

Shuigeng Zhou

List of Publications by Year in Descending Order

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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	GANs for Molecule Generation in Drug Design and Discovery. <i>Intelligent Systems Reference Library</i> , 2022 , 233-273	0.8	1
207	MIMO: A Unified Spatio-Temporal Model for Multi-Scale Sea Surface Temperature Prediction. <i>Remote Sensing</i> , 2022 , 14, 2371	5	1
206	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
205	Universal consistency of twin support vector machines. <i>International Journal of Machine Learning and Cybernetics</i> , 2021 , 12, 1867	3.8	0
204	FraGAT: a fragment-oriented multi-scale graph attention model for molecular property prediction. <i>Bioinformatics</i> , 2021 ,	7.2	5
203	Boosting the Performance of Video Compression Artifact Reduction with Reference Frame Proposals and Frequency Domain Information 2021 ,		2
202	Boosting scRNA-seq data clustering by cluster-aware feature weighting. <i>BMC Bioinformatics</i> , 2021 , 22, 130	3.6	0
201	A general framework for privacy-preserving of data publication based on randomized response techniques. <i>Information Systems</i> , 2021 , 96, 101648	2.7	2
200	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
199	BatchServer: A Web Server for Batch Effect Evaluation, Visualization, and Correction. <i>Journal of Proteome Research</i> , 2021 , 20, 1079-1086	5.6	4
198	Combined cause inference: Definition, model and performance. <i>Information Sciences</i> , 2021 , 574, 431-443	7.7	0
197	ICDAR 2021 Competition on Scene Video Text Spotting. <i>Lecture Notes in Computer Science</i> , 2021 , 650-662	2.9	
196	TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. <i>Methods</i> , 2020 , 179, 55-64	4.6	6
195	Link Weight Prediction Using Weight Perturbation and Latent Factor. <i>IEEE Transactions on Cybernetics</i> , 2020 , PP,	10.2	3
194	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
193	FERRARI: an efficient framework for visual exploratory subgraph search in graph databases. <i>VLDB Journal</i> , 2020 , 29, 973-998	3.9	3
192	Effective and scalable causal partitioning based on low-order conditional independent tests. <i>Neurocomputing</i> , 2020 , 389, 146-154	5.4	1

191	Learning Latent Semantic Attributes for Zero-Shot Object Detection 2020 ,		1
190	A Chaotic Ant Colony Optimized Link Prediction Algorithm. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , 2020 , 1-15	7.3	5
189	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
188	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
187	Computationally identifying hot spots in protein-DNA binding interfaces using an ensemble approach. <i>BMC Bioinformatics</i> , 2020 , 21, 384	3.6	6
186	The Complexities of Random-turn Hex, Square and Triangle Games. <i>IEEE Transactions on Games</i> , 2020 , 1-1	1.2	
185	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
184	ROAM: A Fundamental Routing Query on Road Networks with Efficiency. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020 , 32, 1595-1609	4.2	
183	An Indexing Framework for Efficient Visual Exploratory Subgraph Search in Graph Databases 2019 ,		1
182	Measuring Conditional Independence by Independent Residuals for Causal Discovery. <i>ACM Transactions on Intelligent Systems and Technology</i> , 2019 , 10, 1-19	8	0
181	Single-cell trajectories reconstruction, exploration and mapping of omics data with STREAM. <i>Nature Communications</i> , 2019 , 10, 1903	17.4	97
180	Genome-wide analysis of epigenetic dynamics across human developmental stages and tissues. <i>BMC Genomics</i> , 2019 , 20, 221	4.5	2
179	. <i>Tsinghua Science and Technology</i> , 2019 , 24, 456-467	3.4	2
178	Gaming Temporal Networks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , 2019 , 66, 672-676.5	6.5	8
177	You Only Recognize Once 2019 ,		8
176	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
175	Network Parameter Generation for One-Shot Object Detection 2019 ,		1
174	Non-Local ConvLSTM for Video Compression Artifact Reduction 2019 ,		23

