Yiu, Sm

List of Publications by Year
in descending order

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		125106	23173
170	14,824	35	116
papers	citations	h-index	g-index

179	179	179	25018
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	BitAnalysis: A Visualization System for Bitcoin Wallet Investigation. IEEE Transactions on Big Data, 2023, 9, 621-636.	4.4	3
2	Generic server-aided secure multi-party computation in cloud computing. Computer Standards and Interfaces, 2022, 79, 103552.	3.8	15
3	Compoundâ€“protein interaction prediction by deep learning: Databases, descriptors and models. Drug Discovery Today, 2022, 27, 1350-1366.	3.2	23
4	MLGL-MP: a Multi-Label Graph Learning framework enhanced by pathway interdependence for Metabolic Pathway prediction. Bioinformatics, 2022, 38, i325-i332.	1.8	10
5	NNAN: Nearest Neighbor Attention Network to Predict Drugâ€“Microbe Associations. Frontiers in Microbiology, 2022, 13, 846915.	1.5	2
6	ShadowFPE: New Encrypted Web Application Solution Based on Shadow DOM. Mobile Networks and Applications, 2021, 26, 1733-1746.	2.2	1
7	Understanding deep face anti-spoofing: from the perspective of data. Visual Computer, 2021, 37, 1015-1028.	2.5	12
8	Privacy-Preserving Computing Framework for Encrypted Data Under Multiple Keys. Lecture Notes in Computer Science, 2021, , 215-225.	1.0	0
9	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
10	Privacy-preserving multikey computing framework for encrypted data in the cloud. Information Sciences, 2021, 575, 217-230.	4.0	6
11	Classifying encrypted traffic using adaptive fingerprints with multi-level attributes. World Wide Web, 2021, 24, 2071-2097.	2.7	1
12	Insider threat prediction based on unsupervised anomaly detection scheme for proactive forensic investigation. Forensic Science International: Digital Investigation, 2021, 38, 301126.	1.2	8
13	Incentive evolutionary game model for opportunistic social networks. Future Generation Computer Systems, 2020, 102, 14-29.	4.9	19
14	ThinORAM: Towards Practical Oblivious Data Access in Fog Computing Environment. IEEE Transactions on Services Computing, 2020, 13, 602-612.	3.2	20
15	Coarse-to-fine two-stage semantic video carving approach in digital forensics. Computers and Security, 2020, 97, 101942.	4.0	2
16	Advances in security research in the Asiacrypt region. Communications of the ACM, 2020, 63, 76-81.	3.3	0
17	BitVis: An Interactive Visualization System for Bitcoin Accounts Analysis. , 2019, , .		12
18	Deep Fusion Feature Based Object Detection Method for High Resolution Optical Remote Sensing Images. Applied Sciences (Switzerland), 2019, 9, 1130.	1.3	12

