

Shuigeng Zhou

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

208
papers

4,132
citations

36
h-index

54
g-index

240
ext. papers

5,072
ext. citations

3.6
avg, IF

5.68
L-index

#	Paper	IF	Citations
208	Focusing Attention: Towards Accurate Text Recognition in Natural Images 2017 ,		179
207	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014 , 5, 5110	17.4	156
206	AON: Towards Arbitrarily-Oriented Text Recognition 2018 ,		112
205	Improving compound-protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015 , 31, i221-9	7.2	109
204	Exact solution for mean first-passage time on a pseudofractal scale-free web. <i>Physical Review E</i> , 2009 , 79, 021127	2.4	103
203	Boosting compound-protein interaction prediction by deep learning. <i>Methods</i> , 2016 , 110, 64-72	4.6	102
202	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019 , 10, 1903	17.4	97
201	GString: A Novel Approach for Efficient Search in Graph Databases 2007 ,		91
200	Standard random walks and trapping on the Koch network with scale-free behavior and small-world effect. <i>Physical Review E</i> , 2009 , 79, 061113	2.4	78
199	Distributed Localization Using a Moving Beacon in Wireless Sensor Networks. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2008 , 19, 587-600	3.7	78
198	TEPITOPEpan: extending TEPITOPE for peptide binding prediction covering over 700 HLA-DR molecules. <i>PLoS ONE</i> , 2012 , 7, e30483	3.7	74
197	Edit Probability for Scene Text Recognition 2018 ,		67
196	Epidemic spreading with nonlinear infectivity in weighted scale-free networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011 , 390, 471-481	3.3	63
195	Maximal planar scale-free Sierpinski networks with small-world effect and power law strength-degree correlation. <i>Europhysics Letters</i> , 2007 , 79, 38007	1.6	63
194	MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. <i>BMC Bioinformatics</i> , 2010 , 11 Suppl 11, S11	3.6	62
193	Self-similarity, small-world, scale-free scaling, disassortativity, and robustness in hierarchical lattices. <i>European Physical Journal B</i> , 2007 , 56, 259-271	1.2	59
192	Approaches for scaling DBSCAN algorithm to large spatial databases. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 509-526	1.7	59

191	Determining global mean-first-passage time of random walks on Vicsek fractals using eigenvalues of Laplacian matrices. <i>Physical Review E</i> , 2010 , 81, 031118	2.4	57
190	Prediction of protein-protein interaction sites using an ensemble method. <i>BMC Bioinformatics</i> , 2009 , 10, 426	3.6	54
189	A general geometric growth model for pseudofractal scale-free web. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 377, 329-339	3.3	53
188	Evolving Apollonian networks with small-world scale-free topologies. <i>Physical Review E</i> , 2006 , 74, 046105.4	5.4	52
187	Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , 2009 , 86, 10006	1.6	49
186	PredHS: a web server for predicting protein-protein interaction hot spots by using structural neighborhood properties. <i>Nucleic Acids Research</i> , 2014 , 42, W290-5	20.1	48
185	Enumeration of spanning trees in a pseudofractal scale-free web. <i>Europhysics Letters</i> , 2010 , 90, 68002	1.6	47
184	Analytical solution of average path length for Apollonian networks. <i>Physical Review E</i> , 2008 , 77, 017102	2.4	47
183	Recursive mechanism 2013 ,		43
182	Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. <i>Physical Review E</i> , 2010 , 81, 016114	2.4	43
181	The exact solution of the mean geodesic distance for Vicsek fractals. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 485102	2	42
180	ANGEL: Enhancing the Utility of Generalization for Privacy Preserving Publication. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009 , 21, 1073-1087	4.2	41
179	Finding microRNA targets in plants: current status and perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 264-75	6.5	39
178	Trapping in scale-free networks with hierarchical organization of modularity. <i>Physical Review E</i> , 2009 , 80, 051120	2.4	39
177	Distributed Skyline Retrieval with Low Bandwidth Consumption. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009 , 21, 384-400	4.2	39
176	Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , 2008 , 44, 1397-1409	6.3	39
175	A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , 2014 , 52, 4895-4912	8.1	38
174	Mapping Koch curves into scale-free small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010 , 43, 395101	2	38