173	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
172	Learning Competitive and Discriminative Reconstructions for Anomaly Detection. <i>Proceedings of the AAAI Conference on Artificial Intelligence</i> , 2019 , 33, 5167-5174	5	2
171	DEEPESEN: a convolutional neural network based method for super-enhancer prediction. <i>BMC Bioinformatics</i> , 2019 , 20, 598	3.6	9
170	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
169	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
168	Towards efficiently supporting database as a service with QoS guarantees. <i>Journal of Systems and Software</i> , 2018 , 139, 51-63	3.3	2
167	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
166	Probabilistic Time-Constrained Paths Search over Uncertain Road Networks. <i>IEEE Transactions on Services Computing</i> , 2018 , 11, 399-414	4.8	3
165	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
164	Semi-Group Range Sum Revisited: Query-Space Lower Bound Tightened. <i>Algorithmica</i> , 2018 , 80, 1315-1329	3.9	2
163	A Unified Framework for Predicting KPIs of On-Demand Transport Services. <i>IEEE Access</i> , 2018 , 6, 32005-32014	3.9	6
162	BOOMER 2018 ,		9
161	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
160	EarnCache: Self-adaptive Incremental Caching for Big Data Applications. <i>Lecture Notes in Computer Science</i> , 2018 , 379-393	0.9	
159	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
158	Edit Probability for Scene Text Recognition 2018 ,		67
157	AON: Towards Arbitrarily-Oriented Text Recognition 2018 ,		112
156	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

155	Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. <i>iScience</i> , 2018 , 7, 16-29	6.1	4
154	Knowledge diffusion in complex networks. <i>Concurrency Computation Practice and Experience</i> , 2017 , 29, e3791	1.4	9
153	A new hybrid method for learning bayesian networks: Separation and reunion. <i>Knowledge-Based Systems</i> , 2017 , 121, 185-197	7.3	31
152	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
151	Fusing multiple protein-protein similarity networks to effectively predict lncRNA-protein interactions. <i>BMC Bioinformatics</i> , 2017 , 18, 420	3.6	29
150	A new method for enhancer prediction based on deep belief network. <i>BMC Bioinformatics</i> , 2017 , 18, 418	3.6	32
149	JeCache: Just-Enough Data Caching with Just-in-Time Prefetching for Big Data Applications 2017 ,		2
148	Divide-and-conquer Tournament on Social Networks. <i>Scientific Reports</i> , 2017 , 7, 15484	4.9	
147	Efficient Retrieval of Bounded-Cost Informative Routes. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2017 , 29, 2182-2196	4.2	7
146	iHMS: a database integrating human histone modification data across developmental stages and tissues. <i>BMC Bioinformatics</i> , 2017 , 18, 103	3.6	2
145	Selecting high-quality negative samples for effectively predicting protein-RNA interactions. <i>BMC Systems Biology</i> , 2017 , 11, 9	3.5	18
144	Focusing Attention: Towards Accurate Text Recognition in Natural Images 2017 ,		179
143	PICASSO. <i>Proceedings of the VLDB Endowment</i> , 2017 , 10, 1861-1864	3.1	12
142	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
141	DeepCluster: A General Clustering Framework Based on Deep Learning. <i>Lecture Notes in Computer Science</i> , 2017 , 809-825	0.9	20
140	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
139	Boosting compound-protein interaction prediction by deep learning. <i>Methods</i> , 2016 , 110, 64-72	4.6	102
138	Knowledge-guided fuzzy logic modeling to infer cellular signaling networks from proteomic data. <i>Scientific Reports</i> , 2016 , 6, 35652	4.9	10

137	Robust Median Reversion Strategy for Online Portfolio Selection. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2016 , 28, 2480-2493	4.2	31
136	An integrative analysis of nucleosome occupancy and positioning using diverse sequence dependent properties. <i>Neurocomputing</i> , 2016 , 206, 35-41	5.4	
135	Histone modification patterns in highly differentiation cells. <i>Neurocomputing</i> , 2016 , 206, 42-49	5.4	
134	Computationally predicting protein-RNA interactions using only positive and unlabeled examples. <i>Journal of Bioinformatics and Computational Biology</i> , 2015 , 13, 1541005	1	22
133	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
132	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
131	Unfavorable Individuals in Social Gaming Networks. <i>Scientific Reports</i> , 2015 , 5, 17481	4.9	3
130	Identifying TF-MiRNA Regulatory Relationships Using Multiple Features. <i>PLoS ONE</i> , 2015 , 10, e0125156	3.7	2
129	Deterministic identification of specific individuals from GWAS results. <i>Bioinformatics</i> , 2015 , 31, 1701-7	7.2	22
128	Boosting compound-protein interaction prediction by deep learning 2015 ,		3
127	Improving compound-protein interaction prediction by building up highly credible negative samples. <i>Bioinformatics</i> , 2015 , 31, i221-9	7.2	109
126	Instance-level worst-case query bounds on R-trees. <i>VLDB Journal</i> , 2014 , 23, 591-607	3.9	
125	Cassava genome from a wild ancestor to cultivated varieties. <i>Nature Communications</i> , 2014 , 5, 5110	17.4	156
124	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
123	Private search on key-value stores with hierarchical indexes 2014 ,		7
122	Choosing appropriate models for protein-protein interaction networks: a comparison study. <i>Briefings in Bioinformatics</i> , 2014 , 15, 823-38	13.4	12
121	A comparative evaluation on prediction methods of nucleosome positioning. <i>Briefings in Bioinformatics</i> , 2014 , 15, 1014-27	13.4	19
120	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