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19	Detecting drug communities and predicting comprehensive drugâ€"drug interactions via balance regularized semi-nonnegative matrix factorization. Journal of Cheminformatics, 2019, 11, 28.	2.8	39
20	Deep analysis and optimization of CARD antibiotic resistance gene discovery models. BMC Genomics, 2019, 20, 914.	1.2	7
21	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
22	Anonymous Counting Problem in Trust Level Warning System for VANET. IEEE Transactions on Vehicular Technology, 2019, 68, 34-48.	3.9	7
23	Outsourced privacy-preserving C4.5 decision tree algorithm over horizontally and vertically partitioned dataset among multiple parties. Cluster Computing, 2019, 22, 1581-1593.	3.5	26
24	HybridORAM: Practical oblivious cloud storage with constant bandwidth. Information Sciences, 2019, 479, 651-663.	4.0	32
25	OC-ORAM: Constant Bandwidth ORAM with Smaller Block Size using Oblivious Clear Algorithm. , 2019, , .		0
26	Practical attribute-based encryption: Outsourcing decryption, attribute revocation and policy updating. Journal of Network and Computer Applications, 2018, 108, 112-123.	5.8	73
27	Reconstructing One-Articulated Networks with Distance Matrices. Journal of Computational Biology, 2018, 25, 253-269.	0.8	1
28	TMFUF: a triple matrix factorization-based unified framework for predicting comprehensive drug-drug interactions of new drugs. BMC Bioinformatics, 2018, 19, 411.	1.2	30
29	Secure Compression and Pattern Matching Based on Burrows-Wheeler Transform. , 2018, , .		0
30	MaMPF: Encrypted Traffic Classification Based on Multi-Attribute Markov Probability Fingerprints. , 2018, , .		52
31	A unified solution for different scenarios of predicting drug-target interactions via triple matrix factorization. BMC Systems Biology, 2018, 12, 136.	3.0	18
32	Privacy-preserving verifiable elastic net among multiple institutions in the cloud. Journal of Computer Security, 2018, 26, 791-815.	0.5	5
33	BMCMDA: a novel model for predicting human microbe-disease associations via binary matrix completion. BMC Bioinformatics, 2018, 19, 281.	1.2	26
34	Privacy-Preserving Disease Risk Test Based on Bloom Filters. Lecture Notes in Computer Science, 2018, , 472-486.	1.0	1
35	JPEG image width estimation for file carving. IET Image Processing, 2018, 12, 1245-1252.	1.4	2
36	Predicting and understanding comprehensive drug-drug interactions via semi-nonnegative matrix factorization. BMC Systems Biology, 2018, 12, 14.	3.0	56

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37	DCN: Detector-Corrector Network Against Evasion Attacks on Deep Neural Networks. , 2018, , .		3
38	An Integrated Local Classification Model of Predicting Drug-Drug Interactions via Dempster-Shafer Theory of Evidence. Scientific Reports, 2018, 8, 11829.	1.6	10
39	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
40	Secure Dot Product of Outsourced Encrypted Vectors and its Application to SVM. , 2017, , .		11
41	A survey on cyber attacks against nonlinear state estimation in power systems of ubiquitous cities. Pervasive and Mobile Computing, 2017, 39, 52-64.	2.1	22
42	Reconstructing One-Articulated Networks with Distance Matrices. Lecture Notes in Computer Science, 2017, , 34-45.	1.0	1
43	An Efficient Flicker-Free FEC Coding Scheme for Dimmable Visible Light Communication Based on Polar Codes. IEEE Photonics Journal, 2017, 9, 1-10.	1.0	38
44	Multi-key privacy-preserving deep learning in cloud computing. Future Generation Computer Systems, 2017, 74, 76-85.	4.9	368
45	Failure of phylogeny inferred from multilocus sequence typing to represent bacterial phylogeny. Scientific Reports, 2017, 7, 4536.	1.6	32
46	An iterative algorithm for de novo optical map assembly. , 2017, , .		1
47	Improving somatic variant identification through integration of genome and exome data. BMC Genomics, 2017, 18, 748.	1.2	1
48	Predicting binary, discrete and continued lncRNA-disease associations via a unified framework based on graph regression. BMC Medical Genomics, 2017, 10, 65.	0.7	19
49	Predicting combinative drug pairs towards realistic screening via integrating heterogeneous features. BMC Bioinformatics, 2017, 18, 409.	1.2	18
50	OMSV enables accurate and comprehensive identification of large structural variations from nanochannel-based single-molecule optical maps. Genome Biology, 2017, 18, 230.	3.8	28
51	A Nonoutsourceable Puzzle Under GHOST Rule. , 2017, , .		3
52	A Privacy-Preserving Multi-Pattern Matching Scheme for Searching Strings in Cloud Database. , 2017, , .		2
53	Predicting Comprehensive Drug-Drug Interactions for New Drugs via Triple Matrix Factorization. Lecture Notes in Computer Science, 2017, , 108-117.	1.0	6
54	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

