Refinement and expansion of signaling pathways: The osmotic response network in yeast. Genome Research, 2007, 17, 358-367.	2.4	54
84	Faster and simpler algorithm for sorting signed permutations by reversals. , 1997, , .		52
85	TWO NOTES ON GENOME REARRANGEMENT. Journal of Bioinformatics and Computational Biology, 2003, 01, 71-94.	0.3	51
86	A simpler and faster 1.5-approximation algorithm for sorting by transpositions. Information and Computation, 2006, 204, 275-290.	0.5	51
87	Parallel Profiling of the Transcriptome, Cistrome, and Epigenome in the Cellular Response to Ionizing Radiation. Science Signaling, 2014, 7, rs3.	1.6	51
88	SlimPLS: A Method for Feature Selection in Gene Expression-Based Disease Classification. PLoS ONE, 2009, 4, e6416.	1.1	50
89	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy. Genome Biology, 2011, 12, R61.	13.9	49
90	An algorithm for clustering cDNAs for gene expression analysis. , 1999, , .		48

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91	Gene Expression Signature of Human Cancer Cell Lines Treated with the Ras Inhibitor Salirasib (S-Farnesylthiosalicylic Acid). <i>Cancer Research</i> , 2007, 67, 3320-3328.	0.4	48
92	A Randomization Test for Controlling Population Stratification in Whole-Genome Association Studies. <i>American Journal of Human Genetics</i> , 2007, 81, 895-905.	2.6	48
93	MicroRNAs of the RPE are essential for RPE differentiation and photoreceptor maturation. <i>Development (Cambridge)</i> , 2015, 142, 2487-98.	1.2	48
94	<i>Drosophila</i> TRF2 is a preferential core promoter regulator. <i>Genes and Development</i> , 2014, 28, 2163-2174.	2.7	45
95	Tired and misconnected: A breakdown of brain modularity following sleep deprivation. <i>Human Brain Mapping</i> , 2017, 38, 3300-3314.	1.9	45
96	Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium. <i>Molecular Systems Biology</i> , 2005, 1, 2005.0002.	3.2	44
97	GEVALT: An integrated software tool for genotype analysis. <i>BMC Bioinformatics</i> , 2007, 8, 36.	1.2	43
98	Deciphering Transcriptional Regulatory Elements That Encode Specific Cell-Cycle Phasing by Comparative Genomics Analysis. <i>Cell Cycle</i> , 2005, 4, 1788-1797.	1.3	42
99	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , 2014, 14, 329.	1.6	42
100	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , 2017, 13, e1005777.	1.5	42
101	PIVOT: Protein Interactions VisualizatiOn Tool. <i>Bioinformatics</i> , 2004, 20, 424-425.	1.8	41
102	A Fast Method for Computing High-Significance Disease Association in Large Population-Based Studies. <i>American Journal of Human Genetics</i> , 2006, 79, 481-492.	2.6	41
103	Minimizing the number of tardy job units under release time constraints. <i>Discrete Applied Mathematics</i> , 1990, 28, 45-57.	0.5	40
104	Allegro: Analyzing expression and sequence in concert to discover regulatory programs. <i>Nucleic Acids Research</i> , 2009, 37, 1566-1579.	6.5	40
105			

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109	PrtT-Regulated Proteins Secreted by <i>Aspergillus fumigatus</i> Activate MAPK Signaling in Exposed A549 Lung Cells Leading to Necrotic Cell Death. <i>PLoS ONE</i> , 2011, 6, e17509.	1.1	36
110	DOMINO: a network-based active module identification algorithm with reduced rate of false calls. <i>Molecular Systems Biology</i> , 2021, 17, e9593.	3.2	36
111	Computational expansion of genetic networks. <i>Bioinformatics</i> , 2001, 17, S270-S278.	1.8	36
112	Using the kinetics of C-reactive protein response to improve the differential diagnosis between acute bacterial and viral infections. <i>Infection</i> , 2020, 48, 241-248.	2.3	35
113	PRODIGY: personalized prioritization of driver genes. <i>Bioinformatics</i> , 2020, 36, 1831-1839.	1.8	32
114	Chain functions and scoring functions in genetic networks. <i>Bioinformatics</i> , 2003, 19, i108-i117.	1.8	31
115	Constructing Logical Models of Gene Regulatory Networks by Integrating Transcription Factor-DNA Interactions with Expression Data: An Entropy-Based Approach. <i>Journal of Computational Biology</i> , 2012, 19, 30-41.	0.8	31
116	Systematic inference of highways of horizontal gene transfer in prokaryotes. <i>Bioinformatics</i> , 2013, 29, 571-579.	1.8	31
117	SCAPP: an algorithm for improved plasmid assembly in metagenomes. <i>Microbiome</i> , 2021, 9, 144.	4.9	31
118	An algorithm for the detection and construction of Monge sequences. <i>Linear Algebra and Its Applications</i> , 1989, 114-115, 669-680.	0.4	30
119	Torque: topology-free querying of protein interaction networks. <i>Nucleic Acids Research</i> , 2009, 37, W106-W108.	6.5	30
120	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. <i>Nucleic Acids Research</i> , 2015, 43, 7779-7789.	6.5	30
121	A randomized scheme for speeding up algorithms for linear and convex programming problems with high constraints-to-variables ratio. <i>Mathematical Programming</i> , 1993, 61, 39-52.	1.6	29
122	Network-Induced Classification Kernels for Gene Expression Profile Analysis. <i>Journal of Computational Biology</i> , 2012, 19, 694-709.	0.8	29
123	Constructing module maps for integrated analysis of heterogeneous biological networks. <i>Nucleic Acids Research</i> , 2014, 42, 4208-4219.	6.5	29
124	Transcriptional and Proteomic Analysis of the <i>Aspergillus fumigatus</i> Δ prtT Protease-Deficient Mutant. <i>PLoS ONE</i> , 2012, 7, e33604.	1.1	29
125	A fully dynamic algorithm for modular decomposition and recognition of cographs. <i>Discrete Applied Mathematics</i> , 2004, 136, 329-340.	0.5	28
126	Functional genomic delineation of TLR-induced transcriptional networks. <i>BMC Genomics</i> , 2007, 8, 394.	1.2	28

