Wing-Kin Sung

List of Publications by Year
in descending order

		24978	8138
232 papers	23,961 citations	57 h-index	148 g-index
243 all docs	243 docs citations	243 times ranked	33804 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
2	Integration of External Signaling Pathways with the Core Transcriptional Network in Embryonic Stem Cells. Cell, 2008, 133, 1106-1117.	13.5	2,279
3	An oestrogen-receptor-Î±-bound human chromatin interactome. Nature, 2009, 462, 58-64.	13.7	1,537
4	Extensive Promoter-Centered Chromatin Interactions Provide a Topological Basis for Transcription Regulation. Cell, 2012, 148, 84-98.	13.5	1,096
5	A Global Map of p53 Transcription-Factor Binding Sites in the Human Genome. Cell, 2006, 124, 207-219.	13.5	1,060
6	Genome-wide survey of recurrent HBV integration in hepatocellular carcinoma. Nature Genetics, 2012, 44, 765-769.	9.4	785
7	CTCF-mediated functional chromatin interactome in pluripotent cells. Nature Genetics, 2011, 43, 630-638.	9.4	567
8	Whole-Genome Mapping of Histone H3 Lys4 and 27 Trimethylations Reveals Distinct Genomic Compartments in Human Embryonic Stem Cells. Cell Stem Cell, 2007, 1, 286-298.	5.2	536
9	Exploiting indirect neighbours and topological weight to predict protein function from protein-protein interactions. Bioinformatics, 2006, 22, 1623-1630.	1.8	533
10	A common BIM deletion polymorphism mediates intrinsic resistance and inferior responses to tyrosine kinase inhibitors in cancer. Nature Medicine, 2012, 18, 521-528.	15.2	510
11	Global mapping of c-Myc binding sites and target gene networks in human B cells. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 17834-17839.	3.3	462
12	Whole-genome sequencing identifies recurrent mutations in hepatocellular carcinoma. Genome Research, 2013, 23, 1422-1433.	2.4	457
13	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
14	Chromatin connectivity maps reveal dynamic promoterâ€"enhancer long-range associations. Nature, 2013, 504, 306-310.	13.7	405
15	Jmjd3 contributes to the control of gene expression in LPS-activated macrophages. EMBO Journal, 2009, 28, 3341-3352.	3.5	383
16	Genomic portrait of resectable hepatocellular carcinomas: Implications of *RB1* and *FGF19* aberrations for patient stratification. Hepatology, 2014, 60, 1972-1982.	3.6	345
17	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	9.4	341
18	Telomerase directly regulates NF-Î°B-dependent transcription. Nature Cell Biology, 2012, 14, 1270-1281.	4.6	309

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19	ChIA-PET tool for comprehensive chromatin interaction analysis with paired-end tag sequencing. Genome Biology, 2010, 11, R22.	13.9	255
20	Gene identification signature (GIS) analysis for transcriptome characterization and genome annotation. Nature Methods, 2005, 2, 105-111.	9.0	244
21	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	5.8	233
22	Lethal-7 is down-regulated by the hepatitis B virus x protein and targets signal transducer and activator of transcription 3. Journal of Hepatology, 2010, 53, 57-66.	1.8	212
23	Sall4 Regulates Distinct Transcription Circuitries in Different Blastocyst-Derived Stem Cell Lineages. Cell Stem Cell, 2008, 3, 543-554.	5.2	209
24	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. Journal of Computational Biology, 2011, 18, 1681-1691.	0.8	183
25	Genome-wide Mapping of RELA(p65) Binding Identifies E2F1 as a Transcriptional Activator Recruited by NF-κB upon TLR4 Activation. Molecular Cell, 2007, 27, 622-635.	4.5	180
26	Immune genes are primed for robust transcription by proximal long noncoding RNAs located in nuclear compartments. Nature Genetics, 2019, 51, 138-150.	9.4	177
27	Cellular reprogramming by the conjoint action of ERα, FOXA1, and GATA3 to a ligand€inducible growth state. Molecular Systems Biology, 2011, 7, 526.	3.2	169
