

Yiu, Sm

List of Publications by Year in descending order

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170
papers

14,824
citations

109264

35
h-index

20343

116
g-index

179
all docs

179
docs citations

179
times ranked

22409
citing authors

#	ARTICLE	IF	CITATIONS
1	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. <i>GigaScience</i> , 2012, 1, 18.	3.3	4,510
2	SOAP2: an improved ultrafast tool for short read alignment. <i>Bioinformatics</i> , 2009, 25, 1966-1967.	1.8	3,329
3	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	13.7	1,058
4	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
5	Multi-key privacy-preserving deep learning in cloud computing. <i>Future Generation Computer Systems</i> , 2017, 74, 76-85.	4.9	368
6	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. <i>Nature Communications</i> , 2014, 5, 4340.	5.8	332
7	Redefining the structural motifs that determine <scp>RNA</scp> binding and <scp>RNA</scp> editing by pentatricopeptide repeat proteins in land plants. <i>Plant Journal</i> , 2016, 85, 532-547.	2.8	267
8	SPECS: Secure and privacy enhancing communications schemes for VANETs. <i>Ad Hoc Networks</i> , 2011, 9, 189-203.	3.4	246
9	IDBA-tran: a more robust de novo de Bruijn graph assembler for transcriptomes with uneven expression levels. <i>Bioinformatics</i> , 2013, 29, i326-i334.	1.8	233
10	Predicting Protein Complexes from PPI Data: A Core-Attachment Approach. <i>Journal of Computational Biology</i> , 2009, 16, 133-144.	0.8	204
11	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , 2012, 28, 878-879.	1.8	200
12	COPE: an accurate <i>k</i>-mer-based pair-end reads connection tool to facilitate genome assembly. <i>Bioinformatics</i> , 2012, 28, 2870-2874.	1.8	145
13	An efficient and scalable algorithm for clustering XML documents by structure. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2004, 16, 82-96.	4.0	140
14	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. <i>Genetics</i> , 2016, 202, 351-362.	1.2	126
15	Efficient Identity Based Ring Signature. <i>Lecture Notes in Computer Science</i> , 2005, , 499-512.	1.0	120
16	Filtering of Ineffective siRNAs and Improved siRNA Design Tool. <i>Bioinformatics</i> , 2005, 21, 144-151.	1.8	119
17	A Survey on Regular Expression Matching for Deep Packet Inspection: Applications, Algorithms, and Hardware Platforms. <i>IEEE Communications Surveys and Tutorials</i> , 2016, 18, 2991-3029.	24.8	107
18	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. <i>PLoS ONE</i> , 2013, 8, e65632.	1.1	104

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19	SOAPsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. <i>Frontiers in Genetics</i> , 2011, 2, 46.	1.1	89
20	PRGA: Privacy-Preserving Recording & Gateway-Assisted Authentication of Power Usage Information for Smart Grid. <i>IEEE Transactions on Dependable and Secure Computing</i> , 2015, 12, 85-97.	3.7	87
21	De novo assembly and characterization of <i>Camelina sativa</i> transcriptome by paired-end sequencing. <i>BMC Genomics</i> , 2013, 14, 146.	1.2	83
22	Practical attribute-based encryption: Outsourcing decryption, attribute revocation and policy updating. <i>Journal of Network and Computer Applications</i> , 2018, 108, 112-123.	5.8	73
23	Predicting drug-target interaction for new drugs using enhanced similarity measures and super-target clustering. <i>Methods</i> , 2015, 83, 98-104.	1.9	68
24	Identity-Based Encryption Resilient to Continual Auxiliary Leakage. <i>Lecture Notes in Computer Science</i> , 2012, , 117-134.	1.0	64
25	MetaCluster 4.0: A Novel Binning Algorithm for NGS Reads and Huge Number of Species. <i>Journal of Computational Biology</i> , 2012, 19, 241-249.	0.8	63
26	SmartTutor: An intelligent tutoring system in web-based adult education. <i>Journal of Systems and Software</i> , 2003, 68, 11-25.	3.3	61
27	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. <i>Algorithmica</i> , 2007, 48, 23-36.	1.0	59
28	Predicting and understanding comprehensive drug-drug interactions via semi-nonnegative matrix factorization. <i>BMC Systems Biology</i> , 2018, 12, 14.	3.0	56
29	Secure query processing with data interoperability in a cloud database environment. , 2014, , .		53
30	MaMPF: Encrypted Traffic Classification Based on Multi-Attribute Markov Probability Fingerprints. , 2018, , .		52
31	Predicting RNA Secondary Structures with Arbitrary Pseudoknots by Maximizing the Number of Stacking Pairs. <i>Journal of Computational Biology</i> , 2003, 10, 981-995.	0.8	48
32	IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. <i>Journal of Computational Biology</i> , 2013, 20, 540-550.	0.8	45
33	Secure Hierarchical Identity Based Signature and Its Application. <i>Lecture Notes in Computer Science</i> , 2004, , 480-494.	1.0	42
34	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. <i>Bioinformatics</i> , 2008, 24, 2288-2295.	1.8	41
35	MetaCluster-TA: taxonomic annotation for metagenomic data based on assembly-assisted binning. <i>BMC Genomics</i> , 2014, 15, S12.	1.2	41
36	ARMR: Anonymous routing protocol with multiple routes for communications in mobile ad hoc networks. <i>Ad Hoc Networks</i> , 2009, 7, 1536-1550.	3.4	39

