

Wing-Kin Sung

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.

219
papers

19,881
citations

53
h-index

140
g-index

243
ext. papers

22,396
ext. citations

7.6
avg, IF

5.88
L-index

#	Paper	IF	Citations
219	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007 , 447, 799-816	50.4	4121
218	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. <i>Cell</i> , 2008 , 133, 1106-17	56.2	1978
217	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , 2009 , 462, 58-64	50.4	1243
216	A global map of p53 transcription-factor binding sites in the human genome. <i>Cell</i> , 2006 , 124, 207-19	56.2	958
215	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
214	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012 , 44, 765-9	36.3	627
213	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011 , 43, 630-8	36.3	503
212	Whole-genome mapping of histone H3 Lys4 and 27 trimethylations reveals distinct genomic compartments in human embryonic stem cells. <i>Cell Stem Cell</i> , 2007 , 1, 286-98	18	489
211	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. <i>Bioinformatics</i> , 2006 , 22, 1623-30	7.2	455
210	A common BIM deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. <i>Nature Medicine</i> , 2012 , 18, 521-8	50.5	433
209	Global mapping of c-Myc binding sites and target gene networks in human B cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 17834-9	11.5	411
208	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013 , 23, 1422-33	9.7	371
207	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
206	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , 2009 , 28, 3341-52	13	332
205	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013 , 504, 306-310	50.4	313
204	Genomic portrait of resectable hepatocellular carcinomas: implications of RB1 and FGF19 aberrations for patient stratification. <i>Hepatology</i> , 2014 , 60, 1972-82	11.2	272
203	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013 , 31, 126-34	44.5	268

202	Telomerase directly regulates NF- κ B-dependent transcription. <i>Nature Cell Biology</i> , 2012 , 14, 1270-81	23.4	241
201	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005 , 2, 105-11	21.6	218
200	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010 , 11, R22	18.3	199
199	Genome-wide mutational signatures of aristolochic acid and its application as a screening tool. <i>Science Translational Medicine</i> , 2013 , 5, 197ra101	17.5	194
198	Lethal-7 is down-regulated by the hepatitis B virus x protein and targets signal transducer and activator of transcription 3. <i>Journal of Hepatology</i> , 2010 , 53, 57-66	13.4	186
197	Sall4 regulates distinct transcription circuitries in different blastocyst-derived stem cell lineages. <i>Cell Stem Cell</i> , 2008 , 3, 543-54	18	171
196	Cellular reprogramming by the conjoint action of ER β , FOXA1, and GATA3 to a ligand-inducible growth state. <i>Molecular Systems Biology</i> , 2011 , 7, 526	12.2	151
195	Genome-wide mapping of RELA(p65) binding identifies E2F1 as a transcriptional activator recruited by NF-kappaB upon TLR4 activation. <i>Molecular Cell</i> , 2007 , 27, 622-35	17.6	149
194	Opera: reconstructing optimal genomic scaffolds with high-throughput paired-end sequences. <i>Journal of Computational Biology</i> , 2011 , 18, 1681-91	1.7	139
193	Integration of regulatory networks by NKX3-1 promotes androgen-dependent prostate cancer survival. <i>Molecular and Cellular Biology</i> , 2012 , 32, 399-414	4.8	125
192	AP-2 β regulates oestrogen receptor-mediated long-range chromatin interaction and gene transcription. <i>EMBO Journal</i> , 2011 , 30, 2569-81	13	123
191	An HMM approach to genome-wide identification of differential histone modification sites from ChIP-seq data. <i>Bioinformatics</i> , 2008 , 24, 2344-9	7.2	122
190	A signal-noise model for significance analysis of ChIP-seq with negative control. <i>Bioinformatics</i> , 2010 , 26, 1199-204	7.2	116
189	Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012 , 13, R115	18.3	110
188	Using indirect protein-protein interactions for protein complex prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 435-66	1	103
187	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. <i>Nature Genetics</i> , 2019 , 51, 138-150	36.3	99
186	Deletion of the WD40 domain of LRRK2 in Zebrafish causes Parkinsonism-like loss of neurons and locomotive defect. <i>PLoS Genetics</i> , 2010 , 6, e1000914	6	96
185	Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. <i>Nucleic Acids Research</i> , 2006 , 34, e84	20.1	96