28	Integration of Regulatory Networks by NKX3-1 Promotes Androgen-Dependent Prostate Cancer Survival. Molecular and Cellular Biology, 2012, 32, 399-414.	1.1	165
29	AP-2γ regulates oestrogen receptor-mediated long-range chromatin interaction and gene transcription. EMBO Journal, 2011, 30, 2569-2581.	3.5	144
30	An HMM approach to genome-wide identification of differential histone modification sites from ChIP-seq data. Bioinformatics, 2008, 24, 2344-2349.	1.8	141
31	A signal€"noise model for significance analysis of ChIP-seq with negative control. Bioinformatics, 2010, 26, 1199-1204.	1.8	131
32	Structural variation detection using next-generation sequencing data. Methods, 2016, 102, 36-49.	1.9	129
33	USING INDIRECT PROTEIN€"PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 435-466.	0.3	123
34	A Genomic Survey of Positive Selection in Burkholderia pseudomallei Provides Insights into the Evolution of Accidental Virulence. PLoS Pathogens, 2010, 6, e1000845.	2.1	116
35	Whole-genome reconstruction and mutational signatures in gastric cancer. Genome Biology, 2012, 13, R115.	13.9	116
36	Deletion of the WD40 Domain of LRRK2 in Zebrafish Causes Parkinsonism-Like Loss of Neurons and Locomotive Defect. PLoS Genetics, 2010, 6, e1000914.	1.5	114

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37	Recurrent Fusion Genes in Gastric Cancer: CLDN18-ARHGAP26 Induces Loss of Epithelial Integrity. Cell Reports, 2015, 12, 272-285.	2.9	112
38	Multiplex sequencing of paired-end ditags (MS-PET): a strategy for the ultra-high-throughput analysis of transcriptomes and genomes. Nucleic Acids Research, 2006, 34, e84-e84.	6.5	111
39	3D Chromosome Modeling with Semi-Definite Programming and Hi-C Data. Journal of Computational Biology, 2013, 20, 831-846.	0.8	110
40	PE-Assembler: <i>de novo</i> assembler using short paired-end reads. Bioinformatics, 2011, 27, 167-174.	1.8	98
41	Genome-wide mapping of Myc binding and gene regulation in serum-stimulated fibroblasts. Oncogene, 2012, 31, 1695-1709.	2.6	90
42	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. SIAM Journal on Computing, 2006, 35, 1098-1121.	0.8	88
43	Fusion transcripts and transcribed retrotransposed loci discovered through comprehensive transcriptome analysis using Paired-End diTags (PETs). Genome Research, 2007, 17, 828-838.	2.4	86
44	ChIA-PET analysis of transcriptional chromatin interactions. Methods, 2012, 58, 289-299.	1.9	83
45	Comprehensive evaluation of common genetic variation within LRRK2 reveals evidence for association with sporadic Parkinson's disease. Human Molecular Genetics, 2005, 14, 3549-3556.	1.4	75
46	Oseltamivir Ring Prophylaxis for Containment of 2009 H1N1 Influenza Outbreaks. New England Journal of Medicine, 2010, 362, 2166-2174.	13.9	75
47	Chromatin loops associated with active genes and heterochromatin shape rice genome architecture for transcriptional regulation. Nature Communications, 2019, 10, 3640.	5.8	75
48	Comprehensive long-span paired-end-tag mapping reveals characteristic patterns of structural variations in epithelial cancer genomes. Genome Research, 2011, 21, 665-675.	2.4	74
49	Transcriptional consequences of genomic structural aberrations in breast cancer. Genome Research, 2011, 21, 676-687.	2.4	74
50	Breaking a Time-and-Space Barrier in Constructing Full-Text Indices. SIAM Journal on Computing, 2009, 38, 2162-2178.	0.8	71
51	Genomic acquisition of a capsular polysaccharide virulence cluster by non-pathogenic Burkholderia isolates. Genome Biology, 2010, 11, R89.	13.9	70
52	Protein subcellular localization prediction for Gram-negative bacteria using amino acid subalphabets and a combination of multiple support vector machines. BMC Bioinformatics, 2005, 6, 174.	1.2	68