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37	Detecting drug communities and predicting comprehensive drug-drug interactions via balance regularized semi-nonnegative matrix factorization. <i>Journal of Cheminformatics</i> , 2019, 11, 28.	2.8	39
38	An Efficient Flicker-Free FEC Coding Scheme for Dimmable Visible Light Communication Based on Polar Codes. <i>IEEE Photonics Journal</i> , 2017, 9, 1-10.	1.0	38
39	Unsupervised binning of environmental genomic fragments based on an error robust selection of l-mers. <i>BMC Bioinformatics</i> , 2010, 11, S5.	1.2	35
40	Failure of phylogeny inferred from multilocus sequence typing to represent bacterial phylogeny. <i>Scientific Reports</i> , 2017, 7, 4536.	1.6	32
41	HybridORAM: Practical oblivious cloud storage with constant bandwidth. <i>Information Sciences</i> , 2019, 479, 651-663.	4.0	32
42	An efficient algorithm for finding dense regions for mining quantitative association rules. <i>Computers and Mathematics With Applications</i> , 2005, 50, 471-490.	1.4	30
43	TMFUF: a triple matrix factorization-based unified framework for predicting comprehensive drug-drug interactions of new drugs. <i>BMC Bioinformatics</i> , 2018, 19, 411.	1.2	30
44	Detection of generic spaced motifs using submotif pattern mining. <i>Bioinformatics</i> , 2007, 23, 1476-1485.	1.8	29
45	Providing distributed certificate authority service in cluster-based mobile ad hoc networks. <i>Computer Communications</i> , 2007, 30, 2442-2452.	3.1	28
46	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. <i>Genome Biology</i> , 2017, 18, 230.	3.8	28
47	Promoter-sharing by different genes in human genome – CPNE1 and RBM12 gene pair as an example. <i>BMC Genomics</i> , 2008, 9, 456.	1.2	27
48	BMCMDA: a novel model for predicting human microbe-disease associations via binary matrix completion. <i>BMC Bioinformatics</i> , 2018, 19, 281.	1.2	26
49	Outsourced privacy-preserving C4.5 decision tree algorithm over horizontally and vertically partitioned dataset among multiple parties. <i>Cluster Computing</i> , 2019, 22, 1581-1593.	3.5	26
50	Exposing frame deletion by detecting abrupt changes in video streams. <i>Neurocomputing</i> , 2016, 205, 84-91.	3.5	25
51	SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. <i>Bioinformatics</i> , 2013, 29, 2971-2978.	1.8	23
52	GLProbs: Aligning Multiple Sequences Adaptively. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2015, 12, 67-78.	1.9	23
53	Identity-Based Encryption with Post-Challenge Auxiliary Inputs for Secure Cloud Applications and Sensor Networks. <i>Lecture Notes in Computer Science</i> , 2014, , 130-147.	1.0	23
54	Compound-protein interaction prediction by deep learning: Databases, descriptors and models. <i>Drug Discovery Today</i> , 2022, 27, 1350-1366.	3.2	23

