Jihong Guan

List of Publications by Year
in descending order

179 papers	3,572 citations	147566 31 h-index	197535 49 g-index
183 all docs	183 docs citations	183 times ranked	3290 citing authors

#	ARTICLE	IF	CITATIONS
1	Improving compound–protein interaction prediction by building up highly credible negative samples. Bioinformatics, 2015, 31, i221-i229.	1.8	201
2	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	5.8	198
3	Boosting compound-protein interaction prediction by deep learning. Methods, 2016, 110, 64-72.	1.9	140
4	Exact solution for mean first-passage time on a pseudofractal scale-free web. Physical Review E, 2009, 79, 021127.	0.8	108
5	Standard random walks and trapping on the Koch network with scale-free behavior and small-world effect. Physical Review E, 2009, 79, 061113.	0.8	88
6	Maximal planar scale-free Sierpinski networks with small-world effect and power law strength-degree correlation. Europhysics Letters, 2007, 79, 38007.	0.7	79
7	MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. BMC Bioinformatics, 2010, 11, S11.	1.2	78
8	Epidemic spreading with nonlinear infectivity in weighted scale-free networks. Physica A: Statistical Mechanics and Its Applications, 2011, 390, 471-481.	1.2	73
9	Inferring new indications for approved drugs via random walk on drug-disease heterogenous networks. BMC Bioinformatics, 2016, 17, 539.	1.2	72
10	Determining global mean-first-passage time of random walks on Vicsek fractals using eigenvalues of Laplacian matrices. Physical Review E, 2010, 81, 031118.	0.8	64
11	The exact solution of the mean geodesic distance for Vicsek fractals. Journal of Physics A: Mathematical and Theoretical, 2008, 41, 485102.	0.7	62
12	PredHS: a web server for predicting protein–protein interaction hot spots by using structural neighborhood properties. Nucleic Acids Research, 2014, 42, W290-W295.	6.5	59
13	Finding MicroRNA Targets in Plants: Current Status and Perspectives. Genomics, Proteomics and Bioinformatics, 2012, 10, 264-275.	3.0	56
14	Random walks on the Apollonian network with a single trap. Europhysics Letters, 2009, 86, 10006.	0.7	52
15	Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. Physical Review E, 2010, 81, 016114.	0.8	52
16	Towards effective document clustering: A constrained K-means based approach. Information Processing and Management, 2008, 44, 1397-1409.	5.4	51
17	A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. IEEE Transactions on Geoscience and Remote Sensing, 2014, 52, 4895-4912.	2.7	48
18	A new hybrid method for learning bayesian networks: Separation and reunion. Knowledge-Based Systems, 2017, 121, 185-197.	4.0	48

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19	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. BMC Bioinformatics, 2017, 18, 420.	1.2	47
20	A new method for enhancer prediction based on deep belief network. BMC Bioinformatics, 2017, 18, 418.	1.2	47
21	Mapping Koch curves into scale-free small-world networks. Journal of Physics A: Mathematical and Theoretical, 2010, 43, 395101.	0.7	46
22	Random Sierpinski network with scale-free small-world and modular structure. European Physical Journal B, 2008, 65, 141-147.	0.6	44
23	Trapping in scale-free networks with hierarchical organization of modularity. Physical Review E, 2009, 80, 051120.	0.8	40
24	Epidemic spreading in weighted scale-free networks with community structure. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P07043.	0.9	38
25	Boosting Prediction Performance of Protein–Protein Interaction Hot Spots by Using Structural Neighborhood Properties. Journal of Computational Biology, 2013, 20, 878-891.	0.8	38
26	Mean first-passage time for random walks on the T-graph. New Journal of Physics, 2009, 11, 103043.	1.2	37
27	An empirical study of Chinese language networks. Physica A: Statistical Mechanics and Its Applications, 2008, 387, 3039-3047.	1.2	36
28	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. Bioinformatics, 2021, 37, 2981-2987.	1.8	36
29	Rumor evolution in social networks. Physical Review E, 2013, 87, .	0.8	34
30	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. BMC Systems Biology, 2017, 11, 9.	3.0	34
31	CloudNMF: A MapReduce Implementation of Nonnegative Matrix Factorization for Large-scale Biological Datasets. Genomics, Proteomics and Bioinformatics, 2014, 12, 48-51.	3.0	33
32	Identification of cancer subtypes from single-cell RNA-seq data using a consensus clustering method. BMC Medical Genomics, 2018, 11, 117.	0.7	33
33	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. Journal of Bioinformatics and Computational Biology, 2015, 13, 1541005.	0.3	32
34	Mining frequent closed itemsets from a landmark window over online data streams. Computers and Mathematics With Applications, 2009, 57, 927-936.	1.4	31
35	Evolutionary method for finding communities in bipartite networks. Physical Review E, 2011, 83, 066120.	0.8	31
36	Anomalous behavior of trapping on a fractal scale-free network. Europhysics Letters, 2009, 88, 10001.	0.7	30

