Lusheng Wang

List of Publications by Year
in descending order

183 papers	4,455 citations	159585 30 h-index	123424 61 g-index
192 all docs	192 docs citations	192 times ranked	2614 citing authors

#	ARTICLE	IF	CITATIONS
1	Proteoform identification based on top-down tandem mass spectra with peak error corrections. Briefings in Bioinformatics, 2022, , .	6.5	0
2	mzMD: visualization-oriented MS data storage and retrieval. Bioinformatics, 2022, 38, 2333-2340.	4.1	0
3	Pan€genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. Environmental Microbiology, 2021, 23, 3599-3613.	3.8	4
4	A randomized approximation algorithm for metric triangle packing. Journal of Combinatorial Optimization, 2021, 41, 12-27.	1.3	3
5	SVLR: Genome Structural Variant Detection Using Long-Read Sequencing Data. Journal of Computational Biology, 2021, 28, 774-788.	1.6	4
6	Fast and Accurate Algorithms for Mapping and Aligning Long Reads. Journal of Computational Biology, 2021, 28, 789-803.	1.6	2
7	Integrating pan-genome with metagenome for microbial community profiling. Computational and Structural Biotechnology Journal, 2021, 19, 1458-1466.	4.1	16
8	Identifying Duplications and Lateral Gene Transfers Simultaneously and Rapidly. Journal of Bioinformatics and Computational Biology, 2021, , 2150033.	0.8	0
9	Faster Exact Computation of rSPR Distance via Better Approximation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 916-929.	3.0	2
10	Computing a Consensus Phylogeny via Leaf Removal. Journal of Computational Biology, 2020, 27, 175-188.	1.6	0
11	Improved Practical Algorithms for Rooted Subtree Prune and Regraft (rSPR) Distance and Hybridization Number. Journal of Computational Biology, 2020, 27, 1422-1432.	1.6	1
12	Genetic and clinical analysis in Chinese patients with retinitis pigmentosa caused by <i>EYS</i> mutations. Molecular Genetics & Genomic Medicine, 2020, 8, e1117.	1.2	5
13	Designing and implementing algorithms for the closest string problem. Theoretical Computer Science, 2019, 786, 32-43.	0.9	0
14	Exome sequencing of Saudi Arabian patients with ADPKD. Renal Failure, 2019, 41, 842-849.	2.1	6
15	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. MSystems, 2019, 4, .	3.8	36
16	Approximation Algorithms for the Maximum Weight Internal Spanning Tree Problem. Algorithmica, 2019, 81, 4167-4199.	1.3	5
17	A Randomized Approximation Algorithm for Metric Triangle Packing. Lecture Notes in Computer Science, 2019, , 119-129.	1.3	0
18	Progressive approach for SNP calling and haplotype assembly using single molecular sequencing data. Bioinformatics, 2018, 34, 2012-2018.	4.1	24

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19	An approximation algorithm for maximum internal spanning tree. Journal of Combinatorial Optimization, 2018, 35, 955-979.	1.3	7
20	Comprehensive study of instable regions in Pseudomonas aeruginosa and Mycobacterium tuberculosis. BioMedical Engineering OnLine, 2018, 17, 133.	2.7	3
21	GRSR: a tool for deriving genome rearrangement scenarios from multiple unichromosomal genome sequences. BMC Bioinformatics, 2018, 19, 291.	2.6	2
22	Better ILP models for haplotype assembly. BMC Bioinformatics, 2018, 19, 52.	2.6	2
23	A Polynomial Time Approximation Scheme for the Closest Shared Center Problem. Algorithmica, 2017, 77, 65-83.	1.3	0
24	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. BMC Genomics, 2017, 18, 268.	2.8	11
25	A New 2-Approximation Algorithm for rSPR Distance. Lecture Notes in Computer Science, 2017, , 128-139.	1.3	1
26	Designing and Implementing Algorithms for the Closest String Problem. Lecture Notes in Computer Science, 2017, , 79-90.	1.3	0
27	Randomized Fixed-Parameter Algorithms for the Closest String Problem. Algorithmica, 2016, 74, 466-484.	1.3	5
28	Better ILP-Based Approaches to Haplotype Assembly. Journal of Computational Biology, 2016, 23, 537-552.	1.6	5
29	An Improved Approximation Algorithm for rSPR Distance. Lecture Notes in Computer Science, 2016, , 468-479.	1.3	4
30	Protein–protein interface prediction based on hexagon structure similarity. Computational Biology and Chemistry, 2016, 63, 83-88.	2.3	13
31	Closest String and Substring Problems. , 2016, , 321-324.		0
32	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
33	A Dynamic Programming Algorithm For (1,2)-Exemplar Breakpoint Distance. Journal of Computational Biology, 2015, 22, 666-676.	1.6	3
34	A factor-$(1.408 + \hat{I}\mu)$ approximation for sorting unsigned genomes by reciprocal translocations. Theoretical Computer Science, 2015, 607, 166-180.	0.9	3
35	Faster exact computation of rSPR distance. Journal of Combinatorial Optimization, 2015, 29, 605-635.	1.3	10
36	Identification of Protein Complexes Using Weighted PageRank-Nibble Algorithm and Core-Attachment Structure. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 179-192.	3.0	49