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55	LRCRYPT: Leakage-Resilient Cryptographic System (Design and Implementation). Lecture Notes in Computer Science, 2017, , 233-244.	1.0	0
56	Semantic Video Carving Using Perceptual Hashing and Optical Flow. IFIP Advances in Information and Communication Technology, 2017, , 223-244.	0.5	0
57	Relevant Fact Selection for QA via Sequence Labeling. Lecture Notes in Computer Science, 2017, , 399-409.	1.0	0
58	Tightly-Secure Encryption in the Multi-user, Multi-challenge Setting with Improved Efficiency. Lecture Notes in Computer Science, 2017, , 3-22.	1.0	2
59	Comparison of Small RNA Profiles of Glycine max and Glycine soja at Early Developmental Stages. International Journal of Molecular Sciences, 2016, 17, 2043.	1.8	7
60	Redefining the structural motifs that determine <scp>RNA</scp> binding and <scp>RNA</scp> editing by pentatricopeptide repeat proteins in land plants. Plant Journal, 2016, 85, 532-547.	2.8	267
61	LCM-DS: A novel approach of predicting drug-drug interactions for new drugs via Dempster-Shafer theory of evidence. , 2016, , .		6
62	Dynamic Proofs of Retrievability with improved worst case overhead. , 2016, , .		0
63	Exposing frame deletion by detecting abrupt changes in video streams. Neurocomputing, 2016, 205, 84-91.	3.5	25
64	A Survey on Regular Expression Matching for Deep Packet Inspection: Applications, Algorithms, and Hardware Platforms. IEEE Communications Surveys and Tutorials, 2016, 18, 2991-3029.	24.8	107
65	Faster Algorithms for Computing the R* Consensus Tree. Algorithmica, 2016, 76, 1224-1244.	1.0	0
66	BASE: a practical de novo assembler for large genomes using long NGS reads. BMC Genomics, 2016, 17, 499.	1.2	6
67	Recovery of heavily fragmented JPEG files. Digital Investigation, 2016, 18, S108-S117.	3.2	18
68	Efficient and secure multiâ€functional searchable symmetric encryption schemes. Security and Communication Networks, 2016, 9, 34-42.	1.0	11
69	Towards a More Accurate Error Model for BioNano Optical Maps. Lecture Notes in Computer Science, 2016, , 67-79.	1.0	8
70	Genome-Wide Structural Variation Detection by Genome Mapping on Nanochannel Arrays. Genetics, 2016, 202, 351-362.	1.2	126
71	GIW and InCoB are advancing bioinformatics in the Asia-Pacific. BMC Bioinformatics, 2015, 16, I1.	1.2	1
72	Improving multiple sequence alignment by using better guide trees. BMC Bioinformatics, 2015, 16, S4.	1.2	5