53	Computing the maximum agreement of phylogenetic networks. Theoretical Computer Science, 2005, 335, 93-107.	0.5	66
54	CENTDIST: discovery of co-associated factors by motif distribution. Nucleic Acids Research, 2011, 39, W391-W399.	6.5	66

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55	Target Gene Analysis by Microarrays and Chromatin Immunoprecipition Identifies HEY Proteins as Highly Redundant bHLH Repressors. PLoS Genetics, 2012, 8, e1002728.	1.5	66
56	Differential transcriptomic analyses revealed genes and signaling pathways involved in iono-osmoregulation and cellular remodeling in the gills of euryhaline Mozambique tilapia, Oreochromis mossambicus. BMC Genomics, 2014, 15, 921.	1.2	66
57	Inferring a level-1 phylogenetic network from a dense set of rooted triplets. Theoretical Computer Science, 2006, 363, 60-68.	0.5	60
58	The Brm-HDAC3-Erm repressor complex suppresses dedifferentiation in Drosophila type II neuroblast lineages. ELife, 2014, 3, e01906.	2.8	60
59	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. Algorithmica, 2007, 48, 23-36.	1.0	59
60	An efficient strategy for extensive integration of diverse biological data for protein function prediction. Bioinformatics, 2007, 23, 3364-3373.	1.8	56
61	Association Mapping via Regularized Regression Analysis of Single-Nucleotideâ€"Polymorphism Haplotypes in Variable-Sized Sliding Windows. American Journal of Human Genetics, 2007, 80, 705-715.	2.6	55
62	Using indirect protein interactions for the prediction of Gene Ontology functions. BMC Bioinformatics, 2007, 8, S8.	1.2	54
63	Optimization and clinical validation of a pathogen detection microarray. Genome Biology, 2007, 8, R93.	13.9	51
64	An integrated package for bisulfite DNA methylation data analysis with Indel-sensitive mapping. BMC Bioinformatics, 2019, 20, 47.	1.2	51
65	<i>TP53</i> intron 1 hotspot rearrangements are specific to sporadic osteosarcoma and can cause Li-Fraumeni syndrome. Oncotarget, 2015, 6, 7727-7740.	0.8	51
66	An Even Faster and More Unifying Algorithm for Comparing Trees via Unbalanced Bipartite Matchings. Journal of Algorithms, 2001, 40, 212-233.	0.9	50
67	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. Genomics, 2014, 103, 189-203.	1.3	49
68	Predicting RNA Secondary Structures with Arbitrary Pseudoknots by Maximizing the Number of Stacking Pairs. Journal of Computational Biology, 2003, 10, 981-995.	0.8	48
69	HPV-CCDC106 integration alters local chromosome architecture and hijacks an enhancer by three-dimensional genome structure remodeling in cervical cancer. Journal of Genetics and Genomics, 2020, 47, 437-450.	1.7	48
70	PROTEIN STRUCTURE AND FOLD PREDICTION USING TREE-AUGMENTED NAÃVE BAYESIAN CLASSIFIER. Journal of Bioinformatics and Computational Biology, 2005, 03, 803-819.	0.3	47
71	An AR-ERG transcriptional signature defined by long-range chromatin interactomes in prostate cancer cells. Genome Research, 2019, 29, 223-235.	2.4	46
72	BatMeth: improved mapper for bisulfite sequencing reads on DNA methylation. Genome Biology, 2012, 13, R82.	13.9	45

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73	Ultra-succinct representation of ordered trees with applications. Journal of Computer and System Sciences, 2012, 78, 619-631.	0.9	44
74	Rooted Maximum Agreement Supertrees. Algorithmica, 2005, 43, 293-307.	1.0	43
75	A Decomposition Theorem for Maximum Weight Bipartite Matchings. SIAM Journal on Computing, 2001, 31, 18-26.	0.8	42
76	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. Bioinformatics, 2008, 24, 2288-2295.	1.8	41
77	A correlated motif approach for finding short linear motifs from protein interaction networks. BMC Bioinformatics, 2006, 7, 502.	1.2	40
78	Inherent Signals in Sequencing-Based Chromatin-ImmunoPrecipitation Control Libraries. PLoS ONE, 2009, 4, e5241.	1.1	40