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127	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , 2010, 6, 346.	3.2	28
128	The domatic number problem on some perfect graph families. <i>Information Processing Letters</i> , 1994, 49, 51-56.	0.4	27
129	A Global View of the Selection Forces in the Evolution of Yeast Cis-Regulation. <i>Genome Research</i> , 2004, 14, 829-834.	2.4	27
130	ATM haplotypes and breast cancer risk in Jewish high-risk women. <i>British Journal of Cancer</i> , 2006, 94, 1537-1543.	2.9	27
131	Complexity and algorithms for copy-number evolution problems. <i>Algorithms for Molecular Biology</i> , 2017, 12, 13.	0.3	27
132	In silico identification of transcriptional regulators associated with c-Myc. <i>Nucleic Acids Research</i> , 2004, 32, 4955-4961.	6.5	26
133	Modeling and Analysis of Heterogeneous Regulation in Biological Networks. <i>Journal of Computational Biology</i> , 2004, 11, 1034-1049.	0.8	26
134	E2F1 identified by promoter and biochemical analysis as a central target of glioblastoma cell-cycle arrest in response to ras inhibition. <i>International Journal of Cancer</i> , 2006, 119, 527-538.	2.3	26
135	Fast lossless compression via cascading Bloom filters. <i>BMC Bioinformatics</i> , 2014, 15, S7.	1.2	25
136	Melanoma-Secreted Lysosomes Trigger Monocyte-Derived Dendritic Cell Apoptosis and Limit Cancer Immunotherapy. <i>Cancer Research</i> , 2020, 80, 1942-1956.	0.4	25
137	Towards accurate imputation of quantitative genetic interactions. <i>Genome Biology</i> , 2009, 10, R140.	13.9	24
138	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2016, , 257-268.	1.0	24
139	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , 2019, 431, 2398-2406.	2.0	24
140	Bounded Degree Interval Sandwich Problems. <i>Algorithmica</i> , 1999, 24, 96-104.	1.0	23
141	Degenerate Primer Design. <i>Methods in Molecular Biology</i> , 2007, 402, 220-244.	0.4	23
142	The MORPH Algorithm: Ranking Candidate Genes for Membership in <i>Arabidopsis</i> and Tomato Pathways. <i>Plant Cell</i> , 2012, 24, 4389-4406.	3.1	23
143	Large Scale Sequencing by Hybridization. <i>Journal of Computational Biology</i> , 2002, 9, 413-428.	0.8	22
144	Cluster Graph Modification Problems. <i>Lecture Notes in Computer Science</i> , 2002, , 379-390.	1.0	22