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37	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. Neurocomputing, 2012, 92, 44-53.	3.5	30
38	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. Current Bioinformatics, 2018, 13, 655-660.	0.7	30
39	Incompatibility networks as models of scale-free small-world graphs. European Physical Journal B, 2007, 60, 259-264.	0.6	29
40	miRFam: an effective automatic miRNA classification method based on n-grams and a multiclass SVM. BMC Bioinformatics, 2011, 12, 216.	1.2	29
41	A RAMCloud Storage System based on HDFS: Architecture, implementation and evaluation. Journal of Systems and Software, 2013, 86, 744-750.	3.3	29
42	GITAR: An Open Source Tool for Analysis and Visualization of Hi-C Data. Genomics, Proteomics and Bioinformatics, 2018, 16, 365-372.	3.0	28
43	Topologies and Laplacian spectra of a deterministic uniform recursive tree. European Physical Journal B, 2008, 63, 507-513.	0.6	27
44	Genome-wide search for miRNA-target interactions in Arabidopsis thaliana with an integrated approach. BMC Genomics, 2012, 13, S3.	1.2	27
45	Local-world evolving networks with tunable clustering. Physica A: Statistical Mechanics and Its Applications, 2007, 380, 639-650.	1.2	26
46	Average distance in a hierarchical scale-free network: an exact solution. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P10022.	0.9	24
47	A unified model for Sierpinski networks with scale-free scaling and small-world effect. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 2571-2578.	1.2	24
48	Effective drug–target interaction prediction with mutual interaction neural network. Bioinformatics, 2022, 38, 3582-3589.	1.8	24
49	Different thresholds of bond percolation in scale-free networks with identical degree sequence. Physical Review E, 2009, 79, 031110.	0.8	23
50	A comparative evaluation on prediction methods of nucleosome positioning. Briefings in Bioinformatics, 2014, 15, 1014-1027.	3.2	23
51	Recursive solutions for Laplacian spectra and eigenvectors of a class of growing treelike networks. Physical Review E, 2009, 80, 016104.	0.8	22
52	A new and effective hierarchical overlay structure for Peer-to-Peer networks. Computer Communications, 2011, 34, 862-874.	3.1	22
53	A General Framework for Unmet Demand Prediction in On-Demand Transport Services. IEEE Transactions on Intelligent Transportation Systems, 2019, 20, 2820-2830.	4.7	22
54	Deep structural clustering for single-cell RNA-seq data jointly through autoencoder and graph neural network. Briefings in Bioinformatics, 2022, 23, .	3.2	22

