Lusheng Wang

List of Publications by Year
in descending order

183 papers	4,455 citations	159358 30 h-index	123241 61 g-index
192 all docs	192 docs citations	192 times ranked	2614 citing authors

#	Article	IF	Citations
1	On the Complexity of Multiple Sequence Alignment. Journal of Computational Biology, 1994, 1, 337-348.	0.8	719
2	Relay sensor placement in wireless sensor networks. Wireless Networks, 2008, 14, 347-355.	2.0	386
3	On the closest string and substring problems. Journal of the ACM, 2002, 49, 157-171.	1.8	205
4	On the complexity of comparing evolutionary trees. Discrete Applied Mathematics, 1996, 71, 153-169.	0.5	188
5	Perfect Phylogenetic Networks with Recombination. Journal of Computational Biology, 2001, 8, 69-78.	0.8	187
6	Alignment of trees â€" an alternative to tree edit. Theoretical Computer Science, 1995, 143, 137-148.	0.5	152
7	Computing the maximum similarity bi-clusters of gene expression data. Bioinformatics, 2007, 23, 50-56.	1.8	142
8	Haplotype inference by maximum parsimony. Bioinformatics, 2003, 19, 1773-1780.	1.8	132
9	Finding Similar Regions in Many Sequences. Journal of Computer and System Sciences, 2002, 65, 73-96.	0.9	120
10	Approximations for Steiner Trees with Minimum Number of Steiner Points. Journal of Global Optimization, 2000, 18, 17-33.	1.1	119
11	Finding similar regions in many strings. , 1999, , .		105
12	Exact algorithms for haplotype assembly from whole-genome sequence data. Bioinformatics, 2013, 29, 1938-1945.	1.8	79
13	Genetic Design of Drugs Without Side-Effects. SIAM Journal on Computing, 2003, 32, 1073-1090.	0.8	73
14	Protein-protein binding site identification by enumerating the configurations. BMC Bioinformatics, 2012, 13, 158.	1.2	57
15	Approximations for Steiner trees with minimum number of Steiner points. Theoretical Computer Science, 2001, 262, 83-99.	0.5	52
16	Approximation algorithms for tree alignment with a given phylogeny. Algorithmica, 1996, 16, 302-315.	1.0	49
17	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.	1.9	49
18	Improved Approximation Algorithms for Tree Alignment. Journal of Algorithms, 1997, 25, 255-273.	0.9	46

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19	A group multicast routing algorithm by using multiple minimum Steiner trees. Computer Communications, 1997, 20, 750-758.	3.1	41
20	Hexagonal chains with maximal total Ï€-electron energy. Chemical Physics Letters, 2001, 337, 131-137.	1.2	41
21	Topology control of ad hoc wireless networks for energy efficiency. IEEE Transactions on Computers, 2004, 53, 1629-1635.	2.4	41
22	Hexagonal chains with minimal total Ï€-electron energy. Chemical Physics Letters, 2001, 337, 125-130.	1.2	40
23	On the complexity of finding emerging patterns. Theoretical Computer Science, 2005, 335, 15-27.	0.5	40
24	Identification of linked regions using high-density SNP genotype data in linkage analysis. Bioinformatics, 2008, 24, 86-93.	1.8	40
25	Comprehensive Analysis Reveals the Evolution and Pathogenicity of <i>Aeromonas</i> , Viewed from Both Single Isolated Species and Microbial Communities. MSystems, 2019, 4, .	1.7	36
26	The Inverse Problems for Some Topological Indices in Combinatorial Chemistry. Journal of Computational Biology, 2003, 10, 47-55.	0.8	35
27	Computing similarity between RNA structures. Theoretical Computer Science, 2002, 276, 111-132.	0.5	34
28	Greedy method for inferring tandem duplication history. Bioinformatics, 2003, 19, 1497-1504.	1.8	33
29	Improved deterministic approximation algorithms for Max TSP. Information Processing Letters, 2005, 95, 333-342.	0.4	33
30	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	0.9	31
31	On the complexity of unsigned translocation distance. Theoretical Computer Science, 2006, 352, 322-328.	0.5	31
32	An approximation algorithm for a bottleneck k-Steiner tree problem in the Euclidean plane. Information Processing Letters, 2002, 81, 151-156.	0.4	30
33	Algorithms for Reticulate Networks of Multiple Phylogenetic Trees. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 372-384.	1.9	30
34	Modeling Protein Interacting Groups by Quasi-Bicliques: Complexity, Algorithm, and Application. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 354-364.	1.9	28
35	A More Efficient Approximation Scheme for Tree Alignment. SIAM Journal on Computing, 2000, 30, 283-299.	0.8	27
36	SEGID: Identifying Interesting Segments in (Multiple) Sequence Alignments. Bioinformatics, 2003, 19, 297-298.	1.8	27