184	A genomic survey of positive selection in <i>Burkholderia pseudomallei</i> provides insights into the evolution of accidental virulence. <i>PLoS Pathogens</i> , 2010 , 6, e1000845	7.6	91
183	Structural variation detection using next-generation sequencing data: A comparative technical review. <i>Methods</i> , 2016 , 102, 36-49	4.6	89
182	PE-Assembler: de novo assembler using short paired-end reads. <i>Bioinformatics</i> , 2011 , 27, 167-74	7.2	89
181	3D chromosome modeling with semi-definite programming and Hi-C data. <i>Journal of Computational Biology</i> , 2013 , 20, 831-46	1.7	86
180	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015 , 12, 272-85	10.6	84
179	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). <i>Genome Research</i> , 2007 , 17, 828-38	9.7	80
178	Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts. <i>Oncogene</i> , 2012 , 31, 1695-709	9.2	75
177	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. <i>SIAM Journal on Computing</i> , 2006 , 35, 1098-1121	1.1	72
176	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012 , 58, 289-99	4.6	69
175	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. <i>Genome Research</i> , 2011 , 21, 665-75	9.7	68
174	Comprehensive evaluation of common genetic variation within LRRK2 reveals evidence for association with sporadic Parkinson's disease. <i>Human Molecular Genetics</i> , 2005 , 14, 3549-56	5.6	68
173	Transcriptional consequences of genomic structural aberrations in breast cancer. <i>Genome Research</i> , 2011 , 21, 676-87	9.7	67
172	Oseltamivir ring prophylaxis for containment of 2009 H1N1 influenza outbreaks. <i>New England Journal of Medicine</i> , 2010 , 362, 2166-74	59.2	66
171	Protein subcellular localization prediction for Gram-negative bacteria using amino acid subalphabets and a combination of multiple support vector machines. <i>BMC Bioinformatics</i> , 2005 , 6, 174	3.6	59
170	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic <i>Burkholderia</i> isolates. <i>Genome Biology</i> , 2010 , 11, R89	18.3	58
169	Target gene analysis by microarrays and chromatin immunoprecipitation identifies HEY proteins as highly redundant bHLH repressors. <i>PLoS Genetics</i> , 2012 , 8, e1002728	6	56
168	Computing the maximum agreement of phylogenetic networks. <i>Theoretical Computer Science</i> , 2005 , 335, 93-107	1.1	54
167	Association mapping via regularized regression analysis of single-nucleotide-polymorphism haplotypes in variable-sized sliding windows. <i>American Journal of Human Genetics</i> , 2007 , 80, 705-15	11	53

166	An efficient strategy for extensive integration of diverse biological data for protein function prediction. <i>Bioinformatics</i> , 2007 , 23, 3364-73	7.2	51
165	Differential transcriptomic analyses revealed genes and signaling pathways involved in iono-osmoregulation and cellular remodeling in the gills of euryhaline Mozambique tilapia, <i>Oreochromis mossambicus</i> . <i>BMC Genomics</i> , 2014 , 15, 921	4.5	49
164	Inferring a level-1 phylogenetic network from a dense set of rooted triplets. <i>Theoretical Computer Science</i> , 2006 , 363, 60-68	1.1	48
163	Using indirect protein interactions for the prediction of Gene Ontology functions. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 4, S8	3.6	47
162	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. <i>Algorithmica</i> , 2007 , 48, 23-36	0.9	45
161	Optimization and clinical validation of a pathogen detection microarray. <i>Genome Biology</i> , 2007 , 8, R93	18.3	44
160	TP53 intron 1 hotspot rearrangements are specific to sporadic osteosarcoma and can cause Li-Fraumeni syndrome. <i>Oncotarget</i> , 2015 , 6, 7727-40	3.3	43
159	The Brm-HDAC3-Erm repressor complex suppresses dedifferentiation in <i>Drosophila</i> type II neuroblast lineages. <i>ELife</i> , 2014 , 3, e01906	8.9	43
158	CENTDIST: discovery of co-associated factors by motif distribution. <i>Nucleic Acids Research</i> , 2011 , 39, W391-9	3.9	42
157	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <i>Genome Biology</i> , 2012 , 13, R82	18.3	41
156	Breaking a Time-and-Space Barrier in Constructing Full-Text Indices. <i>SIAM Journal on Computing</i> , 2009 , 38, 2162-2178	1.1	40
155	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. <i>Nature Communications</i> , 2019 , 10, 3640	17.4	39
154	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014 , 103, 189-203	4.3	39
153	An Even Faster and More Unifying Algorithm for Comparing Trees via Unbalanced Bipartite Matchings. <i>Journal of Algorithms</i> , 2001 , 40, 212-233		39
152	Inherent signals in sequencing-based Chromatin-ImmunoPrecipitation control libraries. <i>PLoS ONE</i> , 2009 , 4, e5241	3.7	38
151	Deregulated direct targets of the hepatitis B virus (HBV) protein, HBx, identified through chromatin immunoprecipitation and expression microarray profiling. <i>Journal of Biological Chemistry</i> , 2009 , 284, 21941-21954	5.4	36
150	Protein structure and fold prediction using Tree-Augmented naïve Bayesian classifier. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 803-19	1	34
149	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. <i>Bioinformatics</i> , 2008 , 24, 2288-95	7.2	33