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55	A survey on cyber attacks against nonlinear state estimation in power systems of ubiquitous cities. <i>Pervasive and Mobile Computing</i> , 2017, 39, 52-64.	2.1	22
56	Succinct Text Indexing with Wildcards. <i>Lecture Notes in Computer Science</i> , 2009, , 39-50.	1.0	22
57	Structural Alignment of RNA with Complex Pseudoknot Structure. <i>Journal of Computational Biology</i> , 2011, 18, 97-108.	0.8	21
58	Global small RNA analysis in fast-growing <i>Arabidopsis thaliana</i> with elevated concentrations of ATP and sugars. <i>BMC Genomics</i> , 2014, 15, 116.	1.2	21
59	ThinORAM: Towards Practical Oblivious Data Access in Fog Computing Environment. <i>IEEE Transactions on Services Computing</i> , 2020, 13, 602-612.	3.2	20
60	RECONSTRUCTING AN ULTRAMETRIC GALLED PHYLOGENETIC NETWORK FROM A DISTANCE MATRIX. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 807-832.	0.3	19
61	IDBA-MTP: A Hybrid Metatranscriptomic Assembler Based on Protein Information. <i>Journal of Computational Biology</i> , 2015, 22, 367-376.	0.8	19
62	Predicting binary, discrete and continued lncRNA-disease associations via a unified framework based on graph regression. <i>BMC Medical Genomics</i> , 2017, 10, 65.	0.7	19
63	Incentive evolutionary game model for opportunistic social networks. <i>Future Generation Computer Systems</i> , 2020, 102, 14-29.	4.9	19
64	PERGA: A Paired-End Read Guided De Novo Assembler for Extending Contigs Using SVM and Look Ahead Approach. <i>PLoS ONE</i> , 2014, 9, e114253.	1.1	18
65	Recovery of heavily fragmented JPEG files. <i>Digital Investigation</i> , 2016, 18, S108-S117.	3.2	18
66	Predicting combinative drug pairs towards realistic screening via integrating heterogeneous features. <i>BMC Bioinformatics</i> , 2017, 18, 409.	1.2	18
67	A unified solution for different scenarios of predicting drug-target interactions via triple matrix factorization. <i>BMC Systems Biology</i> , 2018, 12, 136.	3.0	18
68	Finding Motifs with Insufficient Number of Strong Binding Sites. <i>Journal of Computational Biology</i> , 2005, 12, 686-701.	0.8	17
69	VANET-based secure taxi service. <i>Ad Hoc Networks</i> , 2013, 11, 2381-2390.	3.4	16
70	Application of 16S rRNA metagenomics to analyze bacterial communities at a respiratory care centre in Taiwan. <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 2871-2881.	1.7	16
71	MLAS: Multiple level authentication scheme for VANETs. <i>Ad Hoc Networks</i> , 2012, 10, 1445-1456.	3.4	15
72	Generic server-aided secure multi-party computation in cloud computing. <i>Computer Standards and Interfaces</i> , 2022, 79, 103552.	3.8	15