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73	misFinder: identify mis-assemblies in an unbiased manner using reference and paired-end reads. BMC Bioinformatics, 2015, 16, 386.	1.2	14
74	Predicting drugâ€"target interaction for new drugs using enhanced similarity measures and super-target clustering. Methods, 2015, 83, 98-104.	1.9	68
75	SDB. Proceedings of the VLDB Endowment, 2015, 8, 1876-1879.	2.1	9
76	SRP: A concise non-parametric similarity-rank-based model for predicting drug-target interactions. , 2015, , .		13
77	Application of 16S rRNA metagenomics to analyze bacterial communities at a respiratory care centre in Taiwan. Applied Microbiology and Biotechnology, 2015, 99, 2871-2881.	1.7	16
78	GLProbs: Aligning Multiple Sequences Adaptively. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 67-78.	1.9	23
79	IDBA-MTP: A Hybrid Metatranscriptomic Assembler Based on Protein Information. Journal of Computational Biology, 2015, 22, 367-376.	0.8	19
80	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.	3.7	87
81	CCA Secure PKE with Auxiliary Input Security and Leakage Resiliency. Lecture Notes in Computer Science, 2015, , 319-335.	1.0	2
82	Attribute-Based Encryption Resilient to Auxiliary Input. Lecture Notes in Computer Science, 2015, , 371-390.	1.0	8
83	FRAGMENTED JPEG FILE RECOVERY USING PSEUDO HEADERS. IFIP Advances in Information and Communication Technology, 2015, , 215-231.	0.5	0
84	PERGA: A Paired-End Read Guided De Novo Assembler for Extending Contigs Using SVM and Look Ahead Approach. PLoS ONE, 2014, 9, e114253.	1.1	18
85	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. Bioinformatics, 2014, 30, 1049-1055.	1.8	5
86	Sequence assembly using next generation sequencing dataâ€"challenges and solutions. Science China Life Sciences, 2014, 57, 1140-1148.	2.3	14
87	Predicting drug-target interaction for new drugs using enhanced similarity measures and super-target clustering¹. , 2014, , .		5
88	UFLE: a userâ€friendly locationâ€free encryption system for mobile users. Security and Communication Networks, 2014, 7, 1477-1487.	1.0	0
89	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
90	Global small RNA analysis in fast-growing Arabidopsis thaliana with elevated concentrations of ATP and sugars. BMC Genomics, 2014, 15, 116.	1.2	21

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91	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
92	MetaCluster-TA: taxonomic annotation for metagenomic data based on assembly-assisted binning. BMC Genomics, 2014, 15, S12.	1.2	41
93	Secure query processing with data interoperability in a cloud database environment. , 2014, , .		53
94	Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing. Nature Communications, 2014, 5, 4340.	5.8	332
95	Identity-Based Encryption with Post-Challenge Auxiliary Inputs for Secure Cloud Applications and Sensor Networks. Lecture Notes in Computer Science, 2014, , 130-147.	1.0	23
96	Faster Algorithms for Computing theÂR*ÂConsensusÂTree. Lecture Notes in Computer Science, 2014, , 414-425.	1.0	2
97	VANET-based secure taxi service. Ad Hoc Networks, 2013, 11, 2381-2390.	3.4	16
98	De novo assembly and characterization of Camelina sativatranscriptome by paired-end sequencing. BMC Genomics, 2013, 14, 146.	1.2	83
99	IDBA-MT: <i>De Novo</i> Assembler for Metatranscriptomic Data Generated from Next-Generation Sequencing Technology. Journal of Computational Biology, 2013, 20, 540-550.	0.8	45
100	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
101	IDBA-tran: a more robust de novo de Bruijn graph assembler for transcriptomes with uneven expression levels. Bioinformatics, 2013, 29, i326-i334.	1.8	233
102	Unknown Chinese word extraction based on variety of overlapping strings. Information Processing and Management, 2013, 49, 497-512.	5.4	12
103	SOAPfusion: a robust and effective computational fusion discovery tool for RNA-seq reads. Bioinformatics, 2013, 29, 2971-2978.	1.8	23
104	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
105	Lightweight privacy-preserving peer-to-peer data integration. Proceedings of the VLDB Endowment, 2013, 6, 157-168.	2.1	5
106	PERGA. , 2013, , .		2
107	SOAP3-dp: Fast, Accurate and Sensitive GPU-Based Short Read Aligner. PLoS ONE, 2013, 8, e65632.	1.1	104
108	Effective Moment Feature Vectors for Protein Domain Structures. PLoS ONE, 2013, 8, e83788.	1.1	4

