

# Ron Shamir

## 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.

280  
papers

15,605  
citations

61  
h-index

119  
g-index

324  
ext. papers

18,256  
ext. citations

6.2  
avg, IF

6.73  
L-index

#	Paper	IF	Citations
280	Wisdom of crowds for robust gene network inference. <i>Nature Methods</i> , <b>2012</b> , 9, 796-804	21.6	1097
279	Network-based prediction of protein function. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 88	12.2	743
278	Modelling and analysis of gene regulatory networks. <i>Nature Reviews Molecular Cell Biology</i> , <b>2008</b> , 9, 770-807	14.7	718
277	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> , <b>2011</b> , 8, 106-18	18	700
276	Clustering gene expression patterns. <i>Journal of Computational Biology</i> , <b>1999</b> , 6, 281-97	1.7	699
275	Discovering statistically significant biclusters in gene expression data. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S136-44	7.2	576
274	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> , <b>2006</b> , 103, 13004-9	11.5	535
273	A clustering algorithm based on graph connectivity. <i>Information Processing Letters</i> , <b>2000</b> , 76, 175-181	0.8	302
272	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> , <b>2004</b> , 101, 2981-6	11.5	298
271	Regulatory networks define phenotypic classes of human stem cell lines. <i>Nature</i> , <b>2008</b> , 455, 401-5	50.4	283
270	CLICK and EXPANDER: a system for clustering and visualizing gene expression data. <i>Bioinformatics</i> , <b>2003</b> , 19, 1787-99	7.2	283
269	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 126-34	44.5	268
268	How prevalent is functional alternative splicing in the human genome?. <i>Trends in Genetics</i> , <b>2004</b> , 20, 68-78.5	7.5	251
267	Genome-wide in silico identification of transcriptional regulators controlling the cell cycle in human cells. <i>Genome Research</i> , <b>2003</b> , 13, 773-80	9.7	242
266	EXPANDER--an integrative program suite for microarray data analysis. <i>BMC Bioinformatics</i> , <b>2005</b> , 6, 232	3.6	242
265	A global view of pleiotropy and phenotypically derived gene function in yeast. <i>Molecular Systems Biology</i> , <b>2005</b> , 1, 2005.0001	12.2	232
264	A fast algorithm for joint reconstruction of ancestral amino acid sequences. <i>Molecular Biology and Evolution</i> , <b>2000</b> , 17, 890-6	8.3	230

263	Identification of functional modules using network topology and high-throughput data. <i>BMC Systems Biology</i> , <b>2007</b> , 1, 8	3.5	229
262	Conservation and evolvability in regulatory networks: the evolution of ribosomal regulation in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 7203-8	11.5	212
261	Cluster graph modification problems. <i>Discrete Applied Mathematics</i> , <b>2004</b> , 144, 173-182	1	200
260	Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence. <i>Stem Cells</i> , <b>2008</b> , 26, 1506-16	5.8	184
259	Expander: from expression microarrays to networks and functions. <i>Nature Protocols</i> , <b>2010</b> , 5, 303-22	18.8	165
258	Transcription factor and microRNA motif discovery: the Amadeus platform and a compendium of metazoan target sets. <i>Genome Research</i> , <b>2008</b> , 18, 1180-9	9.7	146
257	Multi-omic and multi-view clustering algorithms: review and cancer benchmark. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, 10546-10562	20.1	144
256	Graph Sandwich Problems. <i>Journal of Algorithms</i> , <b>1995</b> , 19, 449-473		125
255	Tractability of Parameterized Completion Problems on Chordal, Strongly Chordal, and Proper Interval Graphs. <i>SIAM Journal on Computing</i> , <b>1999</b> , 28, 1906-1922	1.1	124
254	A Faster and Simpler Algorithm for Sorting Signed Permutations by Reversals. <i>SIAM Journal on Computing</i> , <b>2000</b> , 29, 880-892	1.1	121
253	Four strikes against physical mapping of DNA. <i>Journal of Computational Biology</i> , <b>1995</b> , 2, 139-52	1.7	121
252	Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 835-46	1.7	120
251	Complexity classification of some edge modification problems. <i>Discrete Applied Mathematics</i> , <b>2001</b> , 113, 109-128	1	119
250	Complexity and algorithms for reasoning about time. <i>Journal of the ACM</i> , <b>1993</b> , 40, 1108-1133	2	118
249	Dissection of regulatory networks that are altered in disease via differential co-expression. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1002955	5	104
248	GERBIL: Genotype resolution and block identification using likelihood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2005</b> , 102, 158-62	11.5	99
247	The canine olfactory subgenome. <i>Genomics</i> , <b>2004</b> , 83, 361-72	4.3	97
246	A non-EST-based method for exon-skipping prediction. <i>Genome Research</i> , <b>2004</b> , 14, 1617-23	9.7	94

