

Shuigeng Zhou

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/3328940/shuigeng-zhou-publications-by-year.pdf>

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	5.5	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	DEEPPSEN: 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
21	From regular to growing small-world networks. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2007 , 385, 765-772	3.3	14
20	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
19	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
18	Evolving pseudofractal networks. <i>European Physical Journal B</i> , 2007 , 58, 337-344	1.2	34
17	Recursive weighted treelike networks. <i>European Physical Journal B</i> , 2007 , 59, 99-107	1.2	20
16	Incompatibility networks as models of scale-free small-world graphs. <i>European Physical Journal B</i> , 2007 , 60, 259-264	1.2	26
15	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
14	GPress: Towards Effective GML Documents Compression 2007 ,		1
13	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
12	GString: A Novel Approach for Efficient Search in Graph Databases 2007 ,		91

11	Evolving Apollonian networks with small-world scale-free topologies. <i>Physical Review E</i> , 2006 , 74, 046105.4	5.4	52
10	A new full-text indexing model with low space overhead for chinese text retrieval. <i>International Journal on Digital Libraries</i> , 2004 , 4, 272-282	1.4	0
9	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
8	Fast text classification: a training-corpus pruning based approach 2003 ,		3
7	Incremental mining of the schema of semistructured data. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 241-248	1.7	2
6	Approaches for scaling DBSCAN algorithm to large spatial databases. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 509-526	1.7	59
5	Generalized multidimensional association rules. <i>Journal of Computer Science and Technology</i> , 2000 , 15, 388-392	1.7	1
4	Supporting ranked join in peer-to-peer networks		1
3	Mobile agent-based distributed geographic information systems under Internet environment		1
2	Privacy and efficiency guaranteed social subgraph matching. <i>VLDB Journal</i> ,1	3.9	3
1	STREAM: Single-cell Trajectories Reconstruction, Exploration And Mapping of omics data		4