148	Rooted Maximum Agreement Supertrees. <i>Algorithmica</i> , 2005 , 43, 293-307	0.9	33
147	A Decomposition Theorem for Maximum Weight Bipartite Matchings. <i>SIAM Journal on Computing</i> , 2001 , 31, 18-26	1.1	32
146	Ultra-succinct representation of ordered trees with applications. <i>Journal of Computer and System Sciences</i> , 2012 , 78, 619-631	1	31
145	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs. <i>Journal of Computational Biology</i> , 2003 , 10, 981-95	1.7	31
144	A correlated motif approach for finding short linear motifs from protein interaction networks. <i>BMC Bioinformatics</i> , 2006 , 7, 502	3.6	28
143	Fast relative Lempel-Ziv self-index for similar sequences. <i>Theoretical Computer Science</i> , 2014 , 532, 14-30	1.1	25
142	BatMis: a fast algorithm for k-mismatch mapping. <i>Bioinformatics</i> , 2012 , 28, 2122-8	7.2	25
141	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. <i>Genome Research</i> , 2019 , 29, 223-235	9.7	24
140	Detection of generic spaced motifs using submotif pattern mining. <i>Bioinformatics</i> , 2007 , 23, 1476-85	7.2	23
139	Approximate string matching using compressed suffix arrays. <i>Theoretical Computer Science</i> , 2006 , 352, 240-249	1.1	23
138	PET-Tool: a software suite for comprehensive processing and managing of Paired-End diTag (PET) sequence data. <i>BMC Bioinformatics</i> , 2006 , 7, 390	3.6	22
137	Linked Dynamic Tries with Applications to LZ-Compression in Sublinear Time and Space. <i>Algorithmica</i> , 2015 , 71, 969-988	0.9	21
136	HPV-CCDC106 integration alters local chromosome architecture and hijacks an enhancer by three-dimensional genome structure remodeling in cervical cancer. <i>Journal of Genetics and Genomics</i> , 2020 , 47, 437-450	4	21
135	Pathogen chip for respiratory tract infections. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 945-53	9.7	21
134	Inferring phylogenetic relationships avoiding forbidden rooted triplets. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 59-74	1	21
133	Computational modeling of oligonucleotide positional densities for human promoter prediction. <i>Artificial Intelligence in Medicine</i> , 2005 , 35, 107-19	7.4	21
132	Algorithms in Bioinformatics		21
131	Succinct data structures for Searchable Partial Sums with optimal worst-case performance. <i>Theoretical Computer Science</i> , 2011 , 412, 5176-5186	1.1	19