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37	An efficient algorithm for the blocked pattern matching problem. Bioinformatics, 2015, 31, 532-538.	4.1	11
38	Predicting Human Protein Subcellular Locations by the Ensemble of Multiple Predictors via Protein-Protein Interaction Network with Edge Clustering Coefficients. PLoS ONE, 2014, 9, e86879.	2.5	23
39	A parameterized algorithm for (1,2)-exemplar breakpoint distance. , 2014, , .		0
40	Parameterized and approximation algorithms for finding two disjoint matchings. Theoretical Computer Science, 2014, 556, 85-93.	0.9	0
41	The Parameterized Complexity of the Shared Center Problem. Algorithmica, 2014, 69, 269-293.	1.3	2
42	Probabilistic Models for Capturing More Physicochemical Properties on Protein–Protein Interface. Journal of Chemical Information and Modeling, 2014, 54, 1798-1809.	5.4	13
43	Quantifying Significance of MHC II Residues. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 17-25.	3.0	0
44	A (1.408+Îµ)-Approximation Algorithm for Sorting Unsigned Genomes by Reciprocal Translocations. Lecture Notes in Computer Science, 2014, , 128-140.	1.3	6
45	Identifying Protein-Protein Binding Sites with a Combined Energy Function. Current Protein and Peptide Science, 2014, 15, 540-552.	1.4	2
46	Closest String and Substring Problems. , 2014, , 1-4.		0
47	Randomized and Parameterized Algorithms for the Closest String Problem. Lecture Notes in Computer Science, 2014, , 100-109.	1.3	1
48	Constant time approximation scheme for largest well predicted subset. Journal of Combinatorial Optimization, 2013, 25, 352-367.	1.3	0
49	Near optimal solutions for maximum quasi-bicliques. Journal of Combinatorial Optimization, 2013, 25, 481-497.	1.3	12
50	A highly accurate heuristic algorithm for the haplotype assembly problem. BMC Genomics, 2013, 14, S2.	2.8	27
51	Exact algorithms for haplotype assembly from whole-genome sequence data. Bioinformatics, 2013, 29, 1938-1945.	4.1	79
52	Identifying protein complexes based on density and modularity in protein-protein interaction network. BMC Systems Biology, 2013, 7, S12.	3.0	21
53	Identifying duplications and lateral gene transfers simultaneously and rapidly. , 2013, , .		0
54	An Exact Algorithm for the Zero Exemplar Breakpoint Distance Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1469-1477.	3.0	5