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55	Recursive weighted treelike networks. European Physical Journal B, 2007, 59, 99-107.	0.6	21
56	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1832-1843.	1.9	21
57	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. Methods, 2020, 179, 55-64.	1.9	21
58	D2CL: A Dense Dilated Convolutional LSTM Model for Sea Surface Temperature Prediction. IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing, 2021, 14, 12514-12523.	2.3	21
59	Transition from fractal to non-fractal scalings in growing scale-free networks. European Physical Journal B, 2008, 64, 277-283.	0.6	20
60	Effects of accelerating growth on the evolution of weighted complex networks. Physica A: Statistical Mechanics and Its Applications, 2009, 388, 225-232.	1.2	20
61	Protein Function Prediction Based on PPI Networks: Network Reconstruction vs Edge Enrichment. Frontiers in Genetics, 2021, 12, 758131.	1.1	20
62	Scalable continual top-k keyword search in relational databases. Data and Knowledge Engineering, 2013, 86, 206-223.	2.1	18
63	Active learning for protein function prediction in protein–protein interaction networks. Neurocomputing, 2014, 145, 44-52.	3.5	18
64	An effective approach to detecting both small and large complexes from protein-protein interaction networks. BMC Bioinformatics, 2017, 18, 419.	1.2	18
65	Essential Protein Detection by Random Walk on Weighted Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 377-387.	1.9	18
66	Influences of degree inhomogeneity on average path length and random walks in disassortative scale-free networks. Journal of Mathematical Physics, 2009, 50, 033514.	0.5	17
67	A Chaotic Ant Colony Optimized Link Prediction Algorithm. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2021, 51, 5274-5288.	5.9	17
68	Towards a Secure Medium Access Control Protocol for Cluster-Based Underwater Wireless Sensor Networks. International Journal of Distributed Sensor Networks, 2015, 11, 325474.	1.3	17
69	A path-traceable query routing mechanism for search in unstructured peer-to-peer networks. Journal of Network and Computer Applications, 2010, 33, 115-127.	5.8	16
70	Deterministic weighted scale-free small-world networks. Physica A: Statistical Mechanics and Its Applications, 2010, 389, 3316-3324.	1.2	16
71	Characteristics of real futures trading networks. Physica A: Statistical Mechanics and Its Applications, 2011, 390, 398-409.	1.2	16
72	DISKs. Proceedings of the VLDB Endowment, 2012, 5, 1966-1969.	2.1	16

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73	Single-cell RNA-seq data clustering: A survey with performance comparison study. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040005.	0.3	16
74	Protein–protein interaction prediction based on ordinal regression and recurrent convolutional neural networks. BMC Bioinformatics, 2021, 22, 485.	1.2	16
75	From regular to growing small-world networks. Physica A: Statistical Mechanics and Its Applications, 2007, 385, 765-772.	1.2	15
76	Choosing appropriate models for protein–protein interaction networks: a comparison study. Briefings in Bioinformatics, 2014, 15, 823-838.	3.2	15
77	Screening lifespan-extending drugs in Caenorhabditis elegans via label propagation on drug-protein networks. BMC Systems Biology, 2016, 10, 131.	3.0	15
78	CPredictor3.0: detecting protein complexes from PPI networks with expression data and functional annotations. BMC Systems Biology, 2017, 11, 135.	3.0	15
79	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. BMC Bioinformatics, 2020, 21, 384.	1.2	15
80	Denoising Protein–Protein interaction network via variational graph auto-encoder for protein complex detection. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040010.	0.3	15
81	Group-sparse Modeling Drug-kinase Networks for Predicting Combinatorial Drug Sensitivity in Cancer Cells. Current Bioinformatics, 2018, 13, 437-443.	0.7	15
82	Discovering pattern-based subspace clusters by pattern tree. Knowledge-Based Systems, 2009, 22, 569-579.	4.0	14
83	Knowledge diffusion in complex networks. Concurrency Computation Practice and Experience, 2017, 29, e3791.	1.4	14
84	A Unified Framework for Predicting KPIs of On-Demand Transport Services. IEEE Access, 2018, 6, 32005-32014.	2.6	14
85	Traffic Fluctuations on Weighted Networks. IEEE Circuits and Systems Magazine, 2012, 12, 33-44.	2.6	13
86	WHEN CLOUD COMPUTING MEETS BIOINFORMATICS: A REVIEW. Journal of Bioinformatics and Computational Biology, 2013, 11, 1330002.	0.3	13
87	Local Nash Equilibrium in Social Networks. Scientific Reports, 2014, 4, 6224.	1.6	13
88	Diffusion–annihilation processes in weighted scale-free networks with an identical degree sequence. Journal of Statistical Mechanics: Theory and Experiment, 2011, 2011, P10001.	0.9	12
89	Identifying overlapping communities in networks using evolutionary method. Physica A: Statistical Mechanics and Its Applications, 2016, 442, 182-192.	1.2	12
90	Classifying early and late mild cognitive impairment stages of Alzheimer's disease by fusing default mode networks extracted with multiple seeds. BMC Bioinformatics, 2018, 19, 523.	1.2	12