245	DEGAS: de novo discovery of dysregulated pathways in human diseases. <i>PLoS ONE</i> , <b>2010</b> , 5, e13367	3.7	94
244	Identifying functional modules using expression profiles and confidence-scored protein interactions. <i>Bioinformatics</i> , <b>2009</b> , 25, 1158-64	7.2	93
243	Accurate identification of alternatively spliced exons using support vector machine. <i>Bioinformatics</i> , <b>2005</b> , 21, 897-901	7.2	89
242	Tag SNP selection in genotype data for maximizing SNP prediction accuracy. <i>Bioinformatics</i> , <b>2005</b> , 21 Suppl 1, i195-203	7.2	85
241	Transcription factor/microRNA axis blocks melanoma invasion program by miR-211 targeting NUAK1. <i>Journal of Investigative Dermatology</i> , <b>2014</b> , 134, 441-451	4.3	82
240	Topology-free querying of protein interaction networks. <i>Journal of Computational Biology</i> , <b>2010</b> , 17, 237-52	1.7	80
239	A plasma-membrane E-MAP reveals links of the eisosome with sphingolipid metabolism and endosomal trafficking. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 901-8	17.6	79
238	Towards computational prediction of microRNA function and activity. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, e160	20.1	75
237	Transcriptional modulation induced by ionizing radiation: p53 remains a central player. <i>Molecular Oncology</i> , <b>2011</b> , 5, 336-48	7.9	74
236	Pathwidth, Bandwidth, and Completion Problems to Proper Interval Graphs with Small Cliques. <i>SIAM Journal on Computing</i> , <b>1996</b> , 25, 540-561	1.1	73
235	The degenerate primer design problem. <i>Bioinformatics</i> , <b>2002</b> , 18 Suppl 1, S172-81	7.2	72
234	Environmental stresses disrupt telomere length homeostasis. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003721	6	70
233	Faster Subtree Isomorphism. <i>Journal of Algorithms</i> , <b>1999</b> , 33, 267-280		70
232	A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, e63	20.1	68
231	Enhancer methylation dynamics contribute to cancer plasticity and patient mortality. <i>Genome Research</i> , <b>2016</b> , 26, 601-11	9.7	67
230	On the Complexity of DNA Physical Mapping. <i>Advances in Applied Mathematics</i> , <b>1994</b> , 15, 251-261	0.8	67
229	Integration of transcriptomics, proteomics, and microRNA analyses reveals novel microRNA regulation of targets in the mammalian inner ear. <i>PLoS ONE</i> , <b>2011</b> , 6, e18195	3.7	67
228	Transcription factor family-specific DNA shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , <b>2017</b> , 13, 910	12.2	66

227	An algorithm for clustering cDNA fingerprints. <i>Genomics</i> , <b>2000</b> , 66, 249-56	4.3	66
226	The Efficiency of the Simplex Method: A Survey. <i>Management Science</i> , <b>1987</b> , 33, 301-334	3.9	65
225	Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 9854-61	20.1	63
224	Dissection of a DNA-damage-induced transcriptional network using a combination of microarrays, RNA interference and computational promoter analysis. <i>Genome Biology</i> , <b>2005</b> , 6, R43	18.3	62
223	Parallel induction of ATM-dependent pro- and antiapoptotic signals in response to ionizing radiation in murine lymphoid tissue. <i>Oncogene</i> , <b>2006</b> , 25, 1584-92	9.2	62
222	Recycler: an algorithm for detecting plasmids from de novo assembly graphs. <i>Bioinformatics</i> , <b>2017</b> , 33, 475-482	7.2	62
221	Computing has changed biology--biology education must catch up. <i>Science</i> , <b>2009</b> , 325, 541-2	33.3	61
220	NEMO: cancer subtyping by integration of partial multi-omic data. <i>Bioinformatics</i> , <b>2019</b> , 35, 3348-3356	7.2	60
219	Analysis of blood-based gene expression in idiopathic Parkinson disease. <i>Neurology</i> , <b>2017</b> , 89, 1676-1683	6.5	59
218	SPIKE: a database of highly curated human signaling pathways. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D793-9	20.1	59
217	From E-MAPs to module maps: dissecting quantitative genetic interactions using physical interactions. <i>Molecular Systems Biology</i> , <b>2008</b> , 4, 209	12.2	59
216	A genome-wide analysis in <i>Saccharomyces cerevisiae</i> demonstrates the influence of chromatin modifiers on transcription. <i>Nature Genetics</i> , <b>2007</b> , 39, 303-9	36.3	59
215	Strongly Polynomial Algorithms for the High Multiplicity Scheduling Problem. <i>Operations Research</i> , <b>1991</b> , 39, 648-653	2.3	58
214	A catalog of stability-associated sequence elements in 3SUTRs of yeast mRNAs. <i>Genome Biology</i> , <b>2005</b> , 6, R86	18.3	57
213	Scoring clustering solutions by their biological relevance. <i>Bioinformatics</i> , <b>2003</b> , 19, 2381-9	7.2	56
212	Pediatric onset Crohn's colitis is characterized by genotype-dependent age-related susceptibility. <i>Inflammatory Bowel Diseases</i> , <b>2007</b> , 13, 1509-15	4.5	51
211	A probabilistic methodology for integrating knowledge and experiments on biological networks. <i>Journal of Computational Biology</i> , <b>2006</b> , 13, 165-81	1.7	50
210	The degenerate primer design problem: theory and applications. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 431-56	1.7	49