130	G-PRIMER: greedy algorithm for selecting minimal primer set. <i>Bioinformatics</i> , 2004 , 20, 2473-5	7.2	18
129	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019 , 20, 47	3.6	16
128	Xenopus tropicalis Genome Re-Scaffolding and Re-Annotation Reach the Resolution Required for In Vivo ChIA-PET Analysis. <i>PLoS ONE</i> , 2015 , 10, e0137526	3.7	16
127	Model gene network by semi-fixed Bayesian network. <i>Expert Systems With Applications</i> , 2006 , 30, 42-49	7.8	16
126	Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data. <i>Lecture Notes in Computer Science</i> , 2013 , 317-332	0.9	16
125	An $O(m \log m)$ -Time Algorithm for Detecting Superbubbles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015 , 12, 770-7	3	15
124	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 2218-21	4.7	15
123	Localized motif discovery in gene regulatory sequences. <i>Bioinformatics</i> , 2010 , 26, 1152-9	7.2	15
122	Constructing a Smallest Refining Galled Phylogenetic Network. <i>Lecture Notes in Computer Science</i> , 2005 , 265-280	0.9	15
121	Finding Short Right-Hand-on-the-Wall Walks in Graphs. <i>Lecture Notes in Computer Science</i> , 2005 , 127-139	0.9	15
120	An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins. <i>Nature Communications</i> , 2017 , 8, 122	17.4	14
119	Large-scale evolutionary surveillance of the 2009 H1N1 influenza A virus using resequencing arrays. <i>Nucleic Acids Research</i> , 2010 , 38, e111	20.1	14
118	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION 2007 ,		14
117	A Linear Size Index for Approximate Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2006 , 49-59	0.9	14
116	Comprehensive analysis of transcriptome profiles in hepatocellular carcinoma. <i>Journal of Translational Medicine</i> , 2019 , 17, 273	8.5	13
115	Approximate String Matching Using Compressed Suffix Arrays. <i>Lecture Notes in Computer Science</i> , 2004 , 434-444	0.9	13
114	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. <i>Lecture Notes in Computer Science</i> , 2002 , 401-410	0.9	13
113	A Decomposition Theorem for MaximumWeight Bipartite Matchings with Applications to Evolutionary Trees. <i>Lecture Notes in Computer Science</i> , 1999 , 438-449	0.9	13

112	Platform comparison for evaluation of ALK protein immunohistochemical expression, genomic copy number and hotspot mutation status in neuroblastomas. <i>PLoS ONE</i> , 2014 , 9, e106575	3.7	12
111	Compressed Indexes for Approximate String Matching. <i>Algorithmica</i> , 2010 , 58, 263-281	0.9	12
110	The Integrator Complex Prevents Dedifferentiation of Intermediate Neural Progenitors back into Neural Stem Cells. <i>Cell Reports</i> , 2019 , 27, 987-996.e3	10.6	11
109	Long span DNA paired-end-tag (DNA-PET) sequencing strategy for the interrogation of genomic structural mutations and fusion-point-guided reconstruction of amplicons. <i>PLoS ONE</i> , 2012 , 7, e46152	3.7	11
108	SLiM on Diet: finding short linear motifs on domain interaction interfaces in Protein Data Bank. <i>Bioinformatics</i> , 2010 , 26, 1036-42	7.2	11
107	Structural alignment of RNA with complex pseudoknot structure. <i>Journal of Computational Biology</i> , 2011 , 18, 97-108	1.7	11
106	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. <i>Lecture Notes in Computer Science</i> , 2011 , 437-451	0.9	11
105	CRAM: Compressed Random Access Memory. <i>Lecture Notes in Computer Science</i> , 2012 , 510-521	0.9	11
104	Increasing confidence of protein-protein interactomes. <i>Genome Informatics</i> , 2006 , 17, 284-97		11
103	Simultaneously learning DNA motif along with its position and sequence rank preferences through expectation maximization algorithm. <i>Journal of Computational Biology</i> , 2013 , 20, 237-48	1.7	10
102	More efficient periodic traversal in anonymous undirected graphs. <i>Theoretical Computer Science</i> , 2012 , 444, 60-76	1.1	10
101	Polynomial-time algorithms for building a consensus MUL-tree. <i>Journal of Computational Biology</i> , 2012 , 19, 1073-88	1.7	10
100	Probabilistic prediction of protein-protein interactions from the protein sequences. <i>Computers in Biology and Medicine</i> , 2006 , 36, 1143-54	7	10
99	A linear size index for approximate pattern matching. <i>Journal of Discrete Algorithms</i> , 2011 , 9, 358-364		9
98	Partial convex recolorings of trees and galled networks. <i>ACM Transactions on Algorithms</i> , 2011 , 7, 1-20	1.2	9
97	General techniques for comparing unrooted evolutionary trees 1997 ,		9
96	Next-generation sequencing of apoptotic DNA breakpoints reveals association with actively transcribed genes and gene translocations. <i>PLoS ONE</i> , 2011 , 6, e26054	3.7	9
95	Fast Relative Lempel-Ziv Self-index for Similar Sequences. <i>Lecture Notes in Computer Science</i> , 2012 , 291-303		9