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91	DEEPSEN: a convolutional neural network based method for super-enhancer prediction. BMC Bioinformatics, 2019, 20, 598.	1.2	12
92	Towards More Effective Text Summarization Based on Textual Association Networks. , 2008, , .		11
93	Efficient Retrieval of Bounded-Cost Informative Routes. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 2182-2196.	4.0	11
94	Gaming Temporal Networks. IEEE Transactions on Circuits and Systems II: Express Briefs, 2019, 66, 672-676.	2.2	11
95	Privacy and efficiency guaranteed social subgraph matching. VLDB Journal, 2022, 31, 581-602.	2.7	11
96	The centrality of cancer proteins in human protein-protein interaction network: a revisit. International Journal of Computational Biology and Drug Design, 2014, 7, 146.	0.3	10
97	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5167-5174.	3.6	10
98	Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 777-787.	1.9	10
99	The rigorous solution for the average distance of a Sierpinski network. Journal of Statistical Mechanics: Theory and Experiment, 2009, 2009, P02034.	0.9	8
100	LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. Journal of Systems and Software, 2015, 101, 86-96.	3.3	8
101	Link Prediction based on Quantum-Inspired Ant Colony Optimization. Scientific Reports, 2018, 8, 13389.	1.6	8
102	Learning Causal Structures Based on Divide and Conquer. IEEE Transactions on Cybernetics, 2022, 52, 3232-3243.	6.2	8
103	An empirical study of an agglomeration network. Journal of Physics A: Mathematical and Theoretical, 2007, 40, 12365-12375.	0.7	7
104	GPress: Towards Effective GML Documents Compresssion. , 2007, , .		7
105	Structural and spectral properties of a family of deterministic recursive trees: rigorous solutions. Journal of Physics A: Mathematical and Theoretical, 2009, 42, 165103.	0.7	7
106	Identifying Mammalian MicroRNA Targets Based on Supervised Distance Metric Learning. IEEE Journal of Biomedical and Health Informatics, 2013, 17, 427-435.	3.9	7
107	Link Weight Prediction Using Weight Perturbation and Latent Factor. IEEE Transactions on Cybernetics, 2022, 52, 1785-1797.	6.2	7
108	Efficient Skyline Retrieval on Peer-to-Peer Networks. , 2007, , .		6