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37	A highly accurate heuristic algorithm for the haplotype assembly problem. BMC Genomics, 2013, 14, S2.	1.2	27
38	Efficient Algorithms for the Closest String and Distinguishing String Selection Problems. Lecture Notes in Computer Science, 2009, , 261-270.	1.0	27
39	On bipartite graphs with minimal energy. Discrete Applied Mathematics, 2009, 157, 869-873.	0.5	26
40	A three-string approach to the closest string problem. Journal of Computer and System Sciences, 2012, 78, 164-178.	0.9	26
41	HybridNET: a tool for constructing hybridization networks. Bioinformatics, 2010, 26, 2912-2913.	1.8	25
42	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.	1.9	24
43	Simultaneous Identification of Duplications, Losses, and Lateral Gene Transfers. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1515-1528.	1.9	24
44	Progressive approach for SNP calling and haplotype assembly using single molecular sequencing data. Bioinformatics, 2018, 34, 2012-2018.	1.8	24
45	RANDOMIZED ALGORITHMS FOR MOTIF DETECTION. Journal of Bioinformatics and Computational Biology, 2005, 03, 1039-1052.	0.3	23
46	Fast accurate missing SNP genotype local imputation. BMC Research Notes, 2012, 5, 404.	0.6	23
47	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.	1.1	23
48	On the Inapproximability of Disjoint Paths and Minimum Steiner Forest with Bandwidth Constraints. Journal of Computer and System Sciences, 2000, 60, 1-12.	0.9	22
49	Identifying protein complexes based on density and modularity in protein-protein interaction network. BMC Systems Biology, 2013, 7, S12.	3.0	21
50	k-Resonance of Open-Ended Carbon Nanotubes. Journal of Mathematical Chemistry, 2004, 35, 87-103.	0.7	20
51	Parametric alignment of ordered trees. Bioinformatics, 2003, 19, 2237-2245.	1.8	19
52	Algorithmic approaches for genome rearrangement: a review. IEEE Transactions on Systems, Man and Cybernetics, Part C: Applications and Reviews, 2006, 36, 636-648.	3.3	19
53	An approximation scheme for some Steiner tree problems in the plane. Networks, 1996, 28, 187-193.	1.6	17
54	An Ultrafast Tool for Minimum Reticulate Networks. Journal of Computational Biology, 2013, 20, 38-41.	0.8	17

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55	Integrating pan-genome with metagenome for microbial community profiling. Computational and Structural Biotechnology Journal, 2021, 19, 1458-1466.	1.9	16
56	Quasi-bicliques: Complexity and Binding Pairs. Lecture Notes in Computer Science, 2008, , 255-264.	1.0	16
57	On the Tractability of Maximal Strip Recovery. Journal of Computational Biology, 2010, 17, 907-914.	0.8	15
58	Exact and approximation algorithms forÂtheÂcomplementary maximal strip recovery problem. Journal of Combinatorial Optimization, 2012, 23, 493-506.	0.8	15
59	An improved randomized approximation algorithm for maximum triangle packing. Discrete Applied Mathematics, 2009, 157, 1640-1646.	0.5	14
60	A polynomial time approximation scheme for embedding a directed hypergraph on a ring. Information Processing Letters, 2006, 97, 203-207.	0.4	13
61	Probabilistic Models for Capturing More Physicochemical Properties on Proteinâ€"Protein Interface. Journal of Chemical Information and Modeling, 2014, 54, 1798-1809.	2.5	13
62	Proteinâ€"protein interface prediction based on hexagon structure similarity. Computational Biology and Chemistry, 2016, 63, 83-88.	1.1	13
63	Fitting Distances by Tree Metrics with Increment Error. Journal of Combinatorial Optimization, 1999, 3, 213-225.	0.8	12
64	A (1.5 + Îµ)-Approximation Algorithm for Unsigned Translocation Distance. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 56-66.	1.9	12
65	An improved approximation algorithm for the complementary maximal strip recovery problem. Journal of Computer and System Sciences, 2012, 78, 720-730.	0.9	12
66	Near optimal solutions for maximum quasi-bicliques. Journal of Combinatorial Optimization, 2013, 25, 481-497.	0.8	12
67	A 1.75-approximation algorithm for unsigned translocation distance. Journal of Computer and System Sciences, 2007, 73, 1045-1059.	0.9	11
68	An efficient algorithm for the blocked pattern matching problem. Bioinformatics, 2015, 31, 532-538.	1.8	11
69	Core-genome scaffold comparison reveals the prevalence that inversion events are associated with pairs of inverted repeats. BMC Genomics, 2017, 18, 268.	1.2	11
70	Proteinâ€"Protein Binding Sites Prediction by 3D Structural Similarities. Journal of Chemical Information and Modeling, 2011, 51, 3287-3294.	2.5	10
71	A fast tool for minimum hybridization networks. BMC Bioinformatics, 2012, 13, 155.	1.2	10
72	Faster exact computation of rSPR distance. Journal of Combinatorial Optimization, 2015, 29, 605-635.	0.8	10