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73	Forward-secure multisignature and blind signature schemes. Applied Mathematics and Computation, 2005, 168, 895-908.	1.4	14
74	Sequence assembly using next generation sequencing dataâ€™ challenges and solutions. Science China Life Sciences, 2014, 57, 1140-1148.	2.3	14
75	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. BMC Bioinformatics, 2015, 16, 386.	1.2	14
76	Oblivious Transfer with Access Control : Realizing Disjunction without Duplication. Lecture Notes in Computer Science, 2010, , 96-115.	1.0	14
77	Practical electronic lotteries with offline TTP. Computer Communications, 2006, 29, 2830-2840.	3.1	13
78	SRP: A concise non-parametric similarity-rank-based model for predicting drug-target interactions. , 2015, , .		13
79	Complete plastid genomes of the genus Ammopiptanthus and identification of a novel 23-kb rearrangement. Conservation Genetics Resources, 2017, 9, 647-650.	0.4	13
80	Predicting combinative drug pairs via multiple classifier system with positive samples only. Computer Methods and Programs in Biomedicine, 2019, 168, 1-10.	2.6	13
81	Unknown Chinese word extraction based on variety of overlapping strings. Information Processing and Management, 2013, 49, 497-512.	5.4	12
82	BitVis: An Interactive Visualization System for Bitcoin Accounts Analysis. , 2019, , .		12
83	Deep Fusion Feature Based Object Detection Method for High Resolution Optical Remote Sensing Images. Applied Sciences (Switzerland), 2019, 9, 1130.	1.3	12
84	Understanding deep face anti-spoofing: from the perspective of data. Visual Computer, 2021, 37, 1015-1028.	2.5	12
85	Indexing useful structural patterns for XML query processing. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 997-1009.	4.0	11
86	Finding optimal threshold for correction error reads in DNA assembling. BMC Bioinformatics, 2009, 10, S15.	1.2	11
87	Efficient and secure multiâ€™functional searchable symmetric encryption schemes. Security and Communication Networks, 2016, 9, 34-42.	1.0	11
88	Secure Dot Product of Outsourced Encrypted Vectors and its Application to SVM. , 2017, , .		11
89	A generic anti-spyware solution by access control list at kernel level. Journal of Systems and Software, 2005, 75, 227-234.	3.3	10
90	An Integrated Local Classification Model of Predicting Drug-Drug Interactions via Dempster-Shafer Theory of Evidence. Scientific Reports, 2018, 8, 11829.	1.6	10

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91	MLGL-MP: a Multi-Label Graph Learning framework enhanced by pathway interdependence for Metabolic Pathway prediction. <i>Bioinformatics</i> , 2022, 38, i325-i332.	1.8	10
92	Approximate string matching in DNA sequences. , 2003, , .		9
93	SDB. <i>Proceedings of the VLDB Endowment</i> , 2015, 8, 1876-1879.	2.1	9
94	Automatic construction of online catalog topologies. <i>IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews</i> , 2002, 32, 382-391.	3.3	8
95	Intrusion Detection Routers: Design, Implementation and Evaluation Using an Experimental Testbed. <i>IEEE Journal on Selected Areas in Communications</i> , 2006, 24, 1889-1900.	9.7	8
96	OPQ: OT-Based Private Querying in VANETs. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2011, 12, 1413-1422.	4.7	8
97	Towards a More Accurate Error Model for BioNano Optical Maps. <i>Lecture Notes in Computer Science</i> , 2016, , 67-79.	1.0	8
98	Attribute-Based Encryption Resilient to Auxiliary Input. <i>Lecture Notes in Computer Science</i> , 2015, , 371-390.	1.0	8
99	Insider threat prediction based on unsupervised anomaly detection scheme for proactive forensic investigation. <i>Forensic Science International: Digital Investigation</i> , 2021, 38, 301126.	1.2	8
100	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs. , 2001, , .		7
101	CLUSTERING-BASED APPROACH FOR PREDICTING MOTIF PAIRS FROM PROTEIN INTERACTION DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 701-716.	0.3	7
102	Comparison of Small RNA Profiles of Glycine max and Glycine soja at Early Developmental Stages. <i>International Journal of Molecular Sciences</i> , 2016, 17, 2043.	1.8	7
103	Deep analysis and optimization of CARD antibiotic resistance gene discovery models. <i>BMC Genomics</i> , 2019, 20, 914.	1.2	7
104	Anonymous Counting Problem in Trust Level Warning System for VANET. <i>IEEE Transactions on Vehicular Technology</i> , 2019, 68, 34-48.	3.9	7
105	LCM-DS: A novel approach of predicting drug-drug interactions for new drugs via Dempster-Shafer theory of evidence. , 2016, , .		6
106	BASE: a practical de novo assembler for large genomes using long NGS reads. <i>BMC Genomics</i> , 2016, 17, 499.	1.2	6
107	Privacy-preserving multikey computing framework for encrypted data in the cloud. <i>Information Sciences</i> , 2021, 575, 217-230.	4.0	6
108	Predicting Comprehensive Drug-Drug Interactions for New Drugs via Triple Matrix Factorization. <i>Lecture Notes in Computer Science</i> , 2017, , 108-117.	1.0	6

