

Jihong Guan

List of Publications by Year in descending order

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179
papers

3,572
citations

147801

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49
g-index

183
all docs

183
docs citations

183
times ranked

3290
citing authors

#	ARTICLE	IF	CITATIONS
1	Learning Causal Structures Based on Divide and Conquer. IEEE Transactions on Cybernetics, 2022, 52, 3232-3243.	9.5	8
2	The Complexities of Random-Turn Hex, Square, and Triangle Games. IEEE Transactions on Games, 2022, 14, 180-190.	1.4	0
3	Link Weight Prediction Using Weight Perturbation and Latent Factor. IEEE Transactions on Cybernetics, 2022, 52, 1785-1797.	9.5	7
4	TiC2D: Trajectory Inference From Single-Cell RNA-Seq Data Using Consensus Clustering. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 2512-2522.	3.0	5
5	Privacy and efficiency guaranteed social subgraph matching. VLDB Journal, 2022, 31, 581-602.	4.1	11
6	Deep structural clustering for single-cell RNA-seq data jointly through autoencoder and graph neural network. Briefings in Bioinformatics, 2022, 23, .	6.5	22
7	Causal Gene Identification Using Non-linear Regression-based Independence Tests. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, PP, 1-1.	3.0	2
8	MIMO: A Unified Spatio-Temporal Model for Multi-Scale Sea Surface Temperature Prediction. Remote Sensing, 2022, 14, 2371.	4.0	6
9	Effective drug-target interaction prediction with mutual interaction neural network. Bioinformatics, 2022, 38, 3582-3589.	4.1	24
10	SIM: an improved few-shot image classification model with multi-task learning. Journal of Electronic Imaging, 2022, 31, .	0.9	2
11	A Chaotic Ant Colony Optimized Link Prediction Algorithm. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2021, 51, 5274-5288.	9.3	17
12	A general framework for privacy-preserving of data publication based on randomized response techniques. Information Systems, 2021, 96, 101648.	3.6	2
13	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. Bioinformatics, 2021, 37, 2981-2987.	4.1	36
14	Classifying Cognitive Normal and Early Mild Cognitive Impairment of Alzheimer's Disease by Applying Restricted Boltzmann Machine to fMRI Data. Current Bioinformatics, 2021, 16, 252-260.	1.5	4
15	Classification of Marine Plankton Based on Few-shot Learning. Arabian Journal for Science and Engineering, 2021, 46, 9253-9262.	3.0	3
16	Boosting scRNA-seq data clustering by cluster-aware feature weighting. BMC Bioinformatics, 2021, 22, 130.	2.6	2
17	Combined cause inference: Definition, model and performance. Information Sciences, 2021, 574, 431-443.	6.9	3
18	Protein-protein interaction prediction based on ordinal regression and recurrent convolutional neural networks. BMC Bioinformatics, 2021, 22, 485.	2.6	16

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19	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.	4.9	21
20	Effectively Clustering Single Cell RNA Sequencing Data by Sparse Representation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	3.0	2
21	Protein Function Prediction Based on PPI Networks: Network Reconstruction vs Edge Enrichment. Frontiers in Genetics, 2021, 12, 758131.	2.3	20
22	Accurately Detecting Protein Complexes by Graph Embedding and Combining Functions with Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 777-787.	3.0	10
23	Single-cell RNA-seq data clustering: A survey with performance comparison study. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040005.	0.8	16
24	GRACE: A Graph-Based Cluster Ensemble Approach for Single-Cell RNA-Seq Data Clustering. IEEE Access, 2020, 8, 166730-166741.	4.2	6
25	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. BMC Bioinformatics, 2020, 21, 384.	2.6	15
26	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. Methods, 2020, 179, 55-64.	3.8	21
27	Denoising Protein-Protein interaction network via variational graph auto-encoder for protein complex detection. Journal of Bioinformatics and Computational Biology, 2020, 18, 2040010.	0.8	15
28	Revealing dynamic communities in networks using genetic algorithm with merge and split operators. Physica A: Statistical Mechanics and Its Applications, 2020, 558, 124897.	2.6	4
29	Network as Regularization for Training Deep Neural Networks: Framework, Model and Performance. Proceedings of the AAAI Conference on Artificial Intelligence, 2020, 34, 6013-6020.	4.9	2
30	Gaming Temporal Networks. IEEE Transactions on Circuits and Systems II: Express Briefs, 2019, 66, 672-676.	3.0	11
31	Measuring Conditional Independence by Independent Residuals for Causal Discovery. ACM Transactions on Intelligent Systems and Technology, 2019, 10, 1-19.	4.5	4
32	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. Nature Communications, 2019, 10, 1903.	12.8	198
33	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. BMC Genomics, 2019, 20, 221.	2.8	3
34	Fusion analysis of resting-state networks and its application to Alzheimer's disease. Tsinghua Science and Technology, 2019, 24, 456-467.	6.1	3
35	Recursively Learning Causal Structures Using Regression-Based Conditional Independence Test. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 3108-3115.	4.9	6
36	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. Proceedings of the AAAI Conference on Artificial Intelligence, 2019, 33, 5167-5174.	4.9	10

