

Wing-Kin Sung

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1344210/wing-kin-sung-publications-by-year.pdf>

Version: 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study.. <i>Patterns</i> , 2022 , 3, 100399	5.1	0
218	Single-cell analysis reveals androgen receptor regulates the ER-to-Golgi trafficking pathway with CREB3L2 to drive prostate cancer progression. <i>Oncogene</i> , 2021 , 40, 6479-6493	9.2	0
217	SurVirus: a repeat-aware virus integration caller. <i>Nucleic Acids Research</i> , 2021 , 49, e33	20.1	5
216	ASMDb: a comprehensive database for allele-specific DNA methylation in diverse organisms. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
215	Histone lysine methyltransferase Pr-set7/SETD8 promotes neural stem cell reactivation. <i>EMBO Reports</i> , 2021 , 22, e50994	6.5	4
214	Computing the Rooted Triplet Distance Between Phylogenetic Networks. <i>Algorithmica</i> , 2021 , 83, 1786-1828	18.9	0
213	RiceENCODE: A comprehensive epigenomic database as a rice Encyclopedia of DNA Elements. <i>Molecular Plant</i> , 2021 , 14, 1604-1606	14.4	2
212	HIVID2: an accurate tool to detect virus integrations in the host genome. <i>Bioinformatics</i> , 2021 ,	7.2	2
211	Calling large indels in 1047 Arabidopsis with IndelEnsembler. <i>Nucleic Acids Research</i> , 2021 , 49, 10879-10894	8.9	1
210	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
209	Efficient Identification of k-Closed Strings. <i>International Journal of Foundations of Computer Science</i> , 2020 , 31, 595-610	0.6	1
208	Faster algorithms for 1-mappability of a sequence. <i>Theoretical Computer Science</i> , 2020 , 812, 2-12	1.1	1
207	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <i>BMC Bioinformatics</i> , 2020 , 21, 451	3.6	2
206	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. <i>BMC Bioinformatics</i> , 2019 , 20, 47	3.6	16
205	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
204	An Efficient Algorithm for the Rooted Triplet Distance Between Galled Trees. <i>Journal of Computational Biology</i> , 2019 , 26, 893-907	1.7	1
203	SurVIndel: improving CNV calling from high-throughput sequencing data through statistical testing. <i>Bioinformatics</i> , 2019 ,	7.2	1

202	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
201	Learning Chromatin Interaction Using Hi-C Datasets 2019 , 318-323		
200	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
199	Comprehensive analysis of transcriptome profiles in hepatocellular carcinoma. <i>Journal of Translational Medicine</i> , 2019 , 17, 273	8.5	13
198	Computing the Rooted Triplet Distance Between Phylogenetic Networks. <i>Lecture Notes in Computer Science</i> , 2019 , 290-303	0.9	1
197	Greedy Consensus Tree and Maximum Greedy Consensus Tree Problems. <i>Lecture Notes in Computer Science</i> , 2019 , 305-316	0.9	0
196	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
195	Off-line and on-line algorithms for closed string factorization. <i>Theoretical Computer Science</i> , 2019 , 792, 12-19	1.1	
194	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
193	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
192	Minimal Phylogenetic Supertrees and Local Consensus Trees. <i>AIMS Medical Science</i> , 2018 , 5, 181-203	0.4	
191	Computing Asymmetric Median Tree of Two Trees via Better Bipartite Matching Algorithm. <i>Lecture Notes in Computer Science</i> , 2018 , 356-367	0.9	1
190	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
189	Determining the Consistency of Resolved Triplets and Fan Triplets. <i>Journal of Computational Biology</i> , 2018 , 25, 740-754	1.7	
188	An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins. <i>Nature Communications</i> , 2017 , 8, 122	17.4	14
187	On finding the Adams consensus tree. <i>Information and Computation</i> , 2017 , 256, 334-347	0.8	3
186	An Efficient Algorithm for the Rooted Triplet Distance Between Galled Trees. <i>Lecture Notes in Computer Science</i> , 2017 , 115-126	0.9	1
185	Efficient Identification of k-Closed Strings. <i>Communications in Computer and Information Science</i> , 2017 , 583-595	0.3	1