209	SPIKE--a database, visualization and analysis tool of cellular signaling pathways. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 110	3.6	48
208	A block-free hidden Markov model for genotypes and its application to disease association. <i>Journal of Computational Biology</i> , <b>2005</b> , 12, 1243-60	1.7	48
207	A Fully Dynamic Algorithm for Recognizing and Representing Proper Interval Graphs. <i>SIAM Journal on Computing</i> , <b>2001</b> , 31, 289-305	1.1	46
206	Parallel profiling of the transcriptome, cistrome, and epigenome in the cellular response to ionizing radiation. <i>Science Signaling</i> , <b>2014</b> , 7, rs3	8.8	45
205	Refinement and expansion of signaling pathways: the osmotic response network in yeast. <i>Genome Research</i> , <b>2007</b> , 17, 358-67	9.7	44
204	Reduced changes in protein compared to mRNA levels across non-proliferating tissues. <i>BMC Genomics</i> , <b>2017</b> , 18, 305	4.5	43
203	Gene expression signature of human cancer cell lines treated with the ras inhibitor salirasib (S-farnesylthiosalicylic acid). <i>Cancer Research</i> , <b>2007</b> , 67, 3320-8	10.1	43
202	Two notes on genome rearrangement. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2003</b> , 1, 71-94		43
201	Incomplete Directed Perfect Phylogeny. <i>SIAM Journal on Computing</i> , <b>2004</b> , 33, 590-607	1.1	43
200	MicroRNAs are essential for differentiation of the retinal pigmented epithelium and maturation of adjacent photoreceptors. <i>Development (Cambridge)</i> , <b>2015</b> , 142, 2487-98	6.6	42
199	Element: a computational tool for detecting core promoter elements. <i>Transcription</i> , <b>2015</b> , 6, 41-50	4.8	42
198	Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy. <i>Genome Biology</i> , <b>2011</b> , 12, R61	18.3	42
197	A randomization test for controlling population stratification in whole-genome association studies. <i>American Journal of Human Genetics</i> , <b>2007</b> , 81, 895-905	11	42
196	Expression and methylation patterns partition luminal-A breast tumors into distinct prognostic subgroups. <i>Breast Cancer Research</i> , <b>2016</b> , 18, 74	8.3	41
195	Deciphering transcriptional regulatory elements that encode specific cell cycle phasing by comparative genomics analysis. <i>Cell Cycle</i> , <b>2005</b> , 4, 1788-97	4.7	39
194	Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium. <i>Molecular Systems Biology</i> , <b>2005</b> , 1, 2005.0002	12.2	39
193	A simpler and faster 1.5-approximation algorithm for sorting by transpositions. <i>Information and Computation</i> , <b>2006</b> , 204, 275-290	0.8	39
192	A large-scale perspective on stress-induced alterations in resting-state networks. <i>Scientific Reports</i> , <b>2016</b> , 6, 21503	4.9	39