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55	An Ultrafast Tool for Minimum Reticulate Networks. Journal of Computational Biology, 2013, 20, 38-41.	1.6	17
56	Distances between phylogenetic trees: A survey. Tsinghua Science and Technology, 2013, 18, 490-499.	6.1	4
57	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	1.6	7
58	Faster Exact Computation of rSPR Distance. Lecture Notes in Computer Science, 2013, , 36-47.	1.3	1
59	Parameterized and Approximation Algorithms for Finding Two Disjoint Matchings. Lecture Notes in Computer Science, 2013, , 1-12.	1.3	1
60	A Polynomial Time Approximation Scheme for the Closest Shared Center Problem. Lecture Notes in Computer Science, 2013, , 385-396.	1.3	0
61	Simultaneous Identification of Duplications, Losses, and Lateral Gene Transfers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1515-1528.	3.0	24
62	A polynomial time approximation scheme forÂembedding a directed hypergraph on a weighted ring. Journal of Combinatorial Optimization, 2012, 24, 319-328.	1.3	1
63	Mutation Region Detection for Closely Related Individuals without a Known Pedigree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 499-510.	3.0	6
64	Identifying mutation regions for closely related individuals without a known pedigree. BMC Bioinformatics, 2012, 13, 146.	2.6	3
65	A fast tool for minimum hybridization networks. BMC Bioinformatics, 2012, 13, 155.	2.6	10
66	Protein-protein binding site identification by enumerating the configurations. BMC Bioinformatics, 2012, 13, 158.	2.6	57
67	Fast accurate missing SNP genotype local imputation. BMC Research Notes, 2012, 5, 404.	1.4	23
68	Protein complex prediction based on maximum matching with domainâ€"domain interaction. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1418-1424.	2.3	9
69	Algorithms for Reticulate Networks of Multiple Phylogenetic Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 372-384.	3.0	30
70	Exact and approximation algorithms forÂtheÂcomplementary maximal strip recovery problem. Journal of Combinatorial Optimization, 2012, 23, 493-506.	1.3	15
71	A three-string approach to the closest string problem. Journal of Computer and System Sciences, 2012, 78, 164-178.	1.2	26
72	An improved approximation algorithm for the complementary maximal strip recovery problem. Journal of Computer and System Sciences, 2012, 78, 720-730.	1.2	12

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73	Computing the protein binding sites. BMC Bioinformatics, 2012, 13, S2.	2.6	6
74	P-Binder: A System for the Protein-Protein Binding Sites Identification. Lecture Notes in Computer Science, 2012, , 127-138.	1.3	6
75	An Improved Approximation Algorithm for the Bandpass-2 Problem. Lecture Notes in Computer Science, 2012, , 188-199.	1.3	6
76	The Parameterized Complexity of the Shared Center Problem. Lecture Notes in Computer Science, 2012, , 439-452.	1.3	0
77	Computing Parametric Alignment of RNA Structures: Visualization and Practice. , 2011, , .		0
78	Proteinâ€"Protein Binding Sites Prediction by 3D Structural Similarities. Journal of Chemical Information and Modeling, 2011, 51, 3287-3294.	5.4	10
79	An Approximation Algorithm for the Minimum Co-Path Set Problem. Algorithmica, 2011, 60, 969-986.	1.3	6
80	Discovering almost any hidden motif from multiple sequences. ACM Transactions on Algorithms, 2011, 7, 1-18.	1.0	1
81	Fast Exact Algorithms for the Closest String and Substring Problems with Application to the Planted (L,d)-Motif Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1400-1410.	3.0	24
82	Computing the Protein Binding Sites. Lecture Notes in Computer Science, 2011, , 25-36.	1.3	3
83	Beyond evolutionary trees. Natural Computing, 2010, 9, 421-435.	3.0	2
84	Identification of Distinguishing Motifs. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 53-67.	0.8	0
85	HybridNET: a tool for constructing hybridization networks. Bioinformatics, 2010, 26, 2912-2913.	4.1	25
86	Probabilistic Analysis of a Motif Discovery Algorithm for Multiple Sequences. SIAM Journal on Discrete Mathematics, 2010, 23, 1715-1737.	0.8	2
87	Efficient Algorithms for 3D Protein Substructure Identification. International Conference on Bioinformatics and Biomedical Engineering: [proceedings] International Conference on Bioinformatics and Biomedical Engineering, 2010, , .	0.0	2
88	Modeling Protein Interacting Groups by Quasi-Bicliques: Complexity, Algorithm, and Application. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 354-364.	3.0	28
89	On the Tractability of Maximal Strip Recovery. Journal of Computational Biology, 2010, 17, 907-914.	1.6	15
90	Finding the Nearest Neighbors in Biological Databases Using Less Distance Computations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 669-680.	3.0	6