94	Improved Algorithms for Constructing Consensus Trees. <i>Journal of the ACM</i> , 2016 , 63, 1-24	2	9
93	TranSurVeyor: an improved database-free algorithm for finding non-reference transpositions in high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2018 , 46, e122	20.1	9
92	Improved Approximate String Matching Using Compressed Suffix Data Structures. <i>Lecture Notes in Computer Science</i> , 2005 , 339-348	0.9	9
91	BatAlign: an incremental method for accurate alignment of sequencing reads. <i>Nucleic Acids Research</i> , 2015 , 43, e107	20.1	8
90	Identifying differential histone modification sites from CHIP-seq data. <i>Methods in Molecular Biology</i> , 2012 , 802, 293-303	1.4	8
89	Computing a smallest multilabeled phylogenetic tree from rooted triplets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 1141-7	3	8
88	Improved Approximate String Matching Using Compressed Suffix Data Structures. <i>Algorithmica</i> , 2008 , 51, 298-314	0.9	8
87	Cavity Matchings, Label Compressions, and Unrooted Evolutionary Trees. <i>SIAM Journal on Computing</i> , 2000 , 30, 602-624	1.1	8
86	Inferring a Level-1 Phylogenetic Network from a Dense Set of Rooted Triplets. <i>Lecture Notes in Computer Science</i> , 2004 , 462-471	0.9	8
85	Reconstructing recombination network from sequence data: the small parsimony problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007 , 4, 394-402	3	7
84	CPS-tree: A Compact Partitioned Suffix Tree for Disk-based Indexing on Large Genome Sequences 2007 ,		7
83	Local gapped subforest alignment and its application in finding RNA structural motifs. <i>Journal of Computational Biology</i> , 2006 , 13, 702-18	1.7	7
82	Fast and accurate probe selection algorithm for large genomes		7
81	Brief overview of bioinformatics activities in Singapore. <i>PLoS Computational Biology</i> , 2009 , 5, e1000508	5	6
80	The Maximum Agreement of Two Nested Phylogenetic Networks. <i>Lecture Notes in Computer Science</i> , 2004 , 581-593	0.9	6
79	Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions. <i>Lecture Notes in Computer Science</i> , 2006 , 1-1	0.9	6
78	Bioinformatics Applications in Genomics. <i>Computer</i> , 2012 , 45, 57-63	1.6	5
77	Constructing the R* Consensus Tree of Two Trees in Subcubic Time. <i>Algorithmica</i> , 2013 , 66, 329-345	0.9	5