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37	DEEPSSEN: a convolutional neural network based method for super-enhancer prediction. BMC Bioinformatics, 2019, 20, 598.	2.6	12
38	A General Framework for Unmet Demand Prediction in On-Demand Transport Services. IEEE Transactions on Intelligent Transportation Systems, 2019, 20, 2820-2830.	8.0	22
39	Essential Protein Detection by Random Walk on Weighted Protein-Protein Interaction Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 377-387.	3.0	18
40	RMDB: An Integrated Database of Single-cytosine-resolution DNA Methylation in Oryza Sativa. Current Bioinformatics, 2019, 14, 524-531.	1.5	5
41	Towards efficiently supporting database as a service with QoS guarantees. Journal of Systems and Software, 2018, 139, 51-63.	4.5	3
42	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. IEEE Transactions on Services Computing, 2018, 11, 399-414.	4.6	4
43	Effectively Identifying Compound-Protein Interactions by Learning from Positive and Unlabeled Examples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 1832-1843.	3.0	21
44	Efficient Retrieval of Bounded-Cost Informative Routes. , 2018, , .		0
45	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.	2.6	12
46	GITAR: An Open Source Tool for Analysis and Visualization of Hi-C Data. Genomics, Proteomics and Bioinformatics, 2018, 16, 365-372.	6.9	28
47	Identification of cancer subtypes from single-cell RNA-seq data using a consensus clustering method. BMC Medical Genomics, 2018, 11, 117.	1.5	33
48	Predicting Enhancers from Multiple Cell Lines and Tissues across Different Developmental Stages Based On SVM Method. Current Bioinformatics, 2018, 13, 655-660.	1.5	30
49	Link Prediction based on Quantum-Inspired Ant Colony Optimization. Scientific Reports, 2018, 8, 13389.	3.3	8
50	A Unified Framework for Predicting KPIs of On-Demand Transport Services. IEEE Access, 2018, 6, 32005-32014.	4.2	14
51	Group-sparse Modeling Drug-kinase Networks for Predicting Combinatorial Drug Sensitivity in Cancer Cells. Current Bioinformatics, 2018, 13, 437-443.	1.5	15
52	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
53	A New Method for Extracting the Hierarchical Organization of Networks. International Journal of Information Technology and Decision Making, 2017, 16, 1359-1385.	3.9	0
54	Knowledge diffusion in complex networks. Concurrency Computation Practice and Experience, 2017, 29, e3791.	2.2	14

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55	A new hybrid method for learning bayesian networks: Separation and reunion. Knowledge-Based Systems, 2017, 121, 185-197.	7.1	48
56	Divide-and-conquer Tournament on Social Networks. Scientific Reports, 2017, 7, 15484.	3.3	0
57	Efficient Retrieval of Bounded-Cost Informative Routes. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 2182-2196.	5.7	11
58	iHMS: a database integrating human histone modification data across developmental stages and tissues. BMC Bioinformatics, 2017, 18, 103.	2.6	4
59	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. BMC Systems Biology, 2017, 11, 9.	3.0	34
60	Role of Individual Activity in Rumor Spreading in Scale-free Networks. , 2017, , .		2
61	An effective approach to detecting both small and large complexes from protein-protein interaction networks. BMC Bioinformatics, 2017, 18, 419.	2.6	18
62	Gaussian Weighting Reversion Strategy for Accurate On-Line Portfolio Selection. , 2017, , .		2
63	CPredictor3.0: detecting protein complexes from PPI networks with expression data and functional annotations. BMC Systems Biology, 2017, 11, 135.	3.0	15
64	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. BMC Bioinformatics, 2017, 18, 420.	2.6	47
65	A new method for enhancer prediction based on deep belief network. BMC Bioinformatics, 2017, 18, 418.	2.6	47
66	Boosting compound-protein interaction prediction by deep learning. Methods, 2016, 110, 64-72.	3.8	140
67	Dynamic epigenetic mode analysis using spatial temporal clustering. BMC Bioinformatics, 2016, 17, 537.	2.6	4
68	Screening lifespan-extending drugs in Caenorhabditis elegans via label propagation on drug-protein networks. BMC Systems Biology, 2016, 10, 131.	3.0	15
69	An integrative analysis of nucleosome occupancy and positioning using diverse sequence dependent properties. Neurocomputing, 2016, 206, 35-41.	5.9	0
70	Histone modification patterns in highly differentiation cells. Neurocomputing, 2016, 206, 42-49.	5.9	0
71	Influence of weight heterogeneity on random walks in scale-free networks. Journal of Physics A: Mathematical and Theoretical, 2016, 49, 275101.	2.1	3
72	Side-chain dynamics analysis of KE07 series. Computational Biology and Chemistry, 2016, 65, 148-153.	2.3	2