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109	A new approach to building histogram for selectivity estimation in query processing optimization. Computers and Mathematics With Applications, 2009, 57, 1037-1047.	1.4	6
110	Detecting microarray data supported microRNA-mRNA interactions. International Journal of Data Mining and Bioinformatics, 2010, 4, 639.	0.1	6
111	Recursively Learning Causal Structures Using Regression-Based Conditional Independence Test. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 3108-3115.	3.6	6
112	GRACE: A Graph-Based Cluster Ensemble Approach for Single-Cell RNA-Seq Data Clustering. IEEE Access, 2020, 8, 166730-166741.	2.6	6
113	MIMO: A Unified Spatio-Temporal Model for Multi-Scale Sea Surface Temperature Prediction. Remote Sensing, 2022, 14, 2371.	1.8	6
114	Degree and component size distributions in the generalized uniform recursive tree. Journal of Physics A: Mathematical and Theoretical, 2008, 41, 185101.	0.7	5
115	KORS: Keyword-aware Optimal Route Search System. , 2013, , .		5
116	TiC2D: Trajectory Inference From Single-Cell RNA-Seq Data Using Consensus Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2512-2522.	1.9	5
117	RMDB: An Integrated Database of Single-cytosine-resolution DNA Methylation in Oryza Sativa. Current Bioinformatics, 2019, 14, 524-531.	0.7	5
118	DCAD: a dual clustering algorithm for distributed spatial databases. Geo-Spatial Information Science, 2007, 10, 137-144.	2.4	4
119	LESSON: A system for lecture notes searching and sharing over Internet. Journal of Systems and Software, 2010, 83, 1851-1863.	3.3	4
120	An analytic derivation of clustering coefficients for weighted networks. Journal of Statistical Mechanics: Theory and Experiment, 2010, 2010, P03013.	0.9	4
121	Dynamic epigenetic mode analysis using spatial temporal clustering. BMC Bioinformatics, 2016, 17, 537.	1.2	4
122	iHMS: a database integrating human histone modification data across developmental stages and tissues. BMC Bioinformatics, 2017, 18, 103.	1.2	4
123	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. IEEE Transactions on Services Computing, 2018, 11, 399-414.	3.2	4
124	Measuring Conditional Independence by Independent Residuals for Causal Discovery. ACM Transactions on Intelligent Systems and Technology, 2019, 10, 1-19.	2.9	4
125	Revealing dynamic communities in networks using genetic algorithm with merge and split operators. Physica A: Statistical Mechanics and Its Applications, 2020, 558, 124897.	1.2	4
126	Classifying Cognitive Normal and Early Mild Cognitive Impairment of Alzheimerâ€™s Disease by Applying Restricted Boltzmann Machine to fMRI Data. Current Bioinformatics, 2021, 16, 252-260.	0.7	4

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127	Gene Ontology-Based Protein Function Prediction by Using Sequence Composition Information. Protein and Peptide Letters, 2010, 17, 789-795.	0.4	3
128	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in Arabidopsis thaliana. , 2011, , .		3
129	An improved genetic algorithm for statistical potential function design and protein structure prediction. International Journal of Data Mining and Bioinformatics, 2012, 6, 162.	0.1	3
130	Revisiting topological properties and models of protein–protein interaction networks from the perspective of dataset evolution. IET Systems Biology, 2015, 9, 113-119.	0.8	3
131	Unfavorable Individuals in Social Gaming Networks. Scientific Reports, 2015, 5, 17481.	1.6	3
132	Boosting compound-protein interaction prediction by deep learning. , 2015, , .		3
133	Influence of weight heterogeneity on random walks in scale-free networks. Journal of Physics A: Mathematical and Theoretical, 2016, 49, 275101.	0.7	3
134	Towards efficiently supporting database as a service with QoS guarantees. Journal of Systems and Software, 2018, 139, 51-63.	3.3	3
135	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. BMC Genomics, 2019, 20, 221.	1.2	3
136	Fusion analysis of resting-state networks and its application to Alzheimer's disease. Tsinghua Science and Technology, 2019, 24, 456-467.	4.1	3
137	Classification of Marine Plankton Based on Few-shot Learning. Arabian Journal for Science and Engineering, 2021, 46, 9253-9262.	1.7	3
138	Combined cause inference: Definition, model and performance. Information Sciences, 2021, 574, 431-443.	4.0	3
139	Fast Implementation of Dual Clustering Algorithm for Spatial Data Mining. , 2007, , .		2
140	Routing Based Load Balancing for Unstructured P2P Networks. , 2007, , .		2
141	A GML compression approach based on on-line semantic clustering. , 2010, , .		2
142	Efficient Continual Top-k Keyword Search in Relational Databases. Journal of Information Processing, 2012, 20, 114-127.	0.3	2
143	Effective clustering of microRNA sequences by N-grams and feature weighting. , 2012, , .		2
144	Mean first passage time for random walk on dual structure of dendrimer. Physica A: Statistical Mechanics and Its Applications, 2014, 415, 463-472.	1.2	2