184	Determining the Consistency of Resolved Triplets and Fan Triplets. <i>Lecture Notes in Computer Science</i> , 2017 , 82-98	0.9	2
183	Faster Algorithms for 1-Mappability of a Sequence. <i>Lecture Notes in Computer Science</i> , 2017 , 109-121	0.9	3
182	Comparison of microarray-predicted closest genomes to sequencing for poliovirus vaccine strain similarity and influenza A phylogeny. <i>Diagnostic Microbiology and Infectious Disease</i> , 2016 , 84, 203-6	2.9	
181	Structural variation detection using next-generation sequencing data: A comparative technical review. <i>Methods</i> , 2016 , 102, 36-49	4.6	89
180	Faster Algorithms for Computing the R* Consensus Tree. <i>Algorithmica</i> , 2016 , 76, 1224-1244	0.9	
179	Improved Algorithms for Constructing Consensus Trees. <i>Journal of the ACM</i> , 2016 , 63, 1-24	2	9
178	Linked Dynamic Tries with Applications to LZ-Compression in Sublinear Time and Space. <i>Algorithmica</i> , 2015 , 71, 969-988	0.9	21
177	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
176	BatAlign: an incremental method for accurate alignment of sequencing reads. <i>Nucleic Acids Research</i> , 2015 , 43, e107	20.1	8
175	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. <i>Cell Reports</i> , 2015 , 12, 272-85	10.6	84
174	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
173	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
172	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network 2015 , 1-6		
171	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
170	CWig: compressed representation of Wiggle/BedGraph format. <i>Bioinformatics</i> , 2014 , 30, 2543-50	7.2	3
169	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. <i>Genomics</i> , 2014 , 103, 189-203	4.3	39
168	Fast relative Lempel-Ziv self-index for similar sequences. <i>Theoretical Computer Science</i> , 2014 , 532, 14-30	1.1	25
167	Do triplets have enough information to construct the multi-labeled phylogenetic tree?. <i>PLoS ONE</i> , 2014 , 9, e103622	3.7	2

166	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
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	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
163	Faster Algorithms for Computing the R* Consensus Tree. <i>Lecture Notes in Computer Science</i> , 2014 , 414-425		2
162	Constructing the R* Consensus Tree of Two Trees in Subcubic Time. <i>Algorithmica</i> , 2013 , 66, 329-345	0.9	5
161	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013 , 31, 126-34	44.5	268
160	3D chromosome modeling with semi-definite programming and Hi-C data. <i>Journal of Computational Biology</i> , 2013 , 20, 831-46	1.7	86
159	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
158	Chromatin connectivity maps reveal dynamic promoter-enhancer long-range associations. <i>Nature</i> , 2013 , 504, 306-310	50.4	313
157	International Conference on Genome Informatics (GIW 2013) in Singapore: Introduction to the systems biology contributions. <i>BMC Systems Biology</i> , 2013 , 7 Suppl 6, I1	3.5	
156	Pathogen chip for respiratory tract infections. <i>Journal of Clinical Microbiology</i> , 2013 , 51, 945-53	9.7	21
155	Discovering interacting domains and motifs in protein-protein interactions. <i>Methods in Molecular Biology</i> , 2013 , 939, 9-20	1.4	3
154	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
153	Improved Algorithms for Constructing Consensus Trees 2013 ,		4
152	Algorithms for the Majority Rule (+) Consensus Tree and the Frequency Difference Consensus Tree. <i>Lecture Notes in Computer Science</i> , 2013 , 141-155	0.9	
151	THE 24TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS, GIW2013, IN SINGAPORE. <i>Journal of Bioinformatics and Computational Biology</i> , 2013 , 11, 1302003	1	2
150	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. <i>Genome Research</i> , 2013 , 23, 1422-33	9.7	371
149	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