173	Distinct scalings for mean first-passage time of random walks on scale-free networks with the same degree sequence. <i>Physical Review E</i> , 2009 , 80, 061111	2.4	38
172	Mean first-passage time for random walks on the T-graph. <i>New Journal of Physics</i> , 2009 , 11, 103043	2.9	34
171	Evolving pseudofractal networks. <i>European Physical Journal B</i> , 2007 , 58, 337-344	1.2	34
170	A new method for enhancer prediction based on deep belief network. <i>BMC Bioinformatics</i> , 2017 , 18, 418	3.6	32
169	A new hybrid method for learning bayesian networks: Separation and reunion. <i>Knowledge-Based Systems</i> , 2017 , 121, 185-197	7.3	31
168	Robust Median Reversion Strategy for Online Portfolio Selection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2016 , 28, 2480-2493	4.2	31
167	CloudNMF: a MapReduce implementation of nonnegative matrix factorization for large-scale biological datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2014 , 12, 48-51	6.5	30
166	Epidemic spreading in weighted scale-free networks with community structure. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P07043	1.9	30
165	Random Sierpinski network with scale-free small-world and modular structure. <i>European Physical Journal B</i> , 2008 , 65, 141-147	1.2	30
164	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. <i>BMC Bioinformatics</i> , 2017 , 18, 420	3.6	29
163	Boosting prediction performance of protein-protein interaction hot spots by using structural neighborhood properties. <i>Journal of Computational Biology</i> , 2013 , 20, 878-91	1.7	29
162	Anomalous behavior of trapping on a fractal scale-free network. <i>Europhysics Letters</i> , 2009 , 88, 10001	1.6	29
161	Evolutionary method for finding communities in bipartite networks. <i>Physical Review E</i> , 2011 , 83, 066120	2.4	28
160	An empirical study of Chinese language networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008 , 387, 3039-3047	3.3	27
159	Rumor evolution in social networks. <i>Physical Review E</i> , 2013 , 87,	2.4	26
158	Incompatibility networks as models of scale-free small-world graphs. <i>European Physical Journal B</i> , 2007 , 60, 259-264	1.2	26
157	miRFam: an effective automatic miRNA classification method based on n-grams and a multiclass SVM. <i>BMC Bioinformatics</i> , 2011 , 12, 216	3.6	25
156	Genome-wide search for miRNA-target interactions in <i>Arabidopsis thaliana</i> with an integrated approach. <i>BMC Genomics</i> , 2012 , 13 Suppl 3, S3	4.5	23

155	Local-world evolving networks with tunable clustering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 380, 639-650	3.3	23
154	Correlations in random Apollonian network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 380, 621-628	3.3	23
153	DPHL: A DIA Pan-human Protein Mass Spectrometry Library for Robust Biomarker Discovery. <i>Genomics, Proteomics and Bioinformatics</i> , 2020 , 18, 104-119	6.5	23
152	Non-Local ConvLSTM for Video Compression Artifact Reduction 2019 ,		23
151	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1541005	1	22
150	Deterministic identification of specific individuals from GWAS results. <i>Bioinformatics</i> , 2015 , 31, 1701-7	7.2	22
149	Topologies and Laplacian spectra of a deterministic uniform recursive tree. <i>European Physical Journal B</i> , 2008 , 63, 507-513	1.2	22
148	LIGHT: A Query-Efficient Yet Low-Maintenance Indexing Scheme over DHTs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2010 , 22, 59-75	4.2	21
147	Achieving optimal data storage position in wireless sensor networks. <i>Computer Communications</i> , 2010 , 33, 92-102	5.1	21
146	Fractal scale-free networks resistant to disease spread. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2008 , 2008, P09008	1.9	21
145	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. <i>Current Bioinformatics</i> , 2018 , 13, 655-660	4.7	21
144	MOBCdb: a comprehensive database integrating multi-omics data on breast cancer for precision medicine. <i>Breast Cancer Research and Treatment</i> , 2018 , 169, 625-632	4.4	20
143	Recursive solutions for Laplacian spectra and eigenvectors of a class of growing treelike networks. <i>Physical Review E</i> , 2009 , 80, 016104	2.4	20
142	Average distance in a hierarchical scale-free network: an exact solution. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P10022	1.9	20
141	PRAGUE: Towards Blending Practical Visual Subgraph Query Formulation and Query Processing 2012 ,		20
140	Efficient top-k processing in large-scaled distributed environments. <i>Data and Knowledge Engineering</i> , 2007 , 63, 315-335	1.5	20
139	Recursive weighted treelike networks. <i>European Physical Journal B</i> , 2007 , 59, 99-107	1.2	20
138	DeepCluster: A General Clustering Framework Based on Deep Learning. <i>Lecture Notes in Computer Science</i> , 2017 , 809-825	0.9	20