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73	An Improved Approximation Algorithm for the Capacitated Multicast Tree Routing Problem. Lecture Notes in Computer Science, 2008, , 286-295.	1.0	10
74	On the Tractability of Maximal Strip Recovery. Lecture Notes in Computer Science, 2009, , 400-409.	1.0	10
75	A Linear Kernel for Co-Path/Cycle Packing. Lecture Notes in Computer Science, 2010, , 90-102.	1.0	10
76	An Improved Randomized Approximation Algorithm for Max TSP. Journal of Combinatorial Optimization, 2005, 9, 401-432.	0.8	9
77	An improved approximation algorithm for maximum edge 2-coloring in simple graphs. Journal of Discrete Algorithms, 2008, 6, 205-215.	0.7	9
78	Protein complex prediction based on maximum matching with domain–domain interaction. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2012, 1824, 1418-1424.	1.1	9
79	Minimum k Arborescences with Bandwidth Constraints. Algorithmica, 2004, 38, 529-537.	1.0	8
80	Finding the region of pseudo-periodic tandem repeats in biological sequences. Algorithms for Molecular Biology, 2006, 1, 2.	0.3	8
81	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.	1.4	8
82	Center and Distinguisher for Strings with Unbounded Alphabet. Journal of Combinatorial Optimization, 2002, 6, 383-400.	0.8	7
83	Space Efficient Algorithms for Ordered Tree Comparison. Algorithmica, 2008, 51, 283-297.	1.0	7
84	Detecting Protein Conformational Changes in Interactions via Scaling Known Structures. Journal of Computational Biology, 2013, 20, 765-779.	0.8	7
85	An approximation algorithm for maximum internal spanning tree. Journal of Combinatorial Optimization, 2018, 35, 955-979.	0.8	7
86	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.	0.7	6
87	Optimal Relay Location for Resource-limited Energy-efficient Wireless Communication. Journal of Global Optimization, 2006, 36, 391-399.	1.1	6
88	Some approximation algorithms for the clique partition problem in weighted interval graphs. Theoretical Computer Science, 2007, 381, 124-133.	0.5	6
89	Finding the Nearest Neighbors in Biological Databases Using Less Distance Computations. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2010, 7, 669-680.	1.9	6
90	An Approximation Algorithm for the Minimum Co-Path Set Problem. Algorithmica, 2011, 60, 969-986.	1.0	6

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91	Mutation Region Detection for Closely Related Individuals without a Known Pedigree. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 499-510.	1.9	6
92	Computing the protein binding sites. BMC Bioinformatics, 2012, 13, S2.	1.2	6
93	Exome sequencing of Saudi Arabian patients with ADPKD. Renal Failure, 2019, 41, 842-849.	0.8	6
94	A (1.408+Îµ)-Approximation Algorithm for Sorting Unsigned Genomes by Reciprocal Translocations. Lecture Notes in Computer Science, 2014, , 128-140.	1.0	6
95	P-Binder: A System for the Protein-Protein Binding Sites Identification. Lecture Notes in Computer Science, 2012, , 127-138.	1.0	6
96	An Improved Approximation Algorithm for the Bandpass-2 Problem. Lecture Notes in Computer Science, 2012, , 188-199.	1.0	6
97	Solutions for Two Conjectures on the Inverse Problem of the Wiener Index of Peptoids. SIAM Journal on Discrete Mathematics, 2003, 17, 210-218.	0.4	5
98	CTRD: a fast applet for computing signed translocation distance between genomes. Bioinformatics, 2004, 20, 3256-3257.	1.8	5
99	Maximizing Profits of Routing in WDM Networks. Journal of Combinatorial Optimization, 2005, 10, 99-111.	0.8	5
100	Linked region detection using high-density SNP genotype data via the minimum recombinant model of pedigree haplotype inference. BMC Bioinformatics, 2009, 10, 216.	1.2	5
101	An Exact Algorithm for the Zero Exemplar Breakpoint Distance Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1469-1477.	1.9	5
102	Structural neighboring property for identifying protein-protein binding sites. BMC Systems Biology, 2015, 9, S3.	3.0	5
103	Randomized Fixed-Parameter Algorithms for the Closest String Problem. Algorithmica, 2016, 74, 466-484.	1.0	5
104	Better ILP-Based Approaches to Haplotype Assembly. Journal of Computational Biology, 2016, 23, 537-552.	0.8	5
105	Approximation Algorithms for the Maximum Weight Internal Spanning Tree Problem. Algorithmica, 2019, 81, 4167-4199.	1.0	5
106	Genetic and clinical analysis in Chinese patients with retinitis pigmentosa caused by <i>EYS</i> mutations. Molecular Genetics & Genomic Medicine, 2020, 8, e1117.	0.6	5
107	Approximation Algorithms for Biclustering Problems. SIAM Journal on Computing, 2008, 38, 1504-1518.	0.8	4
108	An Improved Randomized Approximation Algorithm for Maximum Triangle Packing. Lecture Notes in Computer Science, 2008, , 97-108.	1.0	4