148	An Optimal Algorithm for Building the Majority Rule Consensus Tree. <i>Lecture Notes in Computer Science</i> , 2013 , 88-99	0.9	1
147	Ultra-succinct representation of ordered trees with applications. <i>Journal of Computer and System Sciences</i> , 2012 , 78, 619-631	1	31
146	Bioinformatics Applications in Genomics. <i>Computer</i> , 2012 , 45, 57-63	1.6	5
145	Telomerase directly regulates NF- κ B-dependent transcription. <i>Nature Cell Biology</i> , 2012 , 14, 1270-81	23.4	241
144	ChIA-PET analysis of transcriptional chromatin interactions. <i>Methods</i> , 2012 , 58, 289-99	4.6	69
143	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. <i>Genome Biology</i> , 2012 , 13, R82	18.3	41
142	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. <i>Nature Genetics</i> , 2012 , 44, 765-9	36.3	627
141	More efficient periodic traversal in anonymous undirected graphs. <i>Theoretical Computer Science</i> , 2012 , 444, 60-76	1.1	10
140	Constructing phylogenetic supernetworks based on simulated annealing. <i>Molecular Phylogenetics and Evolution</i> , 2012 , 63, 738-44	4.1	3
139	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
138	Extensive promoter-centered chromatin interactions provide a topological basis for transcription regulation. <i>Cell</i> , 2012 , 148, 84-98	56.2	882
137	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
136	Identifying differential histone modification sites from ChIP-seq data. <i>Methods in Molecular Biology</i> , 2012 , 802, 293-303	1.4	8
135	Whole-genome reconstruction and mutational signatures in gastric cancer. <i>Genome Biology</i> , 2012 , 13, R115	18.3	110
134	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
133	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
132	BatMis: a fast algorithm for k-mismatch mapping. <i>Bioinformatics</i> , 2012 , 28, 2122-8	7.2	25
131	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

130	Polynomial-time algorithms for building a consensus MUL-tree. <i>Journal of Computational Biology</i> , 2012 , 19, 1073-88	1.7	10
129	Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts. <i>Oncogene</i> , 2012 , 31, 1695-709	9.2	75
128	Fast Relative Lempel-Ziv Self-index for Similar Sequences. <i>Lecture Notes in Computer Science</i> , 2012 , 291-302	0.9	9
127	CRAM: Compressed Random Access Memory. <i>Lecture Notes in Computer Science</i> , 2012 , 510-521	0.9	11
126	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
125	Cellular reprogramming by the conjoint action of ER α , FOXA1, and GATA3 to a ligand-inducible growth state. <i>Molecular Systems Biology</i> , 2011 , 7, 526	12.2	151
124	AP-2 β regulates oestrogen receptor-mediated long-range chromatin interaction and gene transcription. <i>EMBO Journal</i> , 2011 , 30, 2569-81	13	123
123	Succinct data structures for Searchable Partial Sums with optimal worst-case performance. <i>Theoretical Computer Science</i> , 2011 , 412, 5176-5186	1.1	19
122	A linear size index for approximate pattern matching. <i>Journal of Discrete Algorithms</i> , 2011 , 9, 358-364		9
121	CTCF-mediated functional chromatin interactome in pluripotent cells. <i>Nature Genetics</i> , 2011 , 43, 630-8	36.3	503
120	Improved Algorithms for Maximum Agreement and Compatible Supertrees. <i>Algorithmica</i> , 2011 , 59, 195-214	0.9	4
119	Chromatin interaction networks and higher order architectures of eukaryotic genomes. <i>Journal of Cellular Biochemistry</i> , 2011 , 112, 2218-21	4.7	15
118	Structural alignment of RNA with complex pseudoknot structure. <i>Journal of Computational Biology</i> , 2011 , 18, 97-108	1.7	11
117	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
116	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
115	Partial convex recolorings of trees and galled networks. <i>ACM Transactions on Algorithms</i> , 2011 , 7, 1-20	1.2	9
114	Transcriptional consequences of genomic structural aberrations in breast cancer. <i>Genome Research</i> , 2011 , 21, 676-87	9.7	67
113	Opera: reconstructing optimal genomic scaffolds with high-throughput paired-end sequences. <i>Journal of Computational Biology</i> , 2011 , 18, 1681-91	1.7	139

