Yiu, Sm

List of Publications by Year
in descending order

170 papers	14,824 citations	109321 35 h-index	20358 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. GigaScience, 2012, 1, 18.	6.4	4,510
2	SOAP2: an improved ultrafast tool for short read alignment. Bioinformatics, 2009, 25, 1966-1967.	4.1	3,329
3	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	27.8	1,058
4	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
5	Multi-key privacy-preserving deep learning in cloud computing. Future Generation Computer Systems, 2017, 74, 76-85.	7.5	368
6	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. Nature Communications, 2014, 5, 4340.	12.8	332
7	Redefining the structural motifs that determine RNA binding and RNA editing by pentatricopeptide repeat proteins in land plants. Plant Journal, 2016, 85, 532-547.	5.7	267
8	SPECS: Secure and privacy enhancing communications schemes for VANETs. Ad Hoc Networks, 2011, 9, 189-203.	5.5	246
9	IDBA-tran: a more robust de novo de Bruijn graph assembler for transcriptomes with uneven expression levels. Bioinformatics, 2013, 29, i326-i334.	4.1	233
10	Predicting Protein Complexes from PPI Data: A Core-Attachment Approach. Journal of Computational Biology, 2009, 16, 133-144.	1.6	204
11	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. Bioinformatics, 2012, 28, 878-879.	4.1	200
12	COPE: an accurate k-mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	4.1	145
13	An efficient and scalable algorithm for clustering XML documents by structure. IEEE Transactions on Knowledge and Data Engineering, 2004, 16, 82-96.	5.7	140
14	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. Genetics, 2016, 202, 351-362.	2.9	126
15	Efficient Identity Based Ring Signature. Lecture Notes in Computer Science, 2005, , 499-512.	1.3	120
16	Filtering of Ineffective siRNAs and Improved siRNA Design Tool. Bioinformatics, 2005, 21, 144-151.	4.1	119
17	A Survey on Regular Expression Matching for Deep Packet Inspection: Applications, Algorithms, and Hardware Platforms. IEEE Communications Surveys and Tutorials, 2016, 18, 2991-3029.	39.4	107
18	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	2.5	104

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19	SOAPsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. Frontiers in Genetics, 2011, 2, 46.	2.3	89
20	PRGA: Privacy-Preserving Recording &amp; Gateway-Assisted Authentication of Power Usage Information for Smart Grid. IEEE Transactions on Dependable and Secure Computing, 2015, 12, 85-97.	5.4	87
21	De novo assembly and characterization of Camelina sativatranscriptome by paired-end sequencing. BMC Genomics, 2013, 14, 146.	2.8	83
22	Practical attribute-based encryption: Outsourcing decryption, attribute revocation and policy updating. Journal of Network and Computer Applications, 2018, 108, 112-123.	9.1	73
23	Predicting drugâ€"target interaction for new drugs using enhanced similarity measures and super-target clustering. Methods, 2015, 83, 98-104.	3.8	68
24	Identity-Based Encryption Resilient to Continual Auxiliary Leakage. Lecture Notes in Computer Science, 2012, , 117-134.	1.3	64
25	MetaCluster 4.0: A Novel Binning Algorithm for NGS Reads and Huge Number of Species. Journal of Computational Biology, 2012, 19, 241-249.	1.6	63
26	SmartTutor: An intelligent tutoring system in web-based adult education. Journal of Systems and Software, 2003, 68, 11-25.	4.5	61
27	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. Algorithmica, 2007, 48, 23-36.	1.3	59
28	Predicting and understanding comprehensive drug-drug interactions via semi-nonnegative matrix factorization. BMC Systems Biology, 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. Journal of Computational Biology, 2003, 10, 981-995.	1.6	48
32	IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. Journal of Computational Biology, 2013, 20, 540-550.	1.6	45
33	Secure Hierarchical Identity Based Signature and Its Application. Lecture Notes in Computer Science, 2004, , 480-494.	1.3	42
34	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. Bioinformatics, 2008, 24, 2288-2295.	4.1	41
35	MetaCluster-TA: taxonomic annotation for metagenomic data based on assembly-assisted binning. BMC Genomics, 2014, 15, S12.	2.8	41
36	ARMR: Anonymous routing protocol with multiple routes for communications in mobile ad hoc networks. Ad Hoc Networks, 2009, 7, 1536-1550.	5.5	39