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145	Side-chain dynamics analysis of KE07 series. Computational Biology and Chemistry, 2016, 65, 148-153.	1.1	2
146	Role of Individual Activity in Rumor Spreading in Scale-free Networks. , 2017, , .		2
147	Gaussian Weighting Reversion Strategy for Accurate On-Line Portfolio Selection. , 2017, , .		2
148	A general framework for privacy-preserving of data publication based on randomized response techniques. Information Systems, 2021, 96, 101648.	2.4	2
149	Boosting scRNA-seq data clustering by cluster-aware feature weighting. BMC Bioinformatics, 2021, 22, 130.	1.2	2
150	Network as Regularization for Training Deep Neural Networks: Framework, Model and Performance. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 6013-6020.	3.6	2
151	Effectively Clustering Single Cell RNA Sequencing Data by Sparse Representation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	2
152	Causal Gene Identification Using Non-linear Regression-based Independence Tests. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	1.9	2
153	SIM: an improved few-shot image classification model with multi-task learning. Journal of Electronic Imaging, 2022, 31, .	0.5	2
154	A new full-text indexing model with low space overhead for chinese text retrieval. International Journal on Digital Libraries, 2004, 4, 272-282.	1.1	1
155	A Peer-to-Peer Based Text Sharing and Retrieval System. , 2007, , .		1
156	Empirical Probability Functions Derived from Dihedral Angles for Protein Structure Prediction. , 2009, , .		1
157	Effectively predicting protein functions by collective classification &#x2014; An extended abstract. , 2012, , .		1
158	A comparison study on protein-protein interaction network models. , 2012, , .		1
159	Enhancing Routing Robustness of Unstructured Peer-to-Peer Networks Using Mobile Agents. Journal of Network and Systems Management, 2012, 20, 309-352.	3.3	1
160	GR-tree: An efficient index structure for GML. , 2014, , .		1
161	Determining average path length and average trapping time on generalized dual dendrimer. International Journal of Modern Physics B, 2015, 29, 1550072.	1.0	1
162	CPredictor 4.0: effectively detecting protein complexes in weighted dynamic PPI networks. International Journal of Data Mining and Bioinformatics, 2018, 20, 303.	0.1	1

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163	A Fast Subspace Clustering Algorithm Based on Pattern Similarity. , 2007, , .		0
164	SWER: small world-based efficient routing for wireless sensor networks with mobile sinks. Frontiers of Computer Science, 2009, 3, 427-434.	0.6	0
165	Towards Keyword Search over Relational Databases in DHT Networks. , 2009, , .		0
166	Improving Prediction of the Contact Numbers of Residues in Proteins from Primary Sequences. , 2009, , .		0
167	Querying GML documents: An XQuery based approach. , 2010, , .		0
168	Protein Backbone Dihedral Angle Prediction Based on Probabilistic Models. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	0
169	Building Resilient Unstructured Peer-to-Peer Networks Using Mobile Agents. , 2010, , .		0
170	LRIR: A hybrid semantic Web services matching approach. , 2010, , .		0
171	A self-index GML storage approach based on element coding. , 2011, , .		0
172	Revisiting topological properties of protein-protein interaction networks from the perspective of dataset evolution. , 2014, , .		0
173	Knowledge Diffusion in Complex Networks. , 2015, , .		0
174	An integrative analysis of nucleosome occupancy and positioning using diverse sequence dependent properties. Neurocomputing, 2016, 206, 35-41.	3.5	0
175	Histone modification patterns in highly differentiation cells. Neurocomputing, 2016, 206, 42-49.	3.5	0
176	A New Method for Extracting the Hierarchical Organization of Networks. International Journal of Information Technology and Decision Making, 2017, 16, 1359-1385.	2.3	0
177	Divide-and-conquer Tournament on Social Networks. Scientific Reports, 2017, 7, 15484.	1.6	0
178	Efficient Retrieval of Bounded-Cost Informative Routes. , 2018, , .		0
179	The Complexities of Random-Turn Hex, Square, and Triangle Games. IEEE Transactions on Games, 2022, 14, 180-190.	1.2	0