112	PE-Assembler: de novo assembler using short paired-end reads. <i>Bioinformatics</i> , 2011 , 27, 167-74	7.2	89
111	CENTDIST: discovery of co-associated factors by motif distribution. <i>Nucleic Acids Research</i> , 2011 , 39, W321-9	2.9	42
110	Assemblathon 1: a competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011 , 21, 2224-41	9.7	364
109	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
108	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. <i>Lecture Notes in Computer Science</i> , 2011 , 437-451	0.9	11
107	Algorithms for Building Consensus MUL-trees. <i>Lecture Notes in Computer Science</i> , 2011 , 744-753	0.9	
106	Localized motif discovery in gene regulatory sequences. <i>Bioinformatics</i> , 2010 , 26, 1152-9	7.2	15
105	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
104	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
103	A signal-noise model for significance analysis of ChIP-seq with negative control. <i>Bioinformatics</i> , 2010 , 26, 1199-204	7.2	116
102	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
101	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
100	Oseltamivir ring prophylaxis for containment of 2009 H1N1 influenza outbreaks. <i>New England Journal of Medicine</i> , 2010 , 362, 2166-74	59.2	66
99	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
98	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
97	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. <i>Genome Biology</i> , 2010 , 11, R22	18.3	199
96	Compressed Indexes for Approximate String Matching. <i>Algorithmica</i> , 2010 , 58, 263-281	0.9	12
95	Constructing the R* Consensus Tree of Two Trees in Subcubic Time. <i>Lecture Notes in Computer Science</i> , 2010 , 573-584	0.9	1

94	More Efficient Periodic Traversal in Anonymous Undirected Graphs. <i>Lecture Notes in Computer Science</i> , 2010 , 167-181	0.9	4
93	Adjacent nucleotide dependence in ncRNA and order-1 SCFG for ncRNA identification. <i>PLoS ONE</i> , 2010 , 5, e12848	3.7	1
92	Brief overview of bioinformatics activities in Singapore. <i>PLoS Computational Biology</i> , 2009 , 5, e1000508	5	6
91	Inherent signals in sequencing-based Chromatin-ImmunoPrecipitation control libraries. <i>PLoS ONE</i> , 2009 , 4, e5241	3.7	38
90	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
89	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. <i>EMBO Journal</i> , 2009 , 28, 3341-52	13	332
88	An oestrogen-receptor-alpha-bound human chromatin interactome. <i>Nature</i> , 2009 , 462, 58-64	50.4	1243
87	Breaking a Time-and-Space Barrier in Constructing Full-Text Indices. <i>SIAM Journal on Computing</i> , 2009 , 38, 2162-2178	1.1	40
86	The 2-Interval Pattern Matching Problems and Its Application to ncRNA Scanning. <i>Lecture Notes in Computer Science</i> , 2009 , 79-89	0.9	
85	Structural Alignment of RNA with Complex Pseudoknot Structure. <i>Lecture Notes in Computer Science</i> , 2009 , 403-414	0.9	1
84	Computing a Smallest Multi-labeled Phylogenetic Tree from Rooted Triplets. <i>Lecture Notes in Computer Science</i> , 2009 , 1205-1214	0.9	1
83	Sall4 regulates distinct transcription circuitries in different blastocyst-derived stem cell lineages. <i>Cell Stem Cell</i> , 2008 , 3, 543-54	18	171
82	Integration of external signaling pathways with the core transcriptional network in embryonic stem cells. <i>Cell</i> , 2008 , 133, 1106-17	56.2	1978
81	Using indirect protein-protein interactions for protein complex prediction. <i>Journal of Bioinformatics and Computational Biology</i> , 2008 , 6, 435-66	1	103
80	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. <i>Bioinformatics</i> , 2008 , 24, 2288-95	7.2	33
79	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
78	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
77	Improved Approximate String Matching Using Compressed Suffix Data Structures. <i>Algorithmica</i> , 2008 , 51, 298-314	0.9	8