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109	Identity-Based Encryption Resilient to Continual Auxiliary Leakage. Lecture Notes in Computer Science, 2012, , 117-134.	1.0	64
110	Structural Alignment of RNA with Triple Helix Structure. Journal of Computational Biology, 2012, 19, 365-378.	0.8	5
111	COPE: an accurate <i>k</i>-mer-based pair-end reads connection tool to facilitate genome assembly. Bioinformatics, 2012, 28, 2870-2874.	1.8	145
112	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. Bioinformatics, 2012, 28, 878-879.	1.8	200
113	MLAS: Multiple level authentication scheme for VANETs. Ad Hoc Networks, 2012, 10, 1445-1456.	3.4	15
114	SOAPdenovo2: an empirically improved memory-efficient short-read de novo assembler. GigaScience, 2012, 1, 18.	3.3	4,510
115	MetaCluster 4.0: A Novel Binning Algorithm for NGS Reads and Huge Number of Species. Journal of Computational Biology, 2012, 19, 241-249.	0.8	63
116	Forensic Analysis of Pirated Chinese Shanzhai Mobile Phones. International Federation for Information Processing, 2012, , 129-142.	0.4	6
117	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
118	Structural Alignment of RNA with Complex Pseudoknot Structure. Journal of Computational Biology, 2011, 18, 97-108.	0.8	21
119	SOAPsplice: Genome-Wide ab initio Detection of Splice Junctions from RNA-Seq Data. Frontiers in Genetics, 2011, 2, 46.	1.1	89
120	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
121	OPQ: OT-Based Private Querying in VANETs. IEEE Transactions on Intelligent Transportation Systems, 2011, 12, 1413-1422.	4.7	8
122	Local structural alignment of RNA with affine gap model. BMC Proceedings, 2011, 5, S2.	1.8	0
123	SPECS: Secure and privacy enhancing communications schemes for VANETs. Ad Hoc Networks, 2011, 9, 189-203.	3.4	246
124	Checking key integrity efficiently for high-speed quantum key distribution using combinatorial group testing. Optics Communications, 2011, 284, 531-535.	1.0	3
125	RNASAlign: RNA Structural Alignment System. Bioinformatics, 2011, 27, 2151-2152.	1.8	5
126	Unsupervised binning of environmental genomic fragments based on an error robust selection of l-mers. BMC Bioinformatics, 2010, 11, S5.	1.2	35

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127	Refining orthologue groups at the transcript level. BMC Genomics, 2010, 11, S11.	1.2	5
128	The sequence and de novo assembly of the giant panda genome. Nature, 2010, 463, 311-317.	13.7	1,058
129	Oblivious Transfer with Access Control : Realizing Disjunction without Duplication. Lecture Notes in Computer Science, 2010, , 96-115.	1.0	14
130	A data-mining approach for multiple structural alignment of proteins. Bioinformation, 2010, 4, 366-370.	0.2	4
131	Adjacent Nucleotide Dependence in ncRNA and Order-1 SCFG for ncRNA Identification. PLoS ONE, 2010, 5, e12848.	1.1	2
132	Predicting Protein Complexes from PPI Data: A Core-Attachment Approach. Journal of Computational Biology, 2009, 16, 133-144.	0.8	204
133	CLUSTERING-BASED APPROACH FOR PREDICTING MOTIF PAIRS FROM PROTEIN INTERACTION DATA. Journal of Bioinformatics and Computational Biology, 2009, 07, 701-716.	0.3	7
134	Finding optimal threshold for correction error reads in DNA assembling. BMC Bioinformatics, 2009, 10, S15.	1.2	11
135	ARMR: Anonymous routing protocol with multiple routes for communications in mobile ad hoc networks. Ad Hoc Networks, 2009, 7, 1536-1550.	3.4	39
136	SOAP2: an improved ultrafast tool for short read alignment. Bioinformatics, 2009, 25, 1966-1967.	1.8	3,329
137	Succinct Text Indexing with Wildcards. Lecture Notes in Computer Science, 2009, , 39-50.	1.0	22
138	Non-overlapping Common Substrings Allowing Mutations. Mathematics in Computer Science, 2008, 1, 543-555.	0.2	1
139	Promoter-sharing by different genes in human genome â€“ CPNE1 and RBM12 gene pair as an example. BMC Genomics, 2008, 9, 456.	1.2	27
140	MotifVoter: a novel ensemble method for fine-grained integration of generic motif finders. Bioinformatics, 2008, 24, 2288-2295.	1.8	41
141	Improving Disk Sector Integrity Using K-Dimension Hashing. International Federation for Information Processing, 2008, , 87-98.	0.4	5
142	Detection of generic spaced motifs using submotif pattern mining. Bioinformatics, 2007, 23, 1476-1485.	1.8	29
143	Discovery of transcription factor binding sites through integration of generic motif finders. Nature Precedings, 2007, , .	0.1	0
144	Providing distributed certificate authority service in cluster-based mobile ad hoc networks. Computer Communications, 2007, 30, 2442-2452.	3.1	28