191	Drosophila TRF2 is a preferential core promoter regulator. <i>Genes and Development</i> , <b>2014</b> , 28, 2163-74	12.6	36
190	Allegro: analyzing expression and sequence in concert to discover regulatory programs. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, 1566-79	20.1	36
189	GEVALT: an integrated software tool for genotype analysis. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 36	3.6	36
188	A fast method for computing high-significance disease association in large population-based studies. <i>American Journal of Human Genetics</i> , <b>2006</b> , 79, 481-92	11	36
187	SlimPLS: a method for feature selection in gene expression-based disease classification. <i>PLoS ONE</i> , <b>2009</b> , 4, e6416	3.7	34
186	Detecting Disease-Specific Dysregulated Pathways Via Analysis of Clinical Expression Profiles <b>2008</b> , 347-359		34
185	Tired and misconnected: A breakdown of brain modularity following sleep deprivation. <i>Human Brain Mapping</i> , <b>2017</b> , 38, 3300-3314	5.9	33
184	FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer-promoter map. <i>Genome Biology</i> , <b>2018</b> , 19, 56	18.3	32
183	Faster and simpler algorithm for sorting signed permutations by reversals <b>1997</b> ,		31
182	A Polynomial Approximation Algorithm for the Minimum Fill-In Problem. <i>SIAM Journal on Computing</i> , <b>2000</b> , 30, 1067-1079	1.1	30
181	Minimizing the number of tardy job units under release time constraints. <i>Discrete Applied Mathematics</i> , <b>1990</b> , 28, 45-57	1	30
180	Computational expansion of genetic networks. <i>Bioinformatics</i> , <b>2001</b> , 17 Suppl 1, S270-8	7.2	29
179	Evidence of TAF1 dysfunction in peripheral models of X-linked dystonia-parkinsonism. <i>Cellular and Molecular Life Sciences</i> , <b>2016</b> , 73, 3205-15	10.3	28
178	Improving the performance of minimizers and winnowing schemes. <i>Bioinformatics</i> , <b>2017</b> , 33, i110-i117	7.2	27
177	An algorithm for clustering cDNAs for gene expression analysis <b>1999</b> ,		27
176	An algorithm for the detection and construction of Monge sequences. <i>Linear Algebra and Its Applications</i> , <b>1989</b> , 114-115, 669-680	0.9	26
175	Network-induced classification kernels for gene expression profile analysis. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 694-709	1.7	25
174	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> , <b>2011</b> , 6, e17509	3.7	25

173	ATM haplotypes and breast cancer risk in Jewish high-risk women. <i>British Journal of Cancer</i> , <b>2006</b> , 94, 1537-43	8.7	25
172	Functional genomic delineation of TLR-induced transcriptional networks. <i>BMC Genomics</i> , <b>2007</b> , 8, 394	4.5	24
171	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> , <b>2006</b> , 119, 527-38	7.5	24
170	Constructing module maps for integrated analysis of heterogeneous biological networks. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, 4208-19	20.1	23
169	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> , <b>2012</b> , 19, 30-41	1.7	23
168	TORQUE: topology-free querying of protein interaction networks. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W106-11	6.1	23
167	Chain functions and scoring functions in genetic networks. <i>Bioinformatics</i> , <b>2003</b> , 19 Suppl 1, i108-17	7.2	23
166	In silico identification of transcriptional regulators associated with c-Myc. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, 4955-61	20.1	23
165	PIVOT: protein interactions visualization tool. <i>Bioinformatics</i> , <b>2004</b> , 20, 424-5	7.2	23
164	A fully dynamic algorithm for modular decomposition and recognition of cographs. <i>Discrete Applied Mathematics</i> , <b>2004</b> , 136, 329-340	1	23
163	Modeling and analysis of heterogeneous regulation in biological networks. <i>Journal of Computational Biology</i> , <b>2004</b> , 11, 1034-49	1.7	23
162	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005777	5	22
161	Different sets of QTLs influence fitness variation in yeast. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 346	12.2	21
160	A global view of the selection forces in the evolution of yeast cis-regulation. <i>Genome Research</i> , <b>2004</b> , 14, 829-34	9.7	21
159	A randomized scheme for speeding up algorithms for linear and convex programming problems with high constraints-to-variables ratio. <i>Mathematical Programming</i> , <b>1993</b> , 61, 39-52	2.1	21
158	Using the kinetics of C-reactive protein response to improve the differential diagnosis between acute bacterial and viral infections. <i>Infection</i> , <b>2020</b> , 48, 241-248	5.8	21
157	Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 7779-89	20.1	20
156	Large scale sequencing by hybridization. <i>Journal of Computational Biology</i> , <b>2002</b> , 9, 413-28	1.7	20