119	Active learning for protein function prediction in protein-protein interaction networks. <i>Neurocomputing</i> , 2014 , 145, 44-52	5.4	16
118	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
117	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
116	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
115	MeioBase: a comprehensive database for meiosis. <i>Frontiers in Plant Science</i> , 2014 , 5, 728	6.2	2
114	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
113	Histone modifications involved in cassette exon inclusions: a quantitative and interpretable analysis. <i>BMC Genomics</i> , 2014 , 15, 1148	4.5	9
112	QUBLE: towards blending interactive visual subgraph search queries on large networks. <i>VLDB Journal</i> , 2014 , 23, 401-426	3.9	18
111	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
110	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
109	Scalable continual top-k keyword search in relational databases. <i>Data and Knowledge Engineering</i> , 2013 , 86, 206-223	1.5	14
108	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
107	When cloud computing meets bioinformatics: a review. <i>Journal of Bioinformatics and Computational Biology</i> , 2013 , 11, 1330002	1	10
106	Square++: Making a connection game win-lose complementary and playing-fair. <i>Entertainment Computing</i> , 2013 , 4, 105-113	1.9	7
105	Rumor evolution in social networks. <i>Physical Review E</i> , 2013 , 87,	2.4	26
104	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
103	Recursive mechanism 2013 ,		43
102	QUBLE 2013 ,		8

101	Detecting potential collusive cliques in futures markets based on trading behaviors from real data. <i>Neurocomputing</i> , 2012 , 92, 44-53	5.4	19
100	Group-Theoretical Analysis of Variable Coefficient Nonlinear Telegraph Equations. <i>Acta Applicandae Mathematicae</i> , 2012 , 117, 135-183	1.1	9
99	Traffic Fluctuations on Weighted Networks. <i>IEEE Circuits and Systems Magazine</i> , 2012 , 12, 33-44	3.2	9
98	A comparison study on protein-protein interaction network models 2012 ,		1
97	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
96	Finding microRNA targets in plants: current status and perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , 2012 , 10, 264-75	6.5	39
95	Automatically clustering large-scale miRNA sequences: methods and experiments. <i>BMC Genomics</i> , 2012 , 13 Suppl 8, S15	4.5	3
94	Genome-wide search for miRNA-target interactions in Arabidopsis thaliana with an integrated approach. <i>BMC Genomics</i> , 2012 , 13 Suppl 3, S3	4.5	23
93	Enhancing Routing Robustness of Unstructured Peer-to-Peer Networks Using Mobile Agents. <i>Journal of Network and Systems Management</i> , 2012 , 20, 309-352	2.1	
92	A conversation with Professor Ruqian Lu et al.. <i>SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining</i> , 2012 , 13, 79-81	4.6	
91	DISKs. <i>Proceedings of the VLDB Endowment</i> , 2012 , 5, 1966-1969	3.1	7
90	Effectively predicting protein functions by collective classification [An extended abstract 2012 ,		1
89	PRAGUE: Towards Blending Practical Visual Subgraph Query Formulation and Query Processing 2012 ,		20
88	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
87	TEPITOPEpan: extending TEPITOPE for peptide binding prediction covering over 700 HLA-DR molecules. <i>PLoS ONE</i> , 2012 , 7, e30483	3.7	74
86	Characteristics of real futures trading networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2011 , 390, 398-409	3.3	16
85	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
84	imiRTP: An Integrated Method to Identifying miRNA-target Interactions in Arabidopsis thaliana 2011 ,		3