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145	A Space and Time Efficient Algorithm for Constructing Compressed Suffix Arrays. Algorithmica, 2007, 48, 23-36.	1.0	59
146	An Experimental Study of Compressed Indexing and Local Alignments of DNA. Lecture Notes in Computer Science, 2007, , 242-254.	1.0	0
147	Intrusion Detection Routers: Design, Implementation and Evaluation Using an Experimental Testbed. IEEE Journal on Selected Areas in Communications, 2006, 24, 1889-1900.	9.7	8
148	Sharing and access right delegation for confidential documents: A practical solution. Information and Management, 2006, 43, 607-616.	3.6	5
149	Practical electronic lotteries with offline TTP. Computer Communications, 2006, 29, 2830-2840.	3.1	13
150	RECONSTRUCTING AN ULTRAMETRIC GALLED PHYLOGENETIC NETWORK FROM A DISTANCE MATRIX. Journal of Bioinformatics and Computational Biology, 2006, 04, 807-832.	0.3	19
151	A generic anti-spyware solution by access control list at kernel level. Journal of Systems and Software, 2005, 75, 227-234.	3.3	10
152	An efficient algorithm for finding dense regions for mining quantitative association rules. Computers and Mathematics With Applications, 2005, 50, 471-490.	1.4	30
153	Forward-secure multisignature and blind signature schemes. Applied Mathematics and Computation, 2005, 168, 895-908.	1.4	14
154	Filtering of Ineffective siRNAs and Improved siRNA Design Tool. Bioinformatics, 2005, 21, 144-151.	1.8	119
155	Indexing useful structural patterns for XML query processing. IEEE Transactions on Knowledge and Data Engineering, 2005, 17, 997-1009.	4.0	11
156	Efficient Identity Based Ring Signature. Lecture Notes in Computer Science, 2005, , 499-512.	1.0	120
157	Finding Motifs with Insufficient Number of Strong Binding Sites. Journal of Computational Biology, 2005, 12, 686-701.	0.8	17
158	An efficient and scalable algorithm for clustering XML documents by structure. IEEE Transactions on Knowledge and Data Engineering, 2004, 16, 82-96.	4.0	140
159	SUBTREE TRANSFER DISTANCE FOR DEGREE-D PHYLOGENIES. International Journal of Foundations of Computer Science, 2004, 15, 893-909.	0.8	4
160	Secure Hierarchical Identity Based Signature and Its Application. Lecture Notes in Computer Science, 2004, , 480-494.	1.0	42
161	Non-shared edges and nearest neighbor interchanges revisited. Information Processing Letters, 2004, 91, 129-134.	0.4	5
162	SmartTutor: An intelligent tutoring system in web-based adult education. Journal of Systems and Software, 2003, 68, 11-25.	3.3	61

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163	Approximate string matching in DNA sequences. , 2003, , .		9
164	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
165	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
166	Predicting RNA secondary structures with arbitrary pseudoknots by maximizing the number of stacking pairs. , 2001, , .		7
167	Construction of online catalog topologies using decision trees. , 0, , .		3
168	Compressed index for dynamic text. , 0, , .		0
169	A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	1.5	1
170	Corrigendum to: A Self-Tallying Electronic Voting Based on Blockchain. Computer Journal, 0, , .	1.5	0