155	A simplex variant solving an $m \times d$ linear program in $O(\min(m^2, d^2))$ expected number of pivot steps. <i>Journal of Complexity</i> , <b>1987</b> , 3, 372-387	1.2	20
154	Assessment of algorithms for inferring positional weight matrix motifs of transcription factor binding sites using protein binding microarray data. <i>PLoS ONE</i> , <b>2012</b> , 7, e46145	3.7	20
153	Systematic inference of highways of horizontal gene transfer in prokaryotes. <i>Bioinformatics</i> , <b>2013</b> , 29, 571-9	7.2	19
152	Complexity and algorithms for copy-number evolution problems. <i>Algorithms for Molecular Biology</i> , <b>2017</b> , 12, 13	1.8	19
151	The MORPH algorithm: ranking candidate genes for membership in Arabidopsis and tomato pathways. <i>Plant Cell</i> , <b>2012</b> , 24, 4389-406	11.6	19
150	Towards accurate imputation of quantitative genetic interactions. <i>Genome Biology</i> , <b>2009</b> , 10, R140	18.3	19
149	Evolution and selection in yeast promoters: analyzing the combined effect of diverse transcription factor binding sites. <i>PLoS Computational Biology</i> , <b>2008</b> , 4, e7	5	19
148	Bounded Degree Interval Sandwich Problems. <i>Algorithmica</i> , <b>1999</b> , 24, 96-104	0.9	19
147	The domatic number problem on some perfect graph families. <i>Information Processing Letters</i> , <b>1994</b> , 49, 51-56	0.8	19
146	A polynomial algorithm for an integer quadratic non-separable transportation problem. <i>Mathematical Programming</i> , <b>1992</b> , 55, 359-371	2.1	19
145	Fast lossless compression via cascading Bloom filters. <i>BMC Bioinformatics</i> , <b>2014</b> , 15 Suppl 9, S7	3.6	18
144	Risk factors for perianal Crohn's disease: the role of genotype, phenotype, and ethnicity. <i>American Journal of Gastroenterology</i> , <b>2007</b> , 102, 1702-8	0.7	18
143	Complexity Classification of Some Edge Modification Problems. <i>Lecture Notes in Computer Science</i> , <b>1999</b> , 65-77	0.9	18
142	Evaluation and integration of functional annotation pipelines for newly sequenced organisms: the potato genome as a test case. <i>BMC Plant Biology</i> , <b>2014</b> , 14, 329	5.3	17
141	Ras inhibits endoplasmic reticulum stress in human cancer cells with amplified Myc. <i>International Journal of Cancer</i> , <b>2010</b> , 126, 2268-81	7.5	17
140	Detecting excess radical replacements in phylogenetic trees. <i>Gene</i> , <b>2003</b> , 319, 127-35	3.8	17
139	DEFOG: a practical scheme for deciphering families of genes. <i>Genomics</i> , <b>2002</b> , 80, 295-302	4.3	17
138	Transcriptional and proteomic analysis of the <i>Aspergillus fumigatus</i> prtT protease-deficient mutant. <i>PLoS ONE</i> , <b>2012</b> , 7, e33604	3.7	17

137	A Faster Algorithm for RNA Co-folding. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 174-185	0.9	17
136	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , <b>2016</b> , 257-268	0.9	17
135	A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2011</b> , 8, 848-50	3	16
134	Assessing the number of ancestral alternatively spliced exons in the human genome. <i>BMC Genomics</i> , <b>2006</b> , 7, 273	4.5	16
133	MetaReg: a platform for modeling, analysis and visualization of biological systems using large-scale experimental data. <i>Genome Biology</i> , <b>2008</b> , 9, R1	18.3	15
132	Cluster Graph Modification Problems. <i>Lecture Notes in Computer Science</i> , <b>2002</b> , 379-390	0.9	15
131	Computational Problems in Perfect Phylogeny Haplotyping: Xor-Genotypes and Tag SNPs. <i>Lecture Notes in Computer Science</i> , <b>2004</b> , 14-31	0.9	15
130	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, e51	20.1	14
129	Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 15	3.5	14
128	The incomplete perfect phylogeny haplotype problem. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2005</b> , 3, 359-84	1	14
127	PlasClass improves plasmid sequence classification. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007781	5	14
126	The EXPANDER Integrated Platform for Transcriptome Analysis. <i>Journal of Molecular Biology</i> , <b>2019</b> , 431, 2398-2406	6.5	13
125	RAP: accurate and fast motif finding based on protein-binding microarray data. <i>Journal of Computational Biology</i> , <b>2013</b> , 20, 375-82	1.7	13
124	An $O(n \log 2n)$ algorithm for the maximum weighed tardiness problem. <i>Information Processing Letters</i> , <b>1989</b> , 31, 215-219	0.8	13
123	Topology-Free Querying of Protein Interaction Networks. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 74-89	0.9	13
122	Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications. <i>Oncogene</i> , <b>2017</b> , 36, 3375-3383	9.2	12
121	Detecting highways of horizontal gene transfer. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 1087-114	1.7	12
120	Faster pattern matching with character classes using prime number encoding. <i>Journal of Computer and System Sciences</i> , <b>2009</b> , 75, 155-162	1	12

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