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37	Detecting drug communities and predicting comprehensive drug–drug interactions via balance regularized semi-nonnegative matrix factorization. Journal of Cheminformatics, 2019, 11, 28.	6.1	39
38	An Efficient Flicker-Free FEC Coding Scheme for Dimmable Visible Light Communication Based on Polar Codes. IEEE Photonics Journal, 2017, 9, 1-10.	2.0	38
39	Unsupervised binning of environmental genomic fragments based on an error robust selection of l-mers. BMC Bioinformatics, 2010, 11, S5.	2.6	35
40	Failure of phylogeny inferred from multilocus sequence typing to represent bacterial phylogeny. Scientific Reports, 2017, 7, 4536.	3.3	32
41	HybridORAM: Practical oblivious cloud storage with constant bandwidth. Information Sciences, 2019, 479, 651-663.	6.9	32
42	An efficient algorithm for finding dense regions for mining quantitative association rules. Computers and Mathematics With Applications, 2005, 50, 471-490.	2.7	30
43	TMFUF: a triple matrix factorization-based unified framework for predicting comprehensive drug-drug interactions of new drugs. BMC Bioinformatics, 2018, 19, 411.	2.6	30
44	Detection of generic spaced motifs using submotif pattern mining. Bioinformatics, 2007, 23, 1476-1485.	4.1	29
45	Providing distributed certificate authority service in cluster-based mobile ad hoc networks. Computer Communications, 2007, 30, 2442-2452.	5.1	28
46	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. Genome Biology, 2017, 18, 230.	8.8	28
47	Promoter-sharing by different genes in human genome – CPNE1 and RBM12 gene pair as an example. BMC Genomics, 2008, 9, 456.	2.8	27
48	BMCMDA: a novel model for predicting human microbe-disease associations via binary matrix completion. BMC Bioinformatics, 2018, 19, 281.	2.6	26
49	Outsourced privacy-preserving C4.5 decision tree algorithm over horizontally and vertically partitioned dataset among multiple parties. Cluster Computing, 2019, 22, 1581-1593.	5.0	26
50	Exposing frame deletion by detecting abrupt changes in video streams. Neurocomputing, 2016, 205, 84-91.	5.9	25
51	SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. Bioinformatics, 2013, 29, 2971-2978.	4.1	23
52	GLProbs: Aligning Multiple Sequences Adaptively. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 67-78.	3.0	23
53	Identity-Based Encryption with Post-Challenge Auxiliary Inputs for Secure Cloud Applications and Sensor Networks. Lecture Notes in Computer Science, 2014, , 130-147.	1.3	23
54	Compound–protein interaction prediction by deep learning: Databases, descriptors and models. Drug Discovery Today, 2022, 27, 1350-1366.	6.4	23

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55	A survey on cyber attacks against nonlinear state estimation in power systems of ubiquitous cities. Pervasive and Mobile Computing, 2017, 39, 52-64.	3.3	22
56	Succinct Text Indexing with Wildcards. Lecture Notes in Computer Science, 2009, , 39-50.	1.3	22
57	Structural Alignment of RNA with Complex Pseudoknot Structure. Journal of Computational Biology, 2011, 18, 97-108.	1.6	21
58	Global small RNA analysis in fast-growing Arabidopsis thaliana with elevated concentrations of ATP and sugars. BMC Genomics, 2014, 15, 116.	2.8	21
59	ThinORAM: Towards Practical Oblivious Data Access in Fog Computing Environment. IEEE Transactions on Services Computing, 2020, 13, 602-612.	4.6	20
60	RECONSTRUCTING AN ULTRAMETRIC GALLED PHYLOGENETIC NETWORK FROM A DISTANCE MATRIX. Journal of Bioinformatics and Computational Biology, 2006, 04, 807-832.	0.8	19
61	IDBA-MTP: A Hybrid Metatranscriptomic Assembler Based on Protein Information. Journal of Computational Biology, 2015, 22, 367-376.	1.6	19
62	Predicting binary, discrete and continued lncRNA-disease associations via a unified framework based on graph regression. BMC Medical Genomics, 2017, 10, 65.	1.5	19
63	Incentive evolutionary game model for opportunistic social networks. Future Generation Computer Systems, 2020, 102, 14-29.	7.5	19
64	PERGA: A Paired-End Read Guided De Novo Assembler for Extending Contigs Using SVM and Look Ahead Approach. PLoS ONE, 2014, 9, e114253.	2.5	18
65	Recovery of heavily fragmented JPEG files. Digital Investigation, 2016, 18, S108-S117.	3.2	18
66	Predicting combinative drug pairs towards realistic screening via integrating heterogeneous features. BMC Bioinformatics, 2017, 18, 409.	2.6	18
67	A unified solution for different scenarios of predicting drug-target interactions via triple matrix factorization. BMC Systems Biology, 2018, 12, 136.	3.0	18
68	Finding Motifs with Insufficient Number of Strong Binding Sites. Journal of Computational Biology, 2005, 12, 686-701.	1.6	17
69	VANET-based secure taxi service. Ad Hoc Networks, 2013, 11, 2381-2390.	5.5	16
70	Application of 16S rRNA metagenomics to analyze bacterial communities at a respiratory care centre in Taiwan. Applied Microbiology and Biotechnology, 2015, 99, 2871-2881.	3.6	16
71	MLAS: Multiple level authentication scheme for VANETs. Ad Hoc Networks, 2012, 10, 1445-1456.	5.5	15
72	Generic server-aided secure multi-party computation in cloud computing. Computer Standards and Interfaces, 2022, 79, 103552.	5.4	15