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91	A Three-String Approach to the Closest String Problem. Lecture Notes in Computer Science, 2010, , 449-458.	1.3	4
92	A Linear Kernel for Co-Path/Cycle Packing. Lecture Notes in Computer Science, 2010, , 90-102.	1.3	10
93	Constant Time Approximation Scheme for Largest Well Predicted Subset. Lecture Notes in Computer Science, 2010, , 429-438.	1.3	0
94	Randomized Approaches for Nearest Neighbor Search in Metric Space When Computing the Pairwise Distance Is Extremely Expensive. Lecture Notes in Computer Science, 2010, , 243-252.	1.3	0
95	Near Optimal Solutions for Maximum Quasi-bicliques. Lecture Notes in Computer Science, 2010, , 409-418.	1.3	1
96	Linked region detection using high-density SNP genotype data via the minimum recombinant model of pedigree haplotype inference. BMC Bioinformatics, 2009, 10, 216.	2.6	5
97	Approximation Algorithms for Reconstructing theÂDuplication History ofÂTandemÂRepeats. Algorithmica, 2009, 54, 501-529.	1.3	3
98	An improved randomized approximation algorithm for maximum triangle packing. Discrete Applied Mathematics, 2009, 157, 1640-1646.	0.9	14
99	On bipartite graphs with minimal energy. Discrete Applied Mathematics, 2009, 157, 869-873.	0.9	26
100	Improved Approximation Algorithms for Reconstructing the History of Tandem Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 438-453.	3.0	0
101	On the Tractability of Maximal Strip Recovery. Lecture Notes in Computer Science, 2009, , 400-409.	1.3	10
102	Efficient Algorithms for the Closest String and Distinguishing String Selection Problems. Lecture Notes in Computer Science, 2009, , 261-270.	1.3	27
103	Discovering Almost Any Hidden Motif from Multiple Sequences in Polynomial Time with Low Sample Complexity and High Success Probability. Lecture Notes in Computer Science, 2009, , 231-240.	1.3	0
104	Relay sensor placement in wireless sensor networks. Wireless Networks, 2008, 14, 347-355.	3.0	386
105	Space Efficient Algorithms for Ordered Tree Comparison. Algorithmica, 2008, 51, 283-297.	1.3	7
106	An improved approximation algorithm for maximum edge 2-coloring in simple graphs. Journal of Discrete Algorithms, 2008, 6, 205-215.	0.7	9
107	Predicting the number and sizes of IBD regions among family members and evaluating the family size requirement for linkage studies. European Journal of Human Genetics, 2008, 16, 1535-1543.	2.8	8
108	Approximation Algorithms for Biclustering Problems. SIAM Journal on Computing, 2008, 38, 1504-1518.	1.0	4

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109	An Improved Randomized Approximation Algorithm for Maximum Triangle Packing. Lecture Notes in Computer Science, 2008, , 97-108.	1.3	4
110	A (1.5 + Î¼)-Approximation Algorithm for Unsigned Translocation Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 56-66.	3.0	12
111	Identification of linked regions using high-density SNP genotype data in linkage analysis. Bioinformatics, 2008, 24, 86-93.	4.1	40
112	An Efficient Voting Algorithm for Finding Additive Biclusters with Random Background. Journal of Computational Biology, 2008, 15, 1275-1293.	1.6	4
113	Quasi-bicliques: Complexity and Binding Pairs. Lecture Notes in Computer Science, 2008, , 255-264.	1.3	16
114	An Improved Approximation Algorithm for the Capacitated Multicast Tree Routing Problem. Lecture Notes in Computer Science, 2008, , 286-295.	1.3	10
115	Closest String and Substring Problems. , 2008, , 155-156.		1
116	VOTING ALGORITHMS FOR THE MOTIF FINDING PROBLEM. , 2008, , .		0
117	Finding Additive Biclusters with Random Background. , 2008, , 263-276.		1
118	Efficient Algorithms for Model-Based Motif Discovery from Multiple Sequences. , 2008, , 234-245.		1
119	Computing the maximum similarity bi-clusters of gene expression data. Bioinformatics, 2007, 23, 50-56.	4.1	142
120	Finding Transcription Factor Binding Sites with Indels. , 2007, , .		0
121	Some approximation algorithms for the clique partition problem in weighted interval graphs. Theoretical Computer Science, 2007, 381, 124-133.	0.9	6
122	On packing and coloring hyperedges in a cycle. Discrete Applied Mathematics, 2007, 155, 2140-2151.	0.9	2
123	Near optimal multiple alignment within a band in polynomial time. Journal of Computer and System Sciences, 2007, 73, 997-1011.	1.2	2
124	A 1.75-approximation algorithm for unsigned translocation distance. Journal of Computer and System Sciences, 2007, 73, 1045-1059.	1.2	11
125	Approximation Algorithms for Reconstructing the Duplication History of Tandem Repeats. Lecture Notes in Computer Science, 2007, , 493-503.	1.3	1
126	Finding the region of pseudo-periodic tandem repeats in biological sequences. Algorithms for Molecular Biology, 2006, 1, 2.	1.2	8