76	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
75	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
74	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
73	Using indirect protein interactions for the prediction of Gene Ontology functions. <i>BMC Bioinformatics</i> , 2007 , 8 Suppl 4, S8	3.6	47
72	Fast algorithms for computing the tripartition-based distance between phylogenetic networks. <i>Journal of Combinatorial Optimization</i> , 2007 , 13, 223-242	0.9	4
71	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. <i>Algorithmica</i> , 2007 , 48, 23-36	0.9	45
70	Detection of generic spaced motifs using submotif pattern mining. <i>Bioinformatics</i> , 2007 , 23, 1476-85	7.2	23
69	An efficient strategy for extensive integration of diverse biological data for protein function prediction. <i>Bioinformatics</i> , 2007 , 23, 3364-73	7.2	51
68	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
67	CPS-tree: A Compact Partitioned Suffix Tree for Disk-based Indexing on Large Genome Sequences 2007 ,		7
66	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION 2007 ,		14
65	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
64	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
63	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
62	Optimization and clinical validation of a pathogen detection microarray. <i>Genome Biology</i> , 2007 , 8, R93	18.3	44
61	Application of Bayesian Network in Learning Gene Network 2007 , 319-341		
60	Application of Bayesian Network in Drug Discovery and Development Process 2007 , 254-268		
59	Bayesian Network Modeling of Transcription Factor Binding Sites 2007 , 300-318		

58	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
57	A correlated motif approach for finding short linear motifs from protein interaction networks. <i>BMC Bioinformatics</i> , 2006 , 7, 502	3.6	28
56	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. <i>Bioinformatics</i> , 2006 , 22, 1623-30	7.2	455
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	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
53	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
52	Inferring phylogenetic relationships avoiding forbidden rooted triplets. <i>Journal of Bioinformatics and Computational Biology</i> , 2006 , 4, 59-74	1	21
51	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
50	2006 ,		1
49	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. <i>SIAM Journal on Computing</i> , 2006 , 35, 1098-1121	1.1	72
48	A global map of p53 transcription-factor binding sites in the human genome. <i>Cell</i> , 2006 , 124, 207-19	56.2	958
47	Model gene network by semi-fixed Bayesian network. <i>Expert Systems With Applications</i> , 2006 , 30, 42-49	7.8	16
46	Probabilistic prediction of protein-protein interactions from the protein sequences. <i>Computers in Biology and Medicine</i> , 2006 , 36, 1143-54	7	10
45	Approximate string matching using compressed suffix arrays. <i>Theoretical Computer Science</i> , 2006 , 352, 240-249	1.1	23
44	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
43	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
42	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
41	A Linear Size Index for Approximate Pattern Matching. <i>Lecture Notes in Computer Science</i> , 2006 , 49-59	0.9	14