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109	An Efficient Voting Algorithm for Finding Additive Biclusters with Random Background. Journal of Computational Biology, 2008, 15, 1275-1293.	0.8	4
110	Distances between phylogenetic trees: A survey. Tsinghua Science and Technology, 2013, 18, 490-499.	4.1	4
111	An Improved Approximation Algorithm for rSPR Distance. Lecture Notes in Computer Science, 2016, , 468-479.	1.0	4
112	Pan€genome study of Thermococcales reveals extensive genetic diversity and genetic evidence of thermophilic adaption. Environmental Microbiology, 2021, 23, 3599-3613.	1.8	4
113	SVLR: Genome Structural Variant Detection Using Long-Read Sequencing Data. Journal of Computational Biology, 2021, 28, 774-788.	0.8	4
114	Randomized Algorithms for Motif Detection. Lecture Notes in Computer Science, 2004, , 884-895.	1.0	4
115	A Three-String Approach to the Closest String Problem. Lecture Notes in Computer Science, 2010, , 449-458.	1.0	4
116	Removable edges in a cycle of a 4-connected graph. Discrete Mathematics, 2004, 287, 103-111.	0.4	3
117	On the complexity of finding emerging patterns. , 0, , .		3
118	Approximation Algorithms for Reconstructing theÂDuplication History ofÂTandemÂRepeats. Algorithmica, 2009, 54, 501-529.	1.0	3
119	Identifying mutation regions for closely related individuals without a known pedigree. BMC Bioinformatics, 2012, 13, 146.	1.2	3
120	A Dynamic Programming Algorithm For (1,2)-Exemplar Breakpoint Distance. Journal of Computational Biology, 2015, 22, 666-676.	0.8	3
121	A factor-(1.408 +Îµ) approximation for sorting unsigned genomes by reciprocal translocations. Theoretical Computer Science, 2015, 607, 166-180.	0.5	3
122	Comprehensive study of instable regions in Pseudomonas aeruginosa and Mycobacterium tuberculosis. BioMedical Engineering OnLine, 2018, 17, 133.	1.3	3
123	A randomized approximation algorithm for metric triangle packing. Journal of Combinatorial Optimization, 2021, 41, 12-27.	0.8	3
124	Computing the Protein Binding Sites. Lecture Notes in Computer Science, 2011, , 25-36.	1.0	3
125	On packing and coloring hyperedges in a cycle. Discrete Applied Mathematics, 2007, 155, 2140-2151.	0.5	2
126	Near optimal multiple alignment within a band in polynomial time. Journal of Computer and System Sciences, 2007, 73, 997-1011.	0.9	2