76	D-SLIMMER: domain-SLiM interaction motifs miner for sequence based protein-protein interaction data. <i>Journal of Proteome Research</i> , 2011 , 10, 5285-95	5.6	5
75	A Faster and More Space-Efficient Algorithm for Inferring Arc-Annotations of RNA Sequences through Alignment. <i>Algorithmica</i> , 2006 , 46, 223-245	0.9	5
74	SurVirus: a repeat-aware virus integration caller. <i>Nucleic Acids Research</i> , 2021 , 49, e33	20.1	5
73	Improved Algorithms for Constructing Consensus Trees 2013 ,		4
72	Improved Algorithms for Maximum Agreement and Compatible Supertrees. <i>Algorithmica</i> , 2011 , 59, 195-214	0.9	4
71	Fast algorithms for computing the tripartition-based distance between phylogenetic networks. <i>Journal of Combinatorial Optimization</i> , 2007 , 13, 223-242	0.9	4
70	News sports video shot classification with sports play field and motion features		4
69	Computing the Maximum Agreement of Phylogenetic Networks. <i>Electronic Notes in Theoretical Computer Science</i> , 2004 , 91, 134-147	0.7	4
68	Automatic construction of online catalog topologies. <i>IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews</i> , 2002 , 32, 382-391		4
67	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs 2001 ,		4
66	Rooted Maximum Agreement Supertrees. <i>Lecture Notes in Computer Science</i> , 2004 , 499-508	0.9	4
65	More Efficient Periodic Traversal in Anonymous Undirected Graphs. <i>Lecture Notes in Computer Science</i> , 2010 , 167-181	0.9	4
64	Histone lysine methyltransferase Pr-set7/SETD8 promotes neural stem cell reactivation. <i>EMBO Reports</i> , 2021 , 22, e50994	6.5	4
63	Fast and accurate probe selection algorithm for large genomes 2003 , 2, 65-74		4
62	A Linear Time Algorithm for the r-Gathering Problem on the Line (Extended Abstract). <i>Lecture Notes in Computer Science</i> , 2019 , 56-66	0.9	3
61	CWig: compressed representation of Wiggle/BedGraph format. <i>Bioinformatics</i> , 2014 , 30, 2543-50	7.2	3
60	Discovering interacting domains and motifs in protein-protein interactions. <i>Methods in Molecular Biology</i> , 2013 , 939, 9-20	1.4	3
59	On finding the Adams consensus tree. <i>Information and Computation</i> , 2017 , 256, 334-347	0.8	3

58	Constructing phylogenetic supernetworks based on simulated annealing. <i>Molecular Phylogenetics and Evolution</i> , 2012 , 63, 738-44	4.1	3
57	Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm. <i>Lecture Notes in Computer Science</i> , 2012 , 355-370	0.9	3
56	RB-finder: an improved distance-based sliding window method to detect recombination breakpoints. <i>Journal of Computational Biology</i> , 2008 , 15, 881-98	1.7	3
55	LEARNING GENE NETWORK USING TIME-DELAYED BAYESIAN NETWORK. <i>International Journal on Artificial Intelligence Tools</i> , 2006 , 15, 353-370	0.9	3
54	Effective algorithms for tag SNP selection. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 1089-106	1	3
53	Faster Algorithms for 1-Mappability of a Sequence. <i>Lecture Notes in Computer Science</i> , 2017 , 109-121	0.9	3
52	Algorithms for the Majority Rule (+) Consensus Tree and the Frequency Difference Consensus Tree. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 15-26	3	2
51	Do triplets have enough information to construct the multi-labeled phylogenetic tree?. <i>PLoS ONE</i> , 2014 , 9, e103622	3.7	2
50	THE 24TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS, GIW2013, IN SINGAPORE. <i>Journal of Bioinformatics and Computational Biology</i> , 2013 , 11, 1302003	1	2
49	Non-shared edges and nearest neighbor interchanges revisited. <i>Information Processing Letters</i> , 2004 , 91, 129-134	0.8	2
48	The Enhanced Double Digest Problem for DNA Physical Mapping. <i>Journal of Combinatorial Optimization</i> , 2003 , 7, 69-78	0.9	2
47	Algorithms for Next-Generation Sequencing		2
46	Faster Algorithms for Computing the R* Consensus Tree. <i>Lecture Notes in Computer Science</i> , 2014 , 414-405		2
45	A Streamlined and Generalized Analysis of Chromatin ImmunoPrecipitation Paired-End diTag Data. <i>Lecture Notes in Computer Science</i> , 2008 , 130-139	0.9	2
44	Determining the Consistency of Resolved Triplets and Fan Triplets. <i>Lecture Notes in Computer Science</i> , 2017 , 82-98	0.9	2
43	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <i>BMC Bioinformatics</i> , 2020 , 21, 451	3.6	2
42	ASMcdb: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
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