79	Deregulated Direct Targets of the Hepatitis B Virus (HBV) Protein, HBx, Identified through Chromatin Immunoprecipitation and Expression Microarray Profiling. Journal of Biological Chemistry, 2009, 284, 21941-21954.	1.6	39
80	Fast relative Lempel–Ziv self-index for similar sequences. Theoretical Computer Science, 2014, 532, 14-30.	0.5	34
81	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , .		33
82	BatMis: a fast algorithm for k-mismatch mapping. Bioinformatics, 2012, 28, 2122-2128.	1.8	32
83	Approximate string matching using compressed suffix arrays. Theoretical Computer Science, 2006, 352, 240-249.	0.5	31
84	Inference of Spatial Organizations of Chromosomes Using Semi-definite Embedding Approach and Hi-C Data. Lecture Notes in Computer Science, 2013, , 317-332.	1.0	30
85	PET-Tool: a software suite for comprehensive processing and managing of Paired-End diTag (PET) sequence data. BMC Bioinformatics, 2006, 7, 390.	1.2	29
86	Detection of generic spaced motifs using submotif pattern mining. Bioinformatics, 2007, 23, 1476-1485.	1.8	29
87	Computational modeling of oligonucleotide positional densities for human promoter prediction. Artificial Intelligence in Medicine, 2005, 35, 107-119.	3.8	27
88	INFERRING PHYLOGENETIC RELATIONSHIPS AVOIDING FORBIDDEN ROOTED TRIPLETS. Journal of Bioinformatics and Computational Biology, 2006, 04, 59-74.	0.3	27
89	Algorithms for Combining Rooted Triplets into a Galled Phylogenetic Network. , 2016, , 48-52.		27
90	Pathogen Chip for Respiratory Tract Infections. Journal of Clinical Microbiology, 2013, 51, 945-953.	1.8	25

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91	An intrinsic mechanism controls reactivation of neural stem cells by spindle matrix proteins. Nature Communications, 2017, 8, 122.	5.8	25
92	G-PRIMER: greedy algorithm for selecting minimal primer set. Bioinformatics, 2004, 20, 2473-2475.	1.8	24
93	Linked Dynamic Tries with Applications to LZ-Compression in Sublinear Time and Space. Algorithmica, 2015, 71, 969-988.	1.0	24
94	Comprehensive analysis of transcriptome profiles in hepatocellular carcinoma. Journal of Translational Medicine, 2019, 17, 273.	1.8	23
95	Model gene network by semi-fixed Bayesian network. Expert Systems With Applications, 2006, 30, 42-49.	4.4	22
96	Compressed Indexes forÂApproximate String Matching. Algorithmica, 2010, 58, 263-281.	1.0	22
97	Structural Alignment of RNA with Complex Pseudoknot Structure. Journal of Computational Biology, 2011, 18, 97-108.	0.8	21
98	Succinct data structures for Searchable Partial Sums with optimal worst-case performance. Theoretical Computer Science, 2011, 412, 5176-5186.	0.5	21
99	Xenopus tropicalis Genome Re-Scaffolding and Re-Annotation Reach the Resolution Required for In Vivo ChIA-PET Analysis. PLoS ONE, 2015, 10, e0137526.	1.1	21
100	The Integrator Complex Prevents Dedifferentiation of Intermediate Neural Progenitors back into Neural Stem Cells. Cell Reports, 2019, 27, 987-996.e3.	2.9	21
101	ASMdb: a comprehensive database for allele-specific DNA methylation in diverse organisms. Nucleic Acids Research, 2022, 50, D60-D71.	6.5	20
102	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. Lecture Notes in Computer Science, 2002, , 401-410.	1.0	20
103	Fast and accurate probe selection algorithm for large genomes. , 0, , .		19
104	A Linear Size Index for Approximate Pattern Matching. Lecture Notes in Computer Science, 2006, , 49-59.	1.0	19
105	Constructing a Smallest Refining Galled Phylogenetic Network. Lecture Notes in Computer Science, 2005, , 265-280.	1.0	18
106	Chromatin interaction networks and higher order architectures of eukaryotic genomes. Journal of Cellular Biochemistry, 2011, 112, 2218-2221.	1.2	18
107	Finding Short Right-Hand-on-the-Wall Walks in Graphs. Lecture Notes in Computer Science, 2005, , 127-139.	1.0	17