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127	Beyond evolutionary trees. Natural Computing, 2010, 9, 421-435.	1.8	2
128	Probabilistic Analysis of a Motif Discovery Algorithm for Multiple Sequences. SIAM Journal on Discrete Mathematics, 2010, 23, 1715-1737.	0.4	2
129	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
130	The Parameterized Complexity of the Shared Center Problem. Algorithmica, 2014, 69, 269-293.	1.0	2
131	GRSR: a tool for deriving genome rearrangement scenarios from multiple unichromosomal genome sequences. BMC Bioinformatics, 2018, 19, 291.	1.2	2
132	Better ILP models for haplotype assembly. BMC Bioinformatics, 2018, 19, 52.	1.2	2
133	Faster Exact Computation of rSPR Distance via Better Approximation. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 916-929.	1.9	2
134	Fast and Accurate Algorithms for Mapping and Aligning Long Reads. Journal of Computational Biology, 2021, 28, 789-803.	0.8	2
135	Identifying Protein-Protein Binding Sites with a Combined Energy Function. Current Protein and Peptide Science, 2014, 15, 540-552.	0.7	2
136	AN O(n2) ALGORITHM FOR SIGNED TRANSLOCATION PROBLEM. , 2005, , .		2
137	A Complete Solution to a Conjecture on the Î²-Polynomials of Graphs. Journal of Mathematical Chemistry, 2003, 33, 189-193.	0.7	1
138	Exact matching of RNA secondary structure patterns. Theoretical Computer Science, 2005, 335, 53-66.	0.5	1
139	Decomposing toroidal graphs into circuits and edges. Discrete Applied Mathematics, 2005, 148, 147-159.	0.5	1
140	Discovering almost any hidden motif from multiple sequences. ACM Transactions on Algorithms, 2011, 7, 1-18.	0.9	1
141	A polynomial time approximation scheme forÂembedding a directed hypergraph on a weighted ring. Journal of Combinatorial Optimization, 2012, 24, 319-328.	0.8	1
142	Improved Practical Algorithms for Rooted Subtree Prune and Regraft (rSPR) Distance and Hybridization Number. Journal of Computational Biology, 2020, 27, 1422-1432.	0.8	1
143	Faster Exact Computation of rSPR Distance. Lecture Notes in Computer Science, 2013, , 36-47.	1.0	1
144	Approximation Algorithms for Bi-clustering Problems. Lecture Notes in Computer Science, 2006, , 310-320.	1.0	1

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145	Closest String and Substring Problems. , 2008, , 155-156.		1
146	Near Optimal Solutions for Maximum Quasi-bicliques. Lecture Notes in Computer Science, 2010, , 409-418.	1.0	1
147	Parameterized and Approximation Algorithms for Finding Two Disjoint Matchings. Lecture Notes in Computer Science, 2013, , 1-12.	1.0	1
148	Randomized and Parameterized Algorithms for the Closest String Problem. Lecture Notes in Computer Science, 2014, , 100-109.	1.0	1
149	A New 2-Approximation Algorithm for rSPR Distance. Lecture Notes in Computer Science, 2017, , 128-139.	1.0	1
150	Finding Additive Biclusters with Random Background. , 2008, , 263-276.		1
151	Approximation Algorithms for Reconstructing the Duplication History of Tandem Repeats. Lecture Notes in Computer Science, 2007, , 493-503.	1.0	1
152	Efficient Algorithms for Model-Based Motif Discovery from Multiple Sequences. , 2008, , 234-245.		1
153	On the completeness of incidence calculus. Journal of Automated Reasoning, 1996, 16, 355-368.	1.1	0
154	An Approximation Algorithm for Embedding a Directed Hypergraph on a Ring. Lecture Notes in Computer Science, 2005, , 392-399.	1.0	0
155	Translocation Distance: Algorithms and Complexity. Advances in Computers, 2006, , 105-126.	1.2	0
156	Finding Transcription Factor Binding Sites with Indels. , 2007, , .		0
157	Improved Approximation Algorithms for Reconstructing the History of Tandem Repeats. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 438-453.	1.9	0
158	Identification of Distinguishing Motifs. International Journal of Knowledge Discovery in Bioinformatics, 2010, 1, 53-67.	0.8	0
159	Computing Parametric Alignment of RNA Structures: Visualization and Practice. , 2011, , .		0
160	Mining Protein Interaction Groups. , 0, , .		0
161	Constant time approximation scheme for largest well predicted subset. Journal of Combinatorial Optimization, 2013, 25, 352-367.	0.8	0
162	Identifying duplications and lateral gene transfers simultaneously and rapidly. , 2013, , .		0

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163	A parameterized algorithm for (1,2)-exemplar breakpoint distance. , 2014, , .		0
164	Parameterized and approximation algorithms for finding two disjoint matchings. Theoretical Computer Science, 2014, 556, 85-93.	0.5	0
165	Quantifying Significance of MHC II Residues. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 17-25.	1.9	0
166	A Polynomial Time Approximation Scheme for the Closest Shared Center Problem. Algorithmica, 2017, 77, 65-83.	1.0	0
167	Designing and implementing algorithms for the closest string problem. Theoretical Computer Science, 2