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	A new and effective hierarchical overlay structure for Peer-to-Peer networks. <i>Computer Communications</i> , 2011 , 34, 862-874	5.1	17
81	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
80	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
79	Evolutionary method for finding communities in bipartite networks. <i>Physical Review E</i> , 2011 , 83, 066120	2.4	28
78	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
77	Mapping Koch curves into scale-free small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2010 , 43, 395101	2	38
76	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
75	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
74	Enumeration of spanning trees in a pseudofractal scale-free web. <i>Europhysics Letters</i> , 2010 , 90, 68002	1.6	47
73	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
72	An analytic derivation of clustering coefficients for weighted networks. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2010 , 2010, P03013	1.9	1
71	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
70	Gene ontology-based protein function prediction by using sequence composition information. <i>Protein and Peptide Letters</i> , 2010 , 17, 789-95	1.9	2
69	Prediction of protein-protein interactions from primary sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2010 , 4, 211-27	0.5	9
68	Detecting microarray data supported microRNA-mRNA interactions. <i>International Journal of Data Mining and Bioinformatics</i> , 2010 , 4, 639-55	0.5	4
67	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
66	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

65	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
64	Inferring minimal feasible metabolic networks of Escherichia coli. <i>Applied Biochemistry and Biotechnology</i> , 2010 , 160, 222-31	3.2	0
63	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
62	Group properties of generalized quasi-linear wave equations. <i>Journal of Mathematical Analysis and Applications</i> , 2010 , 366, 460-472	1.1	9
61	Deterministic weighted scale-free small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2010 , 389, 3316-3324	3.3	14
60	Achieving optimal data storage position in wireless sensor networks. <i>Computer Communications</i> , 2010 , 33, 92-102	5.1	21
59	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
58	Different thresholds of bond percolation in scale-free networks with identical degree sequence. <i>Physical Review E</i> , 2009 , 79, 031110	2.4	19
57	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
56	Exact solution for mean first-passage time on a pseudofractal scale-free web. <i>Physical Review E</i> , 2009 , 79, 021127	2.4	103
55	Trapping in scale-free networks with hierarchical organization of modularity. <i>Physical Review E</i> , 2009 , 80, 051120	2.4	39
54	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
53	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
52	Mean first-passage time for random walks on the T-graph. <i>New Journal of Physics</i> , 2009 , 11, 103043	2.9	34
51	Contact graphs of disk packings as a model of spatial planar networks. <i>New Journal of Physics</i> , 2009 , 11, 083007	2.9	7
50	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
49	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
48	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

47	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
46	The prisoner's dilemma in structured scale-free networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2009 , 42, 245002	2	18
45	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
44	Distributed Skyline Retrieval with Low Bandwidth Consumption. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2009 , 21, 384-400	4.2	39
43	Prediction of protein-protein interaction sites using an ensemble method. <i>BMC Bioinformatics</i> , 2009 , 10, 426	3.6	54
42	Compensatory ability to null mutation in metabolic networks. <i>Biotechnology and Bioengineering</i> , 2009 , 103, 361-9	4.9	12
41	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
40	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
39	Anomalous behavior of trapping on a fractal scale-free network. <i>Europhysics Letters</i> , 2009 , 88, 10001	1.6	29
38	Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , 2009 , 86, 10006	1.6	49
37	Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , 2008 , 44, 1397-1409	6.3	39
36	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
35	Fractal scale-free networks resistant to disease spread. <i>Journal of Statistical Mechanics: Theory and Experiment</i> , 2008 , 2008, P09008	1.9	21
34	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
33	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
32	Vertex labeling and routing in expanded Apollonian networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , 2008 , 41, 035004	2	6
31	LHT: A Low-Maintenance Indexing Scheme over DHTs 2008 ,		7
30	Analytical solution of average path length for Apollonian networks. <i>Physical Review E</i> , 2008 , 77, 017102	2.4	47

29	An empirical study of Chinese language networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008 , 387, 3039-3047	3-3	27
28	Topologies and Laplacian spectra of a deterministic uniform recursive tree. <i>European Physical Journal B</i> , 2008 , 63, 507-513	1.2	22
27	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
26	Random Sierpinski network with scale-free small-world and modular structure. <i>European Physical Journal B</i> , 2008 , 65, 141-147	1.2	30
25	Efficient Skyline Retrieval on Peer-to-Peer Networks 2007 ,		6
24	Efficient top-k processing in large-scaled distributed environments. <i>Data and Knowledge Engineering</i> , 2007 , 63, 315-335	1.5	20
23	Local-world evolving networks with tunable clustering. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 380, 639-650	3-3	23
22	Correlations in random Apollonian network. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 380, 621-628	3-3	23
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