108	RiceENCODE: A comprehensive epigenomic database as a rice Encyclopedia of DNA Elements. Molecular Plant, 2021, 14, 1604-1606.	3.9	17

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109	Approximate String Matching Using Compressed Suffix Arrays. Lecture Notes in Computer Science, 2004, , 434-444.	1.0	16
110	Localized motif discovery in gene regulatory sequences. Bioinformatics, 2010, 26, 1152-1159.	1.8	16
111	Improved Algorithms for Constructing Consensus Trees. Journal of the ACM, 2016, 63, 1-24.	1.8	16
112	A Decomposition Theorem for MaximumWeight Bipartite Matchings with Applications to Evolutionary Trees. Lecture Notes in Computer Science, 1999, , 438-449.	1.0	16
113	Large-scale evolutionary surveillance of the 2009 H1N1 influenza A virus using resequencing arrays. Nucleic Acids Research, 2010, 38, e111-e111.	6.5	15
114	SLiM on Diet: finding short linear motifs on domain interaction interfaces in Protein Data Bank. Bioinformatics, 2010, 26, 1036-1042.	1.8	15
115	An <inline-formula><tex-math notation="LaTeX">$m{O(m, log,)$ 1j ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 517 Td (m)Tj xlink:href="sung-ieq1-2385696.gif"/></alternatives></inline-formula>-Time Algorithm for Detecting Superbubbles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 770-777.	1.9	15
116	TranSurVeyor: an improved database-free algorithm for finding non-reference transpositions in high-throughput sequencing data. Nucleic Acids Research, 2018, 46, e122.	6.5	15
117	SurVirus: a repeat-aware virus integration caller. Nucleic Acids Research, 2021, 49, e33-e33.	6.5	15
118	CRAM: Compressed Random Access Memory. Lecture Notes in Computer Science, 2012, , 510-521.	1.0	15
119	A linear size index for approximate pattern matching. Journal of Discrete Algorithms, 2011, 9, 358-364.	0.7	14
120	Improved Approximate String Matching UsingÂCompressed Suffix Data Structures. Algorithmica, 2008, 51, 298-314.	1.0	13
121	Polynomial-Time Algorithms for Building a Consensus MUL-Tree. Journal of Computational Biology, 2012, 19, 1073-1088.	0.8	13
122	Long Span DNA Paired-End-Tag (DNA-PET) Sequencing Strategy for the Interrogation of Genomic Structural Mutations and Fusion-Point-Guided Reconstruction of Amplicons. PLoS ONE, 2012, 7, e46152.	1.1	13
123	Platform Comparison for Evaluation of ALK Protein Immunohistochemical Expression, Genomic Copy Number and Hotspot Mutation Status in Neuroblastomas. PLoS ONE, 2014, 9, e106575.	1.1	13
124	Inferring a Level-1 Phylogenetic Network from a Dense Set of Rooted Triplets. Lecture Notes in Computer Science, 2004, , 462-471.	1.0	13
125	Breaking a time-and-space barrier in constructing full-text indices. , 0, , .		12
126	Probabilistic prediction of proteinâ€"protein interactions from the protein sequences. Computers in Biology and Medicine, 2006, 36, 1143-1154.	3.9	12

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127	Histone lysine methyltransferase Prâ€set7/SETD8 promotes neural stem cell reactivation. EMBO Reports, 2021, 22, e50994.	2.0	12
128	Opera: Reconstructing Optimal Genomic Scaffolds with High-Throughput Paired-End Sequences. Lecture Notes in Computer Science, 2011, , 437-451.	1.0	12
129	General techniques for comparing unrooted evolutionary trees. , 1997, , .		11
130	Partial convex recolorings of trees and galled networks. ACM Transactions on Algorithms, 2011, 7, 1-20.	0.9	11
131	More efficient periodic traversal in anonymous undirected graphs. Theoretical Computer Science, 2012, 444, 60-76.	0.5	11
132	Next-Generation Sequencing of Apoptotic DNA Breakpoints Reveals Association with Actively Transcribed Genes and Gene Translocations. PLoS ONE, 2011, 6, e26054.	1.1	11
133	Increasing confidence of protein-protein interactomes. Genome Informatics, 2006, 17, 284-97.	0.4	11