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73	Forward-secure multisignature and blind signature schemes. Applied Mathematics and Computation, 2005, 168, 895-908.	2.2	14
74	Sequence assembly using next generation sequencing data—challenges and solutions. Science China Life Sciences, 2014, 57, 1140-1148.	4.9	14
75	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. BMC Bioinformatics, 2015, 16, 386.	2.6	14
76	Oblivious Transfer with Access Control : Realizing Disjunction without Duplication. Lecture Notes in Computer Science, 2010, , 96-115.	1.3	14
77	Practical electronic lotteries with offline TTP. Computer Communications, 2006, 29, 2830-2840.	5.1	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.	0.8	13
80	Predicting combinative drug pairs via multiple classifier system with positive samples only. Computer Methods and Programs in Biomedicine, 2019, 168, 1-10.	4.7	13
81	Unknown Chinese word extraction based on variety of overlapping strings. Information Processing and Management, 2013, 49, 497-512.	8.6	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.	2.5	12
84	Understanding deep face anti-spoofing: from the perspective of data. Visual Computer, 2021, 37, 1015-1028.	3.5	12
85	Indexing useful structural patterns for XML query processing. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 997-1009.	5.7	11
86	Finding optimal threshold for correction error reads in DNA assembling. BMC Bioinformatics, 2009, 10, S15.	2.6	11
87	Efficient and secure multi—functional searchable symmetric encryption schemes. Security and Communication Networks, 2016, 9, 34-42.	1.5	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.	4.5	10
90	An Integrated Local Classification Model of Predicting Drug-Drug Interactions via Dempster-Shafer Theory of Evidence. Scientific Reports, 2018, 8, 11829.	3.3	10