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73	Inferring new indications for approved drugs via random walk on drug-disease heterogenous networks. BMC Bioinformatics, 2016, 17, 539.	2.6	72
74	Identifying overlapping communities in networks using evolutionary method. Physica A: Statistical Mechanics and Its Applications, 2016, 442, 182-192.	2.6	12
75	Revisiting topological properties and models of protein-protein interaction networks from the perspective of dataset evolution. IET Systems Biology, 2015, 9, 113-119.	1.5	3
76	Knowledge Diffusion in Complex Networks. , 2015, , .		0
77	Unfavorable Individuals in Social Gaming Networks. Scientific Reports, 2015, 5, 17481.	3.3	3
78	Determining average path length and average trapping time on generalized dual dendrimer. International Journal of Modern Physics B, 2015, 29, 1550072.	2.0	1
79	Boosting compound-protein interaction prediction by deep learning. , 2015, , .		3
80	Improving compound-protein interaction prediction by building up highly credible negative samples. Bioinformatics, 2015, 31, i221-i229.	4.1	201
81	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. Journal of Bioinformatics and Computational Biology, 2015, 13, 1541005.	0.8	32
82	LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. Journal of Systems and Software, 2015, 101, 86-96.	4.5	8
83	Towards a Secure Medium Access Control Protocol for Cluster-Based Underwater Wireless Sensor Networks. International Journal of Distributed Sensor Networks, 2015, 11, 325474.	2.2	17
84	PredHS: a web server for predicting protein-protein interaction hot spots by using structural neighborhood properties. Nucleic Acids Research, 2014, 42, W290-W295.	14.5	59
85	GR-tree: An efficient index structure for GML. , 2014, , .		1
86	Revisiting topological properties of protein-protein interaction networks from the perspective of dataset evolution. , 2014, , .		0
87	Mean first passage time for random walk on dual structure of dendrimer. Physica A: Statistical Mechanics and Its Applications, 2014, 415, 463-472.	2.6	2
88	A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. IEEE Transactions on Geoscience and Remote Sensing, 2014, 52, 4895-4912.	6.3	48
89	Choosing appropriate models for protein-protein interaction networks: a comparison study. Briefings in Bioinformatics, 2014, 15, 823-838.	6.5	15
90	A comparative evaluation on prediction methods of nucleosome positioning. Briefings in Bioinformatics, 2014, 15, 1014-1027.	6.5	23

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91	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014, 145, 44-52.	5.9	18
92	CloudNMF: A MapReduce Implementation of Nonnegative Matrix Factorization for Large-scale Biological Datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2014, 12, 48-51.	6.9	33
93	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.	0.3	10
94	Local Nash Equilibrium in Social Networks. <i>Scientific Reports</i> , 2014, 4, 6224.	3.3	13
95	Boosting Prediction Performance of Protein-Protein Interaction Hot Spots by Using Structural Neighborhood Properties. <i>Journal of Computational Biology</i> , 2013, 20, 878-891.	1.6	38
96	KORS: Keyword-aware Optimal Route Search System. , 2013, , .		5
97	Identifying Mammalian MicroRNA Targets Based on Supervised Distance Metric Learning. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2013, 17, 427-435.	6.3	7
98	Scalable continual top-k keyword search in relational databases. <i>Data and Knowledge Engineering</i> , 2013, 86, 206-223.	3.4	18
99	A RAMCloud Storage System based on HDFS: Architecture, implementation and evaluation. <i>Journal of Systems and Software</i> , 2013, 86, 744-750.	4.5	29
100	WHEN CLOUD COMPUTING MEETS BIOINFORMATICS: A REVIEW. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1330002.	0.8	13
101	Rumor evolution in social networks. <i>Physical Review E</i> , 2013, 87, .	2.1	34
102	DISKs. <i>Proceedings of the VLDB Endowment</i> , 2012, 5, 1966-1969.	3.8	16
103	Effectively predicting protein functions by collective classification — An extended abstract. , 2012, , .		1
104	Efficient Continual Top-k Keyword Search in Relational Databases. <i>Journal of Information Processing</i> , 2012, 20, 114-127.	0.4	2
105	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.	0.1	3
106	Traffic Fluctuations on Weighted Networks. <i>IEEE Circuits and Systems Magazine</i> , 2012, 12, 33-44.	2.3	13
107	Effective clustering of microRNA sequences by N-grams and feature weighting. , 2012, , .		2
108	A comparison study on protein-protein interaction network models. , 2012, , .		1