134	Identifying Differential Histone Modification Sites from ChIPâ€seq Data. Methods in Molecular Biology, 2012, 802, 293-303.	0.4	10
135	Simultaneously Learning DNA Motif Along with Its Position and Sequence Rank Preferences Through Expectation Maximization Algorithm. Journal of Computational Biology, 2013, 20, 237-248.	0.8	10
136	Calling large indels in 1047 <i>Arabidopsis</i> with IndelEnsembler. Nucleic Acids Research, 2021, 49, 10879-10894.	6.5	10
137	Improved Approximate String Matching Using Compressed Suffix Data Structures. Lecture Notes in Computer Science, 2005, , 339-348.	1.0	10
138	Single-cell analysis reveals androgen receptor regulates the ER-to-Golgi trafficking pathway with CREB3L2 to drive prostate cancer progression. Oncogene, 2021, 40, 6479-6493.	2.6	10
139	Cavity Matchings, Label Compressions, and Unrooted Evolutionary Trees. SIAM Journal on Computing, 2000, 30, 602-624.	0.8	9
140	News sports video shot classification with sports play field and motion features. , 0, , .		9
141	Reconstructing Recombination Network from Sequence Data: The Small Parsimony Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 394-402.	1.9	9
142	Computing a Smallest Multilabeled Phylogenetic Tree from Rooted Triplets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1141-1147.	1.9	9
143	BatAlign: an incremental method for accurate alignment of sequencing reads. Nucleic Acids Research, 2015, 43, e107-e107.	6.5	9
144	Fast Relative Lempel-Ziv Self-index for Similar Sequences. Lecture Notes in Computer Science, 2012, , 291-302.	1.0	9

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145	Automatic construction of online catalog topologies. IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews, 2002, 32, 382-391.	3.3	8
146	Computing the Maximum Agreement of Phylogenetic Networks. Electronic Notes in Theoretical Computer Science, 2004, 91, 134-147.	0.9	8
147	Local Gapped Subforest Alignment and Its Application in Finding RNA Structural Motifs. Journal of Computational Biology, 2006, 13, 702-718.	0.8	8
148	CPS-tree: A Compact Partitioned Suffix Tree for Disk-based Indexing on Large Genome Sequences. , 2007, , .		8
149	SurVIndel: improving CNV calling from high-throughput sequencing data through statistical testing. Bioinformatics, 2021, 37, 1497-1505.	1.8	8
150	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs. , 2001, , .		7
151	A Faster and More Space-Efficient Algorithm for Inferring Arc-Annotations of RNA Sequences through Alignment. Algorithmica, 2006, 46, 223-245.	1.0	7
152	Brief Overview of Bioinformatics Activities in Singapore. PLoS Computational Biology, 2009, 5, e1000508.	1.5	7
153	Constructing the R* Consensus Tree of Two Trees in Subcubic Time. Algorithmica, 2013, 66, 329-345.	1.0	7
154	D-SLIMMER: Domainâ€"SLiM Interaction Motifs Miner for Sequence Based Proteinâ€"Protein Interaction Data. Journal of Proteome Research, 2011, 10, 5285-5295.	1.8	6
155	Improved Algorithms for Maximum Agreement andÂCompatible Supertrees. Algorithmica, 2011, 59, 195-214.	1.0	6
156	Bioinformatics Applications in Genomics. Computer, 2012, 45, 57-63.	1.2	6
157	Exploiting Indirect Neighbours and Topological Weight to Predict Protein Function from Protein-Protein Interactions. Lecture Notes in Computer Science, 2006, , 1-1.	1.0	6
158	Faster Algorithms for 1-Mappability of a Sequence. Lecture Notes in Computer Science, 2017, , 109-121.	1.0	6
159	Obtaining spatially resolved tumor purity maps using deep multiple instance learning in a pan-cancer study. Patterns, 2022, 3, 100399.	3.1	6
160	Non-shared edges and nearest neighbor interchanges revisited. Information Processing Letters, 2004, 91, 129-134.	0.4	5
161	MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. BMC Bioinformatics, 2020, 21, 451.	1.2	5
162	Algorithms for Next-Generation Sequencing. , 0, , .		5