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127	Algorithmic approaches for genome rearrangement: a review. IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews, 2006, 36, 636-648.	2.9	19
128	Translocation Distance: Algorithms and Complexity. Advances in Computers, 2006, , 105-126.	1.6	0
129	A polynomial time approximation scheme for embedding a directed hypergraph on a ring. Information Processing Letters, 2006, 97, 203-207.	0.6	13
130	On the complexity of unsigned translocation distance. Theoretical Computer Science, 2006, 352, 322-328.	0.9	31
131	Optimal Relay Location for Resource-limited Energy-efficient Wireless Communication. Journal of Global Optimization, 2006, 36, 391-399.	1.8	6
132	Approximation Algorithms for Bi-clustering Problems. Lecture Notes in Computer Science, 2006, , 310-320.	1.3	1
133	An Approximation Algorithm for Embedding a Directed Hypergraph on a Ring. Lecture Notes in Computer Science, 2005, , 392-399.	1.3	0
134	An <mml:math altimg="si1.gif" overflow="scroll" xmlns:xocs="http://www.elsevier.com/xml/xocs/dtd" xmlns:xs="http://www.w3.org/2001/XMLSchema" xmlns:xsi="http://www.w3.org/2001/XMLSchema-instance" xmlns="http://www.elsevier.com/xml/ja/dtd" xmlns:ja="http://www.elsevier.com/xml/ja/dtd" xmlns:mml="http://www.w3.org/1998/Math/MathML" xmlns:tb="http://www.elsevier.com/xml/common/table/dtd" xmlns:sb="http://www.elsevier.com/xml/common/struct-bib/dtd" xmlns:ce="http://www.elsevier.com/x	1.2	31
135	On the complexity of finding emerging patterns. Theoretical Computer Science, 2005, 335, 15-27.	0.9	40
136	Exact matching of RNA secondary structure patterns. Theoretical Computer Science, 2005, 335, 53-66.	0.9	1
137	Improved deterministic approximation algorithms for Max TSP. Information Processing Letters, 2005, 95, 333-342.	0.6	33
138	Decomposing toroidal graphs into circuits and edges. Discrete Applied Mathematics, 2005, 148, 147-159.	0.9	1
139	An Improved Randomized Approximation Algorithm for Max TSP. Journal of Combinatorial Optimization, 2005, 9, 401-432.	1.3	9
140	Maximizing Profits of Routing in WDM Networks. Journal of Combinatorial Optimization, 2005, 10, 99-111.	1.3	5
141	On the ordering of benzenoid chains and cyclo-polyphenacenes with respect to their numbers of Clar aromatic sextets. Journal of Mathematical Chemistry, 2005, 38, 293-309.	1.5	6
142	RANDOMIZED ALGORITHMS FOR MOTIF DETECTION. Journal of Bioinformatics and Computational Biology, 2005, 03, 1039-1052.	0.8	23
143	Space Efficient Algorithms for Ordered Tree Comparison. Lecture Notes in Computer Science, 2005, , 380-391.	1.3	0
144	AN O(n2) ALGORITHM FOR SIGNED TRANSLOCATION PROBLEM. , 2005, , .		2