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109	Finding MicroRNA Targets in Plants: Current Status and Perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , 2012, 10, 264-275.	6.9	56
110	Genome-wide search for miRNA-target interactions in <i>Arabidopsis thaliana</i> with an integrated approach. <i>BMC Genomics</i> , 2012, 13, S3.	2.8	27
111	Enhancing Routing Robustness of Unstructured Peer-to-Peer Networks Using Mobile Agents. <i>Journal of Network and Systems Management</i> , 2012, 20, 309-352.	4.9	1
112	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. <i>Neurocomputing</i> , 2012, 92, 44-53.	5.9	30
113	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in <i>Arabidopsis thaliana</i> . , 2011, , .		3
114	Characteristics of real futures trading networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011, 390, 398-409.	2.6	16
115	miRFam: an effective automatic miRNA classification method based on n-grams and a multiclass SVM. <i>BMC Bioinformatics</i> , 2011, 12, 216.	2.6	29
116	A new and effective hierarchical overlay structure for Peer-to-Peer networks. <i>Computer Communications</i> , 2011, 34, 862-874.	5.1	22
117	Epidemic spreading with nonlinear infectivity in weighted scale-free networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011, 390, 471-481.	2.6	73
118	Diffusionâ€“annihilation processes in weighted scale-free networks with an identical degree sequence. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2011, 2011, P10001.	2.3	12
119	Evolutionary method for finding communities in bipartite networks. <i>Physical Review E</i> , 2011, 83, 066120.	2.1	31
120	A self-index GML storage approach based on element coding. , 2011, , .		0
121	Gene Ontology-Based Protein Function Prediction by Using Sequence Composition Information. <i>Protein and Peptide Letters</i> , 2010, 17, 789-795.	0.9	3
122	Querying GML documents: An XQuery based approach. , 2010, , .		0
123	Detecting microarray data supported microRNA-mRNA interactions. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 639.	0.1	6
124	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.	9.1	16
125	LESSON: A system for lecture notes searching and sharing over Internet. <i>Journal of Systems and Software</i> , 2010, 83, 1851-1863.	4.5	4
126	MiRenSVM: towards better prediction of microRNA precursors using an ensemble SVM classifier with multi-loop features. <i>BMC Bioinformatics</i> , 2010, 11, S11.	2.6	78

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127	Deterministic weighted scale-free small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010, 389, 3316-3324.	2.6	16
128	Mapping Koch curves into scale-free small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010, 43, 395101.	2.1	46
129	A GML compression approach based on on-line semantic clustering. , 2010, , .		2
130	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.	2.1	64
131	Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. <i>Physical Review E</i> , 2010, 81, 016114.	2.1	52
132	Protein Backbone Dihedral Angle Prediction Based on Probabilistic Models. <i>International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering</i> , 2010, , .	0.0	0
133	An analytic derivation of clustering coefficients for weighted networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010, 2010, P03013.	2.3	4
134	Building Resilient Unstructured Peer-to-Peer Networks Using Mobile Agents. , 2010, , .		0
135	LRIR: A hybrid semantic Web services matching approach. , 2010, , .		0
136	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.	2.1	88
137	Different thresholds of bond percolation in scale-free networks with identical degree sequence. <i>Physical Review E</i> , 2009, 79, 031110.	2.1	23
138	Recursive solutions for Laplacian spectra and eigenvectors of a class of growing treelike networks. <i>Physical Review E</i> , 2009, 80, 016104.	2.1	22
139	Exact solution for mean first-passage time on a pseudofractal scale-free web. <i>Physical Review E</i> , 2009, 79, 021127.	2.1	108
140	Trapping in scale-free networks with hierarchical organization of modularity. <i>Physical Review E</i> , 2009, 80, 051120.	2.1	40
141	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.	1.1	17
142	Mean first-passage time for random walks on the T-graph. <i>New Journal of Physics</i> , 2009, 11, 103043.	2.9	37
143	Epidemic spreading in weighted scale-free networks with community structure. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P07043.	2.3	38
144	Average distance in a hierarchical scale-free network: an exact solution. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P10022.	2.3	24