137	A comparative evaluation on prediction methods of nucleosome positioning. <i>Briefings in Bioinformatics</i> , 2014 , 15, 1014-27	13.4	19
136	A New Unsupervised Binning Approach for Metagenomic Sequences Based on N-grams and Automatic Feature Weighting. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 42-54	3	19
135	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. <i>Neurocomputing</i> , 2012 , 92, 44-53	5.4	19
134	A RAMCloud Storage System based on HDFS: Architecture, implementation and evaluation. <i>Journal of Systems and Software</i> , 2013 , 86, 744-750	3.3	19
133	Different thresholds of bond percolation in scale-free networks with identical degree sequence. <i>Physical Review E</i> , 2009 , 79, 031110	2.4	19
132	A unified model for Sierpinski networks with scale-free scaling and small-world effect. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009 , 388, 2571-2578	3.3	19
131	A geometric growth model interpolating between regular and small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2007 , 40, 11863-11876	2	19
130	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. <i>BMC Systems Biology</i> , 2017 , 11, 9	3.5	18
129	QUBLE: towards blending interactive visual subgraph search queries on large networks. <i>VLDB Journal</i> , 2014 , 23, 401-426	3.9	18
128	The prisoner's dilemma in structured scale-free networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009 , 42, 245002	2	18
127	Transition from fractal to non-fractal scalings in growing scale-free networks. <i>European Physical Journal B</i> , 2008 , 64, 277-283	1.2	18
126	Effects of accelerating growth on the evolution of weighted complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009 , 388, 225-232	3.3	17
125	A new and effective hierarchical overlay structure for Peer-to-Peer networks. <i>Computer Communications</i> , 2011 , 34, 862-874	5.1	17
124	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014 , 145, 44-52	5.4	16
123	Characteristics of real futures trading networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011 , 390, 398-409	3.3	16
122	Influences of degree inhomogeneity on average path length and random walks in disassortative scale-free networks. <i>Journal of Mathematical Physics</i> , 2009 , 50, 033514	1.2	16
121	Scalable continual top-k keyword search in relational databases. <i>Data and Knowledge Engineering</i> , 2013 , 86, 206-223	1.5	14
120	A path-traceable query routing mechanism for search in unstructured peer-to-peer networks. <i>Journal of Network and Computer Applications</i> , 2010 , 33, 115-127	7.9	14