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163	SUBTREE TRANSFER DISTANCE FOR DEGREE-D PHYLOGENIES. International Journal of Foundations of Computer Science, 2004, 15, 893-909.	0.8	4
164	Learning multi-time delay gene network using Bayesian network framework. , 0, , .		4
165	Discriminative Fusion Approach for Automatic Image Annotation. , 2005, , .		4
166	Learning Gene Network Using Conditional Dependence. , 2006, , .		4
167	LEARNING GENE NETWORK USING TIME-DELAYED BAYESIAN NETWORK. International Journal on Artificial Intelligence Tools, 2006, 15, 353-370.	0.7	4
168	Fast algorithms for computing the tripartition-based distance between phylogenetic networks. Journal of Combinatorial Optimization, 2007, 13, 223-242.	0.8	4
169	Constructing phylogenetic supernetworks based on simulated annealing. Molecular Phylogenetics and Evolution, 2012, 63, 738-744.	1.2	4
170	Discovering Interacting Domains and Motifs in Protein–Protein Interactions. Methods in Molecular Biology, 2013, 939, 9-20.	0.4	4
171	Improved Algorithms for Constructing Consensus Trees. , 2013, , .		4
172	CWig: compressed representation of Wiggle/BedGraph format. Bioinformatics, 2014, 30, 2543-2550.	1.8	4
173	On finding the Adams consensus tree. Information and Computation, 2017, 256, 334-347.	0.5	4
174	Algorithms for the Majority Rule (+) Consensus Tree and the Frequency Difference Consensus Tree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 15-26.	1.9	4
175	HIVID2: an accurate tool to detect virus integrations in the host genome. Bioinformatics, 2021, 37, 1821-1827.	1.8	4
176	More Efficient Periodic Traversal in Anonymous Undirected Graphs. Lecture Notes in Computer Science, 2010, , 167-181.	1.0	4
177	Determining the Consistency of Resolved Triplets and Fan Triplets. Lecture Notes in Computer Science, 2017, , 82-98.	1.0	4
178	Fast and accurate probe selection algorithm for large genomes. Proceedings, 2003, 2, 65-74.	0.1	4
179	Construction of online catalog topologies using decision trees. , 0, , .		3
180	EFFECTIVE ALGORITHMS FOR TAG SNP SELECTION. Journal of Bioinformatics and Computational Biology, 2005, 03, 1089-1106.	0.3	3

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181	RB-Finder: An Improved Distance-Based Sliding Window Method to Detect Recombination Breakpoints. Journal of Computational Biology, 2008, 15, 881-898.	0.8	3
182	Simultaneously Learning DNA Motif along with Its Position and Sequence Rank Preferences through EM Algorithm. Lecture Notes in Computer Science, 2012, , 355-370.	1.0	3
183	A Linear Time Algorithm for the r-Gathering Problem on the Line (Extended Abstract). Lecture Notes in Computer Science, 2019, , 56-66.	1.0	3
184	Compressed Indexes for Approximate String Matching. Lecture Notes in Computer Science, 2006, , 208-219.	1.0	3
185	The Enhanced Double Digest Problem for DNA Physical Mapping. Journal of Combinatorial Optimization, 2003, 7, 69-78.	0.8	2
186	THE 24TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS, GIW2013, IN SINGAPORE. Journal of Bioinformatics and Computational Biology, 2013, 11, 1302003.	0.3	2
187	Do Triplets Have Enough Information to Construct the Multi-Labeled Phylogenetic Tree?. PLoS ONE, 2014, 9, e103622.	1.1	2
188	Computing the Rooted Triplet Distance Between Phylogenetic Networks. Lecture Notes in Computer Science, 2019, , 290-303.	1.0	2
189	Greedy Consensus Tree and Maximum Greedy Consensus Tree Problems. Lecture Notes in Computer Science, 2019, , 305-316.	1.0	2
190	Faster Algorithms for Computing theÂR*ÂConsensusÂTree. Lecture Notes in Computer Science, 2014, , 414-425.	1.0	2
191	A Streamlined and Generalized Analysis of Chromatin ImmunoPrecipitation Paired-End diTag Data. Lecture Notes in Computer Science, 2008, , 130-139.	1.0	2
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