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109	Forensic Analysis of Pirated Chinese Shanzhai Mobile Phones. International Federation for Information Processing, 2012, , 129-142.	0.4	6
110	Non-shared edges and nearest neighbor interchanges revisited. Information Processing Letters, 2004, 91, 129-134.	0.4	5
111	Sharing and access right delegation for confidential documents: A practical solution. Information and Management, 2006, 43, 607-616.	3.6	5
112	Refining orthologue groups at the transcript level. BMC Genomics, 2010, 11, S11.	1.2	5
113	RNASAlign: RNA Structural Alignment System. Bioinformatics, 2011, 27, 2151-2152.	1.8	5
114	Structural Alignment of RNA with Triple Helix Structure. Journal of Computational Biology, 2012, 19, 365-378.	0.8	5
115	Lightweight privacy-preserving peer-to-peer data integration. Proceedings of the VLDB Endowment, 2013, 6, 157-168.	2.1	5
116	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. Bioinformatics, 2014, 30, 1049-1055.	1.8	5
117	Predicting drug-target interaction for new drugs using enhanced similarity measures and super-target clustering ¹ . , 2014, , .		5
118	Improving multiple sequence alignment by using better guide trees. BMC Bioinformatics, 2015, 16, S4.	1.2	5
119	Privacy-preserving verifiable elastic net among multiple institutions in the cloud. Journal of Computer Security, 2018, 26, 791-815.	0.5	5
120	Improving Disk Sector Integrity Using K-Dimension Hashing. International Federation for Information Processing, 2008, , 87-98.	0.4	5
121	Privacy-Preserving Elastic Net for Data Encrypted by Different Keys - With an Application on Biomarker Discovery. Lecture Notes in Computer Science, 2017, , 185-204.	1.0	5
122	SUBTREE TRANSFER DISTANCE FOR DEGREE-D PHYLOGENIES. International Journal of Foundations of Computer Science, 2004, 15, 893-909.	0.8	4
123	Effective Moment Feature Vectors for Protein Domain Structures. PLoS ONE, 2013, 8, e83788.	1.1	4
124	A Multiple Sieve Approach Based on Artificial Intelligent Techniques and Correlation Power Analysis. ACM Transactions on Multimedia Computing, Communications and Applications, 2021, 17, 1-21.	3.0	4
125	A data-mining approach for multiple structural alignment of proteins. Bioinformatics, 2010, 4, 366-370.	0.2	4
126	Construction of online catalog topologies using decision trees. , 0, , .		3

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127	Checking key integrity efficiently for high-speed quantum key distribution using combinatorial group testing. Optics Communications, 2011, 284, 531-535.	1.0	3
128	Modeling the initial stage of a file sharing process on a BitTorrent network. Peer-to-Peer Networking and Applications, 2014, 7, 311-319.	2.6	3
129	A Nonoutsourcable Puzzle Under GHOST Rule. , 2017, , .		3
130	DCN: Detector-Corrector Network Against Evasion Attacks on Deep Neural Networks. , 2018, , .		3
131	Whole Genome Sequencing On Donor Cell Leukemia in a Patient with Multiple Myeloma Identified Gene Mutations That May Provide Insights to Leukemogenesis.. Blood, 2012, 120, 2414-2414.	0.6	3
132	BitAnalysis: A Visualization System for Bitcoin Wallet Investigation. IEEE Transactions on Big Data, 2023, 9, 621-636.	4.4	3
133	PERGA. , 2013, , .		2
134	A Privacy-Preserving Multi-Pattern Matching Scheme for Searching Strings in Cloud Database. , 2017, , .		2
135	JPEG image width estimation for file carving. IET Image Processing, 2018, 12, 1245-1252.	1.4	2
136	Coarse-to-fine two-stage semantic video carving approach in digital forensics. Computers and Security, 2020, 97, 101942.	4.0	2
137	Faster Algorithms for Computing the \hat{R}^* Consensus Tree. Lecture Notes in Computer Science, 2014, , 414-425.	1.0	2
138	CCA Secure PKE with Auxiliary Input Security and Leakage Resiliency. Lecture Notes in Computer Science, 2015, , 319-335.	1.0	2
139	Adjacent Nucleotide Dependence in ncRNA and Order-1 SCFG for ncRNA Identification. PLoS ONE, 2010, 5, e12848.	1.1	2
140	Tightly-Secure Encryption in the Multi-user, Multi-challenge Setting with Improved Efficiency. Lecture Notes in Computer Science, 2017, , 3-22.	1.0	2
141	NNAN: Nearest Neighbor Attention Network to Predict Drug-Microbe Associations. Frontiers in Microbiology, 2022, 13, 846915.	1.5	2
142	Non-overlapping Common Substrings Allowing Mutations. Mathematics in Computer Science, 2008, 1, 543-555.	0.2	1
143	Maintaining Hard Disk Integrity With Digital Legal Professional Privilege (LPP) Data. IEEE Transactions on Information Forensics and Security, 2013, 8, 821-828.	4.5	1
144	Improved key integrity checking for high-speed quantum key distribution using combinatorial group testing with strongly selective family design. Quantum Information Processing, 2014, 13, 1425-1435.	1.0	1