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145	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.	2.1	7
146	The rigorous solution for the average distance of a Sierpinski network. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2009, 2009, P02034.	2.3	8
147	Effects of accelerating growth on the evolution of weighted complex networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2009, 388, 225-232.	2.6	20
148	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.	2.6	24
149	A new approach to building histogram for selectivity estimation in query processing optimization. <i>Computers and Mathematics With Applications</i> , 2009, 57, 1037-1047.	2.7	6
150	SWER: small world-based efficient routing for wireless sensor networks with mobile sinks. <i>Frontiers of Computer Science</i> , 2009, 3, 427-434.	0.6	0
151	Discovering pattern-based subspace clusters by pattern tree. <i>Knowledge-Based Systems</i> , 2009, 22, 569-579.	7.1	14
152	Mining frequent closed itemsets from a landmark window over online data streams. <i>Computers and Mathematics With Applications</i> , 2009, 57, 927-936.	2.7	31
153	Anomalous behavior of trapping on a fractal scale-free network. <i>Europhysics Letters</i> , 2009, 88, 10001.	2.0	30
154	Towards Keyword Search over Relational Databases in DHT Networks. , 2009, , .		0
155	Empirical Probability Functions Derived from Dihedral Angles for Protein Structure Prediction. , 2009, , .		1
156	Improving Prediction of the Contact Numbers of Residues in Proteins from Primary Sequences. , 2009, , .		0
157	Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , 2009, 86, 10006.	2.0	52
158	An empirical study of Chinese language networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008, 387, 3039-3047.	2.6	36
159	Topologies and Laplacian spectra of a deterministic uniform recursive tree. <i>European Physical Journal B</i> , 2008, 63, 507-513.	1.5	27
160	Transition from fractal to non-fractal scalings in growing scale-free networks. <i>European Physical Journal B</i> , 2008, 64, 277-283.	1.5	20
161	Random Sierpinski network with scale-free small-world and modular structure. <i>European Physical Journal B</i> , 2008, 65, 141-147.	1.5	44
162	Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , 2008, 44, 1397-1409.	8.6	51

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163	Towards More Effective Text Summarization Based on Textual Association Networks. , 2008, , .		11
164	Degree and component size distributions in the generalized uniform recursive tree. Journal of Physics A: Mathematical and Theoretical, 2008, 41, 185101.	2.1	5
165	The exact solution of the mean geodesic distance for Vicsek fractals. Journal of Physics A: Mathematical and Theoretical, 2008, 41, 485102.	2.1	62
166	Fast Implementation of Dual Clustering Algorithm for Spatial Data Mining. , 2007, , .		2
167	An empirical study of an agglomeration network. Journal of Physics A: Mathematical and Theoretical, 2007, 40, 12365-12375.	2.1	7
168	A Peer-to-Peer Based Text Sharing and Retrieval System. , 2007, , .		1
169	GPress: Towards Effective GML Documents Compression. , 2007, , .		7
170	Maximal planar scale-free Sierpinski networks with small-world effect and power law strength-degree correlation. Europhysics Letters, 2007, 79, 38007.	2.0	79
171	Efficient Skyline Retrieval on Peer-to-Peer Networks. , 2007, , .		6
172	A Fast Subspace Clustering Algorithm Based on Pattern Similarity. , 2007, , .		0
173	Routing Based Load Balancing for Unstructured P2P Networks. , 2007, , .		2
174	Local-world evolving networks with tunable clustering. Physica A: Statistical Mechanics and Its Applications, 2007, 380, 639-650.	2.6	26
175	From regular to growing small-world networks. Physica A: Statistical Mechanics and Its Applications, 2007, 385, 765-772.	2.6	15
176	Recursive weighted treelike networks. European Physical Journal B, 2007, 59, 99-107.	1.5	21
177	Incompatibility networks as models of scale-free small-world graphs. European Physical Journal B, 2007, 60, 259-264.	1.5	29
178	DCAD: a dual clustering algorithm for distributed spatial databases. Geo-Spatial Information Science, 2007, 10, 137-144.	5.3	4
179	A new full-text indexing model with low space overhead for chinese text retrieval. International Journal on Digital Libraries, 2004, 4, 272-282.	1.5	1