119	Deterministic weighted scale-free small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010 , 389, 3316-3324	3.3	14
118	From regular to growing small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 385, 765-772	3.3	14
117	An effective approach to detecting both small and large complexes from protein-protein interaction networks. <i>BMC Bioinformatics</i> , 2017 , 18, 419	3.6	13
116	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2018 , 15, 1832-1843	3	12
115	NEpiC: a network-assisted algorithm for epigenetic studies using mean and variance combined signals. <i>Nucleic Acids Research</i> , 2016 , 44, e134	20.1	12
114	Choosing appropriate models for protein-protein interaction networks: a comparison study. <i>Briefings in Bioinformatics</i> , 2014 , 15, 823-38	13.4	12
113	PICASSO. <i>Proceedings of the VLDB Endowment</i> , 2017 , 10, 1861-1864	3.1	12
112	Compensatory ability to null mutation in metabolic networks. <i>Biotechnology and Bioengineering</i> , 2009 , 103, 361-9	4.9	12
111	Diffusion-Annihilation processes in weighted scale-free networks with an identical degree sequence. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2011 , 2011, P10001	1.9	12
110	CPredictor3.0: detecting protein complexes from PPI networks with expression data and functional annotations. <i>BMC Systems Biology</i> , 2017 , 11, 135	3.5	11
109	Group-sparse Modeling Drug-kinase Networks for Predicting Combinatorial Drug Sensitivity in Cancer Cells. <i>Current Bioinformatics</i> , 2018 , 13, 437-443	4.7	11
108	When cloud computing meets bioinformatics: a review. <i>Journal of Bioinformatics and Computational Biology</i> , 2013 , 11, 1330002	1	10
107	Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. <i>Scientific Reports</i> , 2016 , 6, 35652	4.9	10
106	Knowledge diffusion in complex networks. <i>Concurrency Computation Practice and Experience</i> , 2017 , 29, e3791	1.4	9
105	BOOMER 2018 ,		9
104	Group-Theoretical Analysis of Variable Coefficient Nonlinear Telegraph Equations. <i>Acta Applicandae Mathematicae</i> , 2012 , 117, 135-183	1.1	9
103	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. <i>BMC Genomics</i> , 2014 , 15, 1148	4.5	9
102	Traffic Fluctuations on Weighted Networks. <i>IEEE Circuits and Systems Magazine</i> , 2012 , 12, 33-44	3.2	9

101	Prediction of protein-protein interactions from primary sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2010 , 4, 211-27	0.5	9
100	Group properties of generalized quasi-linear wave equations. <i>Journal of Mathematical Analysis and Applications</i> , 2010 , 366, 460-472	1.1	9
99	DEEPESEN: a convolutional neural network based method for super-enhancer prediction. <i>BMC Bioinformatics</i> , 2019 , 20, 598	3.6	9
98	A General Framework for Unmet Demand Prediction in On-Demand Transport Services. <i>IEEE Transactions on Intelligent Transportation Systems</i> , 2019 , 20, 2820-2830	6.1	9
97	Gaming Temporal Networks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2019 , 66, 672-676	9.5	8
96	You Only Recognize Once 2019 ,		8
95	QUBLE 2013 ,		8
94	HNet-DNN: Inferring New Drug-Disease Associations with Deep Neural Network Based on Heterogeneous Network Features. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 2367-2376	6.1	7
93	Private search on key-value stores with hierarchical indexes 2014 ,		7
92	The centrality of cancer proteins in human protein-protein interaction network: a revisit. <i>International Journal of Computational Biology and Drug Design</i> , 2014 , 7, 146-56	0.4	7
91	Square++: Making a connection game win-lose complementary and playing-fair. <i>Entertainment Computing</i> , 2013 , 4, 105-113	1.9	7
90	Efficient Retrieval of Bounded-Cost Informative Routes. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017 , 29, 2182-2196	4.2	7
89	Contact graphs of disk packings as a model of spatial planar networks. <i>New Journal of Physics</i> , 2009 , 11, 083007	2.9	7
88	Structural and spectral properties of a family of deterministic recursive trees: rigorous solutions. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009 , 42, 165103	2	7
87	DISKs. <i>Proceedings of the VLDB Endowment</i> , 2012 , 5, 1966-1969	3.1	7
86	LHT: A Low-Maintenance Indexing Scheme over DHTs 2008 ,		7
85	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. <i>Methods</i> , 2020 , 179, 55-64	4.6	6
84	A Unified Framework for Predicting KPIs of On-Demand Transport Services. <i>IEEE Access</i> , 2018 , 6, 32005-32014	3.9	6