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145	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. BMC Bioinformatics, 2015, 16, 11.	1.2	1
146	Reconstructing One-Articulated Networks with Distance Matrices. Lecture Notes in Computer Science, 2017, , 34-45.	1.0	1
147	An iterative algorithm for de novo optical map assembly. , 2017, , .		1
148	Improving somatic variant identification through integration of genome and exome data. BMC Genomics, 2017, 18, 748.	1.2	1
149	Reconstructing One-Articulated Networks with Distance Matrices. Journal of Computational Biology, 2018, 25, 253-269.	0.8	1
150	Privacy-Preserving Disease Risk Test Based on Bloom Filters. Lecture Notes in Computer Science, 2018, , 472-486.	1.0	1
151	ShadowFPE: New Encrypted Web Application Solution Based on Shadow DOM. Mobile Networks and Applications, 2021, 26, 1733-1746.	2.2	1
152	A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	1.5	1
153	Classifying encrypted traffic using adaptive fingerprints with multi-level attributes. World Wide Web, 2021, 24, 2071-2097.	2.7	1
154	Compressed index for dynamic text. , 0, , .		0
155	Discovery of transcription factor binding sites through integration of generic motif finders. Nature Precedings, 2007, , .	0.1	0
156	k-Dimensional hashing scheme for hard disk integrity verification in computer forensics. Journal of Zhejiang University: Science C, 2011, 12, 809-818.	0.7	0
157	Local structural alignment of RNA with affine gap model. BMC Proceedings, 2011, 5, S2.	1.8	0
158	UFLE: a user-friendly location-free encryption system for mobile users. Security and Communication Networks, 2014, 7, 1477-1487.	1.0	0
159	Dynamic Proofs of Retrievability with improved worst case overhead. , 2016, , .		0
160	Faster Algorithms for Computing the R* Consensus Tree. Algorithmica, 2016, 76, 1224-1244.	1.0	0
161	Secure Compression and Pattern Matching Based on Burrows-Wheeler Transform. , 2018, , .		0
162	Privacy-Preserving Computing Framework for Encrypted Data Under Multiple Keys. Lecture Notes in Computer Science, 2021, , 215-225.	1.0	0

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163	Corrigendum to: A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	1.5	0
164	FRAGMENTED JPEG FILE RECOVERY USING PSEUDO HEADERS. IFIP Advances in Information and Communication Technology, 2015, , 215-231.	0.5	0
165	LRCRYPT: Leakage-Resilient Cryptographic System (Design and Implementation). Lecture Notes in Computer Science, 2017, , 233-244.	1.0	0
166	Semantic Video Carving Using Perceptual Hashing and Optical Flow. IFIP Advances in Information and Communication Technology, 2017, , 223-244.	0.5	0
167	Relevant Fact Selection for QA via Sequence Labeling. Lecture Notes in Computer Science, 2017, , 399-409.	1.0	0
168	OC-ORAM: Constant Bandwidth ORAM with Smaller Block Size using Oblivious Clear Algorithm. , 2019, , .		0
169	Advances in security research in the Asiacrypt region. Communications of the ACM, 2020, 63, 76-81.	3.3	0
170	An Experimental Study of Compressed Indexing and Local Alignments of DNA. Lecture Notes in Computer Science, 2007, , 242-254.	1.0	0