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145	PROMO: an interactive tool for analyzing clinically-labeled multi-omic cancer datasets. BMC Bioinformatics, 2019, 20, 732.	1.2	22
146	Unravelling plasmidome distribution and interaction with its hosting microbiome. Environmental Microbiology, 2020, 22, 32-44.	1.8	22
147	A polynomial algorithm for an integer quadratic non-separable transportation problem. Mathematical Programming, 1992, 55, 359-371.	1.6	21
148	Ras inhibits endoplasmic reticulum stress in human cancer cells with amplified <i>Myc</i> . International Journal of Cancer, 2010, 126, 2268-2281.	2.3	21
149	Assessment of Algorithms for Inferring Positional Weight Matrix Motifs of Transcription Factor Binding Sites Using Protein Binding Microarray Data. PLoS ONE, 2012, 7, e46145.	1.1	21
150	A machine learning model for predicting deterioration of COVID-19 inpatients. Scientific Reports, 2022, 12, 2630.	1.6	21
151	DEFOG: A Practical Scheme for Deciphering Families of Genes. Genomics, 2002, 80, 295-302.	1.3	20
152	Tracing the Neural Carryover Effects of Interpersonal Anger on Resting-State fMRI in Men and Their Relation to Traumatic Stress Symptoms in a Subsample of Soldiers. Frontiers in Behavioral Neuroscience, 2017, 11, 252.	1.0	20
153	A Faster Algorithm for RNA Co-folding. Lecture Notes in Computer Science, 2008, , 174-185.	1.0	20
154	Risk Factors for Perianal Crohn's Disease: The Role of Genotype, Phenotype, and Ethnicity. American Journal of Gastroenterology, 2007, 102, 1702-1708.	0.2	19
155	Evolution and Selection in Yeast Promoters: Analyzing the Combined Effect of Diverse Transcription Factor Binding Sites. PLoS Computational Biology, 2008, 4, e7.	1.5	19
156	A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 848-850.	1.9	19
157	A hierarchical Bayesian model for flexible module discovery in three-way time-series data. Bioinformatics, 2015, 31, i17-i26.	1.8	19
158	A Family of Simplex Variants Solving an m -Dimensional Linear Program in Expected Number of Pivot Steps Depending on n Only. Mathematics of Operations Research, 1986, 11, 570-590.	0.8	18
159	Assessing the number of ancestral alternatively spliced exons in the human genome. BMC Genomics, 2006, 7, 273.	1.2	18
160	MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data. Genome Biology, 2008, 9, R1.	13.9	18
161	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. BMC Systems Biology, 2010, 4, 15.	3.0	18
162	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. Nucleic Acids Research, 2016, 44, e51-e51.	6.5	18

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163	Complexity Classification of Some Edge Modification Problems. Lecture Notes in Computer Science, 1999, , 65-77.	1.0	18
164	Detecting excess radical replacements in phylogenetic trees. Gene, 2003, 319, 127-135.	1.0	17
165	Maximum likelihood resolution of multi-block genotypes. , 2004, , .		17
166	Copy-Number Evolution Problems: Complexity and Algorithms. Lecture Notes in Computer Science, 2016, , 137-149.	1.0	17
167	SELMAP - SELEX affinity landscape MAPping of transcription factor binding sites using integrated microfluidics. Scientific Reports, 2016, 6, 33351.	1.6	17
168	Realizing Interval Graphs with Size and Distance Constraints. SIAM Journal on Discrete Mathematics, 1997, 10, 662-687.	0.4	16
169	The Restriction Scaffold Problem. Journal of Computational Biology, 2003, 10, 385-398.	0.8	16
170	THE INCOMPLETE PERFECT PHYLOGENY HAPLOTYPE PROBLEM. Journal of Bioinformatics and Computational Biology, 2005, 03, 359-384.	0.3	16
171	Detecting Highways of Horizontal Gene Transfer. Journal of Computational Biology, 2011, 18, 1087-1114.	0.8	16
172	Computational Problems in Perfect Phylogeny Haplotyping: Xor-Genotypes and Tag SNPs. Lecture Notes in Computer Science, 2004, , 14-31.	1.0	16
173	Faster pattern matching with character classes using prime number encoding. Journal of Computer and System Sciences, 2009, 75, 155-162.	0.9	15
174	Topology-Free Querying of Protein Interaction Networks. Lecture Notes in Computer Science, 2009, , 74-89.	1.0	15
175	An $O(n \log 2n)$ algorithm for the maximum weighed tardiness problem. Information Processing Letters, 1989, 31, 215-219.	0.4	14
176	Nonlinear partial differential equations and applications: A computational method for resequencing long DNA targets by universal oligonucleotide arrays. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 15492-15496.	3.3	14
177	RAP: Accurate and Fast Motif Finding Based on Protein-Binding Microarray Data. Journal of Computational Biology, 2013, 20, 375-382.	0.8	14
178	Modeling proteinâ€™DNA binding via high-throughput<i>in vitro</i> technologies. Briefings in Functional Genomics, 2017, 16, elw030.	1.3	14
179	Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications. Oncogene, 2017, 36, 3375-3383.	2.6	14
180	Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling the false discovery rate. PLoS Computational Biology, 2017, 13, e1005700.	1.5	14

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181	Satisfiability problems on intervals and unit intervals. <i>Theoretical Computer Science</i> , 1997, 175, 349-372.	0.5	13
182	On the Complexity of Positional Sequencing by Hybridization. <i>Journal of Computational Biology</i> , 2001, 8, 361-371.	0.8	13
183	Design of shortest double-stranded DNA sequences covering all k -mers with applications to protein-binding microarrays and synthetic enhancers. <i>Bioinformatics</i> , 2013, 29, i71-i79.	1.8	13
184	A Point Mutation in Translation Initiation Factor eIF2B Leads to Function- and Time-Specific Changes in Brain Gene Expression. <i>PLoS ONE</i> , 2011, 6, e26992.	1.1	13
185	A fast algorithm for constructing monge sequences in transportation problems with forbidden arcs. <i>Discrete Mathematics</i> , 1993, 114, 435-444.	0.4	12
186	Monge and feasibility sequences in general flow problems. <i>Discrete Applied Mathematics</i> , 1993, 44, 21-38.	0.5	12
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