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145	CTRD: a fast applet for computing signed translocation distance between genomes. Bioinformatics, 2004, 20, 3256-3257.	4.1	5
146	k-Resonance of Open-Ended Carbon Nanotubes. Journal of Mathematical Chemistry, 2004, 35, 87-103.	1.5	20
147	Minimum k Arborescences with Bandwidth Constraints. Algorithmica, 2004, 38, 529-537.	1.3	8
148	Removable edges in a cycle of a 4-connected graph. Discrete Mathematics, 2004, 287, 103-111.	0.7	3
149	Topology control of ad hoc wireless networks for energy efficiency. IEEE Transactions on Computers, 2004, 53, 1629-1635.	3.4	41
150	Randomized Algorithms for Motif Detection. Lecture Notes in Computer Science, 2004, , 884-895.	1.3	4
151	A Complete Solution to a Conjecture on the Î²-Polynomials of Graphs. Journal of Mathematical Chemistry, 2003, 33, 189-193.	1.5	1
152	Genetic Design of Drugs Without Side-Effects. SIAM Journal on Computing, 2003, 32, 1073-1090.	1.0	73
153	Solutions for Two Conjectures on the Inverse Problem of the Wiener Index of Peptoids. SIAM Journal on Discrete Mathematics, 2003, 17, 210-218.	0.8	5
154	SEGID: Identifying Interesting Segments in (Multiple) Sequence Alignments. Bioinformatics, 2003, 19, 297-298.	4.1	27
155	Parametric alignment of ordered trees. Bioinformatics, 2003, 19, 2237-2245.	4.1	19
156	The Inverse Problems for Some Topological Indices in Combinatorial Chemistry. Journal of Computational Biology, 2003, 10, 47-55.	1.6	35
157	Haplotype inference by maximum parsimony. Bioinformatics, 2003, 19, 1773-1780.	4.1	132
158	Greedy method for inferring tandem duplication history. Bioinformatics, 2003, 19, 1497-1504.	4.1	33
159	On the closest string and substring problems. Journal of the ACM, 2002, 49, 157-171.	2.2	205
160	Finding Similar Regions in Many Sequences. Journal of Computer and System Sciences, 2002, 65, 73-96.	1.2	120
161	Computing similarity between RNA structures. Theoretical Computer Science, 2002, 276, 111-132.	0.9	34
162	An approximation algorithm for a bottleneck k-Steiner tree problem in the Euclidean plane. Information Processing Letters, 2002, 81, 151-156.	0.6	30

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163	Center and Distinguisher for Strings with Unbounded Alphabet. Journal of Combinatorial Optimization, 2002, 6, 383-400.	1.3	7
164	Approximations for Steiner trees with minimum number of Steiner points. Theoretical Computer Science, 2001, 262, 83-99.	0.9	52
165	Hexagonal chains with minimal total Ï€-electron energy. Chemical Physics Letters, 2001, 337, 125-130.	2.6	40
166	Hexagonal chains with maximal total Ï€-electron energy. Chemical Physics Letters, 2001, 337, 131-137.	2.6	41
167	Perfect Phylogenetic Networks with Recombination. Journal of Computational Biology, 2001, 8, 69-78.	1.6	187
168	On the Inapproximability of Disjoint Paths and Minimum Steiner Forest with Bandwidth Constraints. Journal of Computer and System Sciences, 2000, 60, 1-12.	1.2	22
169	Approximations for Steiner Trees with Minimum Number of Steiner Points. Journal of Global Optimization, 2000, 18, 17-33.	1.8	119
170	A More Efficient Approximation Scheme for Tree Alignment. SIAM Journal on Computing, 2000, 30, 283-299.	1.0	27
171	Finding similar regions in many strings. , 1999, , .		105
172	Fitting Distances by Tree Metrics with Increment Error. Journal of Combinatorial Optimization, 1999, 3, 213-225.	1.3	12
173	A group multicast routing algorithm by using multiple minimum Steiner trees. Computer Communications, 1997, 20, 750-758.	5.1	41
174	Improved Approximation Algorithms for Tree Alignment. Journal of Algorithms, 1997, 25, 255-273.	0.9	46
175	Approximation algorithms for tree alignment with a given phylogeny. Algorithmica, 1996, 16, 302-315.	1.3	49
176	An approximation scheme for some Steiner tree problems in the plane. Networks, 1996, 28, 187-193.	2.7	17
177	On the complexity of comparing evolutionary trees. Discrete Applied Mathematics, 1996, 71, 153-169.	0.9	188
178	On the completeness of incidence calculus. Journal of Automated Reasoning, 1996, 16, 355-368.	1.4	0
179	Alignment of trees â€" an alternative to tree edit. Theoretical Computer Science, 1995, 143, 137-148.	0.9	152
180	On the Complexity of Multiple Sequence Alignment. Journal of Computational Biology, 1994, 1, 337-348.	1.6	719

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181	On the complexity of finding emerging patterns. , 0, , .		3
182	Mining Protein Interaction Groups. , 0, , .		0
183	Identification of Distinguishing Motifs. , 0, , 1-14.		0