83	A Lightweight Multidimensional Index for Complex Queries over DHTs. <i>IEEE Transactions on Parallel and Distributed Systems</i> , 2011 , 22, 2046-2054	3.7	6
82	Vertex labeling and routing in expanded Apollonian networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 035004	2	6
81	Efficient Skyline Retrieval on Peer-to-Peer Networks 2007 ,		6
80	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. <i>BMC Bioinformatics</i> , 2020 , 21, 384	3.6	6
79	Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2020 , 17, 777-787	3	6
78	Classifying early and late mild cognitive impairment stages of Alzheimer's disease by fusing default mode networks extracted with multiple seeds. <i>BMC Bioinformatics</i> , 2018 , 19, 523	3.6	6
77	The rigorous solution for the average distance of a Sierpinski network. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009 , 2009, P02034	1.9	5
76	Degree and component size distributions in the generalized uniform recursive tree. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 185101	2	5
75	RMDB: An Integrated Database of Single-cytosine-resolution DNA Methylation in <i>Oryza Sativa</i> . <i>Current Bioinformatics</i> , 2019 , 14, 524-531	4.7	5
74	A Chaotic Ant Colony Optimized Link Prediction Algorithm. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2020 , 1-15	7.3	5
73	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. <i>Bioinformatics</i> , 2021 ,	7.2	5
72	FREE: A Fast and Robust End-to-End Video Text Spotter. <i>IEEE Transactions on Image Processing</i> , 2021 , 30, 822-837	8.7	5
71	Different behaviors of epidemic spreading in scale-free networks with identical degree sequence. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010 , 43, 065001	2	4
70	A machine learning-based method for protein global model quality assessment. <i>International Journal of General Systems</i> , 2011 , 40, 417-425	2.1	4
69	Detecting microarray data supported microRNA-mRNA interactions. <i>International Journal of Data Mining and Bioinformatics</i> , 2010 , 4, 639-55	0.5	4
68	Symbolic analysis and exact travelling wave solutions to a new modified Novikov equation. <i>Applied Mathematics and Computation</i> , 2010 , 217, 590-598	2.7	4
67	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4
66	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021 , 20, 1079-1086	5.6	4

65	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. <i>IScience</i> , 2018 , 7, 16-29	6.1	4
64	LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. <i>Journal of Systems and Software</i> , 2015 , 101, 86-96	3.3	3
63	Link Weight Prediction Using Weight Perturbation and Latent Factor. <i>IEEE Transactions on Cybernetics</i> , 2020 , PP,	10.2	3
62	FERRARI: an efficient framework for visual exploratory subgraph search in graph databases. <i>VLDB Journal</i> , 2020 , 29, 973-998	3.9	3
61	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. <i>IEEE Transactions on Services Computing</i> , 2018 , 11, 399-414	4.8	3
60	Revisiting topological properties and models of protein-protein interaction networks from the perspective of dataset evolution. <i>IET Systems Biology</i> , 2015 , 9, 113-9	1.4	3
59	Unfavorable Individuals in Social Gaming Networks. <i>Scientific Reports</i> , 2015 , 5, 17481	4.9	3
58	Boosting compound-protein interaction prediction by deep learning 2015 ,		3
57	Automatically clustering large-scale miRNA sequences: methods and experiments. <i>BMC Genomics</i> , 2012 , 13 Suppl 8, S15	4.5	3
56	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in Arabidopsis thaliana 2011 ,		3
55	An improved genetic algorithm for statistical potential function design and protein structure prediction. <i>International Journal of Data Mining and Bioinformatics</i> , 2012 , 6, 162-77	0.5	3
54	Data management in Peer-to-Peer environment: A perspective of BestPeer. <i>Journal of Computer Science and Technology</i> , 2003 , 18, 452-461	1.7	3
53	Fast text classification: a training-corpus pruning based approach 2003 ,		3
52	Privacy and efficiency guaranteed social subgraph matching. <i>VLDB Journal</i> ,1	3.9	3
51	D2CL: A Dense Dilated Convolutional LSTM Model for Sea Surface Temperature Prediction. <i>IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing</i> , 2021 , 14, 12514-12523	4.7	3
50	Single-cell RNA-seq data clustering: A survey with performance comparison study. <i>Journal of Bioinformatics and Computational Biology</i> , 2020 , 18, 2040005	1	3
49	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. <i>BMC Genomics</i> , 2019 , 20, 221	4.5	2
48	. <i>Tsinghua Science and Technology</i> , 2019 , 24, 456-467	3.4	2

