

# Shuigeng Zhou

## List of Publications by Citations

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

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|--------------------|-------------------------|----------------|-----------------|
| 208<br>papers      | 4,132<br>citations      | 36<br>h-index  | 54<br>g-index   |
| 240<br>ext. papers | 5,072<br>ext. citations | 3.6<br>avg, IF | 5.68<br>L-index |

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

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|-----|---|------|----|
| 191 | Determining global mean-first-passage time of random walks on Vicsek fractals using eigenvalues of Laplacian matrices. <i>Physical Review E</i> , <b>2010</b> , 81, 031118      | 2.4  | 57 |
| 190 | Prediction of protein-protein interaction sites using an ensemble method. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 426   | 3.6  | 54 |
| 189 | A general geometric growth model for pseudofractal scale-free web. <i>Physica A: Statistical Mechanics and Its Applications</i> , <b>2007</b> , 377, 329-339                    | 3.3  | 53 |
| 188 | Evolving Apollonian networks with small-world scale-free topologies. <i>Physical Review E</i> , <b>2006</b> , 74, 046105  | 5.4  | 52 |
| 187 | Random walks on the Apollonian network with a single trap. <i>Europhysics Letters</i> , <b>2009</b> , 86, 10006   | 1.6  | 49 |
| 186 | PredHS: a web server for predicting protein-protein interaction hot spots by using structural neighborhood properties. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W290-5 | 20.1 | 48 |
| 185 | Enumeration of spanning trees in a pseudofractal scale-free web. <i>Europhysics Letters</i> , <b>2010</b> , 90, 68002   | 1.6  | 47 |
| 184 | Analytical solution of average path length for Apollonian networks. <i>Physical Review E</i> , <b>2008</b> , 77, 017102   | 2.4  | 47 |
| 183 | Recursive mechanism <b>2013</b> ,   |      | 43 |
| 182 | Explicit determination of mean first-passage time for random walks on deterministic uniform recursive trees. <i>Physical Review E</i> , <b>2010</b> , 81, 016114                | 2.4  | 43 |
| 181 | The exact solution of the mean geodesic distance for Vicsek fractals. <i>Journal of Physics A: Mathematical and Theoretical</i> , <b>2008</b> , 41, 485102                      | 2    | 42 |
| 180 | ANGEL: Enhancing the Utility of Generalization for Privacy Preserving Publication. <i>IEEE Transactions on Knowledge and Data Engineering</i> , <b>2009</b> , 21, 1073-1087     | 4.2  | 41 |
| 179 | Finding microRNA targets in plants: current status and perspectives. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2012</b> , 10, 264-75                                  | 6.5  | 39 |
| 178 | Trapping in scale-free networks with hierarchical organization of modularity. <i>Physical Review E</i> , <b>2009</b> , 80, 051120   | 2.4  | 39 |
| 177 | Distributed Skyline Retrieval with Low Bandwidth Consumption. <i>IEEE Transactions on Knowledge and Data Engineering</i> , <b>2009</b> , 21, 384-400                            | 4.2  | 39 |
| 176 | Towards effective document clustering: A constrained K-means based approach. <i>Information Processing and Management</i> , <b>2008</b> , 44, 1397-1409                         | 6.3  | 39 |
| 175 | A Novel Image Registration Algorithm for Remote Sensing Under Affine Transformation. <i>IEEE Transactions on Geoscience and Remote Sensing</i> , <b>2014</b> , 52, 4895-4912    | 8.1  | 38 |
| 174 | Mapping Koch curves into scale-free small-world networks. <i>Journal of Physics A: Mathematical and Theoretical</i> , <b>2010</b> , 43, 395101                                  | 2    | 38 |

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

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

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

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



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| 101 | Prediction of protein-protein interactions from primary sequences. <i>International Journal of Data Mining and Bioinformatics</i> , <b>2010</b> , 4, 211-27   | 0.5 | 9 |
| 100 | Group properties of generalized quasi-linear wave equations. <i>Journal of Mathematical Analysis and Applications</i> , <b>2010</b> , 366, 460-472  | 1.1 | 9 |
| 99  | DEESEN: a convolutional neural network based method for super-enhancer prediction. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 598  | 3.6 | 9 |
| 98  | A General Framework for Unmet Demand Prediction in On-Demand Transport Services. <i>IEEE Transactions on Intelligent Transportation Systems</i> , <b>2019</b> , 20, 2820-2830                         | 6.1 | 9 |
| 97  | Gaming Temporal Networks. <i>IEEE Transactions on Circuits and Systems II: Express Briefs</i> , <b>2019</b> , 66, 672-676   | 5.5 | 8 |
| 96  | You Only Recognize Once <b>2019</b> ,   |     | 8 |
| 95  | QUBLE <b>2013</b> ,   |     | 8 |
| 94  | HNet-DNN: Inferring New Drug-Disease Associations with Deep Neural Network Based on Heterogeneous Network Features. <i>Journal of Chemical Information and Modeling</i> , <b>2020</b> , 60, 2367-2376 | 6.1 | 7 |
| 93  | Private search on key-value stores with hierarchical indexes <b>2014</b> ,  |     | 7 |
| 92  | The centrality of cancer proteins in human protein-protein interaction network: a revisit. <i>International Journal of Computational Biology and Drug Design</i> , <b>2014</b> , 7, 146-56            | 0.4 | 7 |
| 91  | Square++: Making a connection game win-lose complementary and playing-fair. <i>Entertainment Computing</i> , <b>2013</b> , 4, 105-113   | 1.9 | 7 |
| 90  | Efficient Retrieval of Bounded-Cost Informative Routes. <i>IEEE Transactions on Knowledge and Data Engineering</i> , <b>2017</b> , 29, 2182-2196  | 4.2 | 7 |
| 89  | Contact graphs of disk packings as a model of spatial planar networks. <i>New Journal of Physics</i> , <b>2009</b> , 11, 083007   | 2.9 | 7 |
| 88  | Structural and spectral properties of a family of deterministic recursive trees: rigorous solutions. <i>Journal of Physics A: Mathematical and Theoretical</i> , <b>2009</b> , 42, 165103             | 2   | 7 |
| 87  | DISKs. <i>Proceedings of the VLDB Endowment</i> , <b>2012</b> , 5, 1966-1969  | 3.1 | 7 |
| 86  | LHT: A Low-Maintenance Indexing Scheme over DHTs <b>2008</b> ,  |     | 7 |
| 85  | TOP: A deep mixture representation learning method for boosting molecular toxicity prediction. <i>Methods</i> , <b>2020</b> , 179, 55-64  | 4.6 | 6 |
| 84  | A Unified Framework for Predicting KPIs of On-Demand Transport Services. <i>IEEE Access</i> , <b>2018</b> , 6, 32005-32014  | 3.9 | 6 |



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

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| 65 | Rainbow-Seq: Combining Cell Lineage Tracing with Single-Cell RNA Sequencing in Preimplantation Embryos. <i>IScience</i> , <b>2018</b> , 7, 16-29   | 6.1  | 4 |
| 64 | LAYER: A cost-efficient mechanism to support multi-tenant database as a service in cloud. <i>Journal of Systems and Software</i> , <b>2015</b> , 101, 86-96  | 3.3  | 3 |
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