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91	MLGL-MP: a Multi-Label Graph Learning framework enhanced by pathway interdependence for Metabolic Pathway prediction. Bioinformatics, 2022, 38, i325-i332.	4.1	10
92	Approximate string matching in DNA sequences. , 2003, , .		9
93	SDB. Proceedings of the VLDB Endowment, 2015, 8, 1876-1879.	3.8	9
94	Automatic construction of online catalog topologies. IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews, 2002, 32, 382-391.	2.9	8
95	Intrusion Detection Routers: Design, Implementation and Evaluation Using an Experimental Testbed. IEEE Journal on Selected Areas in Communications, 2006, 24, 1889-1900.	14.0	8
96	OPQ: OT-Based Private Querying in VANETs. IEEE Transactions on Intelligent Transportation Systems, 2011, 12, 1413-1422.	8.0	8
97	Towards a More Accurate Error Model for BioNano Optical Maps. Lecture Notes in Computer Science, 2016, , 67-79.	1.3	8
98	Attribute-Based Encryption Resilient to Auxiliary Input. Lecture Notes in Computer Science, 2015, , 371-390.	1.3	8
99	Insider threat prediction based on unsupervised anomaly detection scheme for proactive forensic investigation. Forensic Science International: Digital Investigation, 2021, 38, 301126.	1.7	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. Journal of Bioinformatics and Computational Biology, 2009, 07, 701-716.	0.8	7
102	Comparison of Small RNA Profiles of Glycine max and Glycine soja at Early Developmental Stages. International Journal of Molecular Sciences, 2016, 17, 2043.	4.1	7
103	Deep analysis and optimization of CARD antibiotic resistance gene discovery models. BMC Genomics, 2019, 20, 914.	2.8	7
104	Anonymous Counting Problem in Trust Level Warning System for VANET. IEEE Transactions on Vehicular Technology, 2019, 68, 34-48.	6.3	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. BMC Genomics, 2016, 17, 499.	2.8	6
107	Privacy-preserving multikey computing framework for encrypted data in the cloud. Information Sciences, 2021, 575, 217-230.	6.9	6
108	Predicting Comprehensive Drug-Drug Interactions for New Drugs via Triple Matrix Factorization. Lecture Notes in Computer Science, 2017, , 108-117.	1.3	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.	0.6	5
111	Sharing and access right delegation for confidential documents: A practical solution. Information and Management, 2006, 43, 607-616.	6.5	5
112	Refining orthologue groups at the transcript level. BMC Genomics, 2010, 11, S11.	2.8	5
113	RNASAlign: RNA Structural Alignment System. Bioinformatics, 2011, 27, 2151-2152.	4.1	5
114	Structural Alignment of RNA with Triple Helix Structure. Journal of Computational Biology, 2012, 19, 365-378.	1.6	5
115	Lightweight privacy-preserving peer-to-peer data integration. Proceedings of the VLDB Endowment, 2013, 6, 157-168.	3.8	5
116	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. Bioinformatics, 2014, 30, 1049-1055.	4.1	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.	2.6	5
119	Privacy-preserving verifiable elastic net among multiple institutions in the cloud. Journal of Computer Security, 2018, 26, 791-815.	0.8	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.	1.3	5
122	SUBTREE TRANSFER DISTANCE FOR DEGREE-D PHYLOGENIES. International Journal of Foundations of Computer Science, 2004, 15, 893-909.	1.1	4
123	Effective Moment Feature Vectors for Protein Domain Structures. PLoS ONE, 2013, 8, e83788.	2.5	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.	4.3	4
125	A data-mining approach for multiple structural alignment of proteins. Bioinformation, 2010, 4, 366-370.	0.5	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.	2.1	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.	3.9	3
129	A Nonoutsourceable 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.	1.4	3
132	BitAnalysis: A Visualization System for Bitcoin Wallet Investigation. IEEE Transactions on Big Data, 2023, 9, 621-636.	6.1	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.	2.5	2
136	Coarse-to-fine two-stage semantic video carving approach in digital forensics. Computers and Security, 2020, 97, 101942.	6.0	2
137	Faster Algorithms for Computing theÂR*ÂConsensusÂTree. Lecture Notes in Computer Science, 2014, , 414-425.	1.3	2
138	CCA Secure PKE with Auxiliary Input Security and Leakage Resiliency. Lecture Notes in Computer Science, 2015, , 319-335.	1.3	2
139	Adjacent Nucleotide Dependence in ncRNA and Order-1 SCFG for ncRNA Identification. PLoS ONE, 2010, 5, e12848.	2.5	2
140	Tightly-Secure Encryption in the Multi-user, Multi-challenge Setting with Improved Efficiency. Lecture Notes in Computer Science, 2017, , 3-22.	1.3	2
141	NNAN: Nearest Neighbor Attention Network to Predict Drugâ€"Microbe Associations. Frontiers in Microbiology, 2022, 13, 846915.	3.5	2
142	Non-overlapping Common Substrings Allowing Mutations. Mathematics in Computer Science, 2008, 1, 543-555.	0.4	1
143	Maintaining Hard Disk Integrity With Digital Legal Professional Privilege (LPP) Data. IEEE Transactions on Information Forensics and Security, 2013, 8, 821-828.	6.9	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.	2.2	1

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145	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. BMC Bioinformatics, 2015, 16, I1.	2.6	1
146	Reconstructing One-Articulated Networks with Distance Matrices. Lecture Notes in Computer Science, 2017, , 34-45.	1.3	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.	2.8	1
149	Reconstructing One-Articulated Networks with Distance Matrices. Journal of Computational Biology, 2018, 25, 253-269.	1.6	1
150	Privacy-Preserving Disease Risk Test Based on Bloom Filters. Lecture Notes in Computer Science, 2018, , 472-486.	1.3	1
151	ShadowFPE: New Encrypted Web Application Solution Based on Shadow DOM. Mobile Networks and Applications, 2021, 26, 1733-1746.	3.3	1
152	A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	2.4	1
153	Classifying encrypted traffic using adaptive fingerprints with multi-level attributes. World Wide Web, 2021, 24, 2071-2097.	4.0	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.	1.6	0
158	UFLE: a userâ€friendly locationâ€free encryption system for mobile users. Security and Communication Networks, 2014, 7, 1477-1487.	1.5	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.	1.3	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.	1.3	0

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163	Corrigendum to: A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	2.4	0
164	FRAGMENTED JPEG FILE RECOVERY USING PSEUDO HEADERS. IFIP Advances in Information and Communication Technology, 2015, , 215-231.	0.7	0
165	LRCRYPT: Leakage-Resilient Cryptographic System (Design and Implementation). Lecture Notes in Computer Science, 2017, , 233-244.	1.3	0
166	Semantic Video Carving Using Perceptual Hashing and Optical Flow. IFIP Advances in Information and Communication Technology, 2017, , 223-244.	0.7	0
167	Relevant Fact Selection for QA via Sequence Labeling. Lecture Notes in Computer Science, 2017, , 399-409.	1.3	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.	4.5	0
170	An Experimental Study of Compressed Indexing and Local Alignments of DNA. Lecture Notes in Computer Science, 2007, , 242-254.	1.3	0