47	Towards efficiently supporting database as a service with QoS guarantees. <i>Journal of Systems and Software</i> , 2018 , 139, 51-63	3.3	2
46	JeCache: Just-Enough Data Caching with Just-in-Time Prefetching for Big Data Applications 2017 ,		2
45	iHMS: a database integrating human histone modification data across developmental stages and tissues. <i>BMC Bioinformatics</i> , 2017 , 18, 103	3.6	2
44	Identifying TF-MiRNA Regulatory Relationships Using Multiple Features. <i>PLoS ONE</i> , 2015 , 10, e0125156	3.7	2
43	MeioBase: a comprehensive database for meiosis. <i>Frontiers in Plant Science</i> , 2014 , 5, 728	6.2	2
42	Mean first passage time for random walk on dual structure of dendrimer. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2014 , 415, 463-472	3.3	2
41	A new algorithm for automatic computation of solitary wave solutions to nonlinear partial differential equations based on the Exp-function method. <i>Applied Mathematics and Computation</i> , 2012 , 219, 1890-1896	2.7	2
40	Gene ontology-based protein function prediction by using sequence composition information. <i>Protein and Peptide Letters</i> , 2010 , 17, 789-95	1.9	2
39	LESSON: A system for lecture notes searching and sharing over Internet. <i>Journal of Systems and Software</i> , 2010 , 83, 1851-1863	3.3	2
38	Incremental mining of the schema of semistructured data. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 241-248	1.7	2
37	Boosting the Performance of Video Compression Artifact Reduction with Reference Frame Proposals and Frequency Domain Information 2021 ,		2
36	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019 , 33, 5167-5174	5	2
35	Statistical learning with group invariance: problem, method and consistency. <i>International Journal of Machine Learning and Cybernetics</i> , 2019 , 10, 1503-1511	3.8	2
34	A general framework for privacy-preserving of data publication based on randomized response techniques. <i>Information Systems</i> , 2021 , 96, 101648	2.7	2
33	An Indexing Framework for Efficient Visual Exploratory Subgraph Search in Graph Databases 2019 ,		1
32	Effective and scalable causal partitioning based on low-order conditional independent tests. <i>Neurocomputing</i> , 2020 , 389, 146-154	5.4	1
31	A comparison study on protein-protein interaction network models 2012 ,		1
30	Group properties and invariant solutions of a sixth-order thin film equation in viscous fluid. <i>Journal of Mathematical Physics</i> , 2013 , 54, 013510	1.2	1

29	An analytic derivation of clustering coefficients for weighted networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010 , 2010, P03013	1.9	1
28	Effectively predicting protein functions by collective classification [An extended abstract 2012 ,		1
27	GPress: Towards Effective GML Documents Compression 2007 ,		1
26	Supporting ranked join in peer-to-peer networks		1
25	Generalized multidimensional association rules. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 388-392	1.7	1
24	Mobile agent-based distributed geographic information systems under Internet environment		1
23	Learning Latent Semantic Attributes for Zero-Shot Object Detection 2020 ,		1
22	GANs for Molecule Generation in Drug Design and Discovery. <i>Intelligent Systems Reference Library</i> , 2022 , 233-273	0.8	1
21	Calculating the Crossing Probability on the Square Tessellation of a Connection Game with Random Move Order: The Algorithm and Its Complexity. <i>Lecture Notes in Computer Science</i> , 2014 , 288-297	0.9	1
20	Network Parameter Generation for One-Shot Object Detection 2019 ,		1
19	Recursively Learning Causal Structures Using Regression-Based Conditional Independence Test. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019 , 33, 3108-3115	5	1
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