40	Compressed Indexes for Approximate String Matching. <i>Lecture Notes in Computer Science</i> , 2006 , 208-219	0.9	1
39	Increasing confidence of protein-protein interactomes. <i>Genome Informatics</i> , 2006 , 17, 284-97		11
38	Constructing a Smallest Refining Galled Phylogenetic Network. <i>Lecture Notes in Computer Science</i> , 2005 , 265-280	0.9	15
37	Computing the maximum agreement of phylogenetic networks. <i>Theoretical Computer Science</i> , 2005 , 335, 93-107	1.1	54
36	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. <i>Nature Methods</i> , 2005 , 2, 105-11	21.6	218
35	Computational modeling of oligonucleotide positional densities for human promoter prediction. <i>Artificial Intelligence in Medicine</i> , 2005 , 35, 107-19	7.4	21
34	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
33	Rooted Maximum Agreement Supertrees. <i>Algorithmica</i> , 2005 , 43, 293-307	0.9	33
32	Finding Short Right-Hand-on-the-Wall Walks in Graphs. <i>Lecture Notes in Computer Science</i> , 2005 , 127-139	0.9	15
31	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
30	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
29	Effective algorithms for tag SNP selection. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 1089-106	1	3
28	Adaptive control of hybridization noise in DNA sequencing-by-hybridization. <i>Journal of Bioinformatics and Computational Biology</i> , 2005 , 3, 79-98	1	1
27	Fast Algorithms for Computing the Tripartition-Based Distance Between Phylogenetic Networks. <i>Lecture Notes in Computer Science</i> , 2005 , 402-411	0.9	
26	Improved Approximate String Matching Using Compressed Suffix Data Structures. <i>Lecture Notes in Computer Science</i> , 2005 , 339-348	0.9	9
25	Approximate String Matching Using Compressed Suffix Arrays. <i>Lecture Notes in Computer Science</i> , 2004 , 434-444	0.9	13
24	SUBTREE TRANSFER DISTANCE FOR DEGREE-D PHYLOGENIES. <i>International Journal of Foundations of Computer Science</i> , 2004 , 15, 893-909	0.6	1
23	G-PRIMER: greedy algorithm for selecting minimal primer set. <i>Bioinformatics</i> , 2004 , 20, 2473-5	7.2	18

22	Computing the Maximum Agreement of Phylogenetic Networks. <i>Electronic Notes in Theoretical Computer Science</i> , 2004 , 91, 134-147	0.7	4
21	Non-shared edges and nearest neighbor interchanges revisited. <i>Information Processing Letters</i> , 2004 , 91, 129-134	0.8	2
20	Rooted Maximum Agreement Supertrees. <i>Lecture Notes in Computer Science</i> , 2004 , 499-508	0.9	4
19	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
18	The Maximum Agreement of Two Nested Phylogenetic Networks. <i>Lecture Notes in Computer Science</i> , 2004 , 581-593	0.9	6
17	The Enhanced Double Digest Problem for DNA Physical Mapping. <i>Journal of Combinatorial Optimization</i> , 2003 , 7, 69-78	0.9	2
16	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
15	Fast and accurate probe selection algorithm for large genomes 2003 , 2, 65-74		4
14	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
13	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. <i>Lecture Notes in Computer Science</i> , 2002 , 401-410	0.9	13
12	An Even Faster and More Unifying Algorithm for Comparing Trees via Unbalanced Bipartite Matchings. <i>Journal of Algorithms</i> , 2001 , 40, 212-233		39
11	A Decomposition Theorem for Maximum Weight Bipartite Matchings. <i>SIAM Journal on Computing</i> , 2001 , 31, 18-26	1.1	32
10	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs 2001 ,		4
9	Cavity Matchings, Label Compressions, and Unrooted Evolutionary Trees. <i>SIAM Journal on Computing</i> , 2000 , 30, 602-624	1.1	8
8	Unbalanced and Hierarchical Bipartite Matchings with Applications to Labeled Tree Comparison. <i>Lecture Notes in Computer Science</i> , 2000 , 479-490	0.9	
7	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
6	General techniques for comparing unrooted evolutionary trees 1997 ,		9
5	News sports video shot classification with sports play field and motion features		4

4	Fast and accurate probe selection algorithm for large genomes	7
3	Breaking a time-and-space barrier in constructing full-text indices	1
2	Algorithms for Next-Generation Sequencing	2
1	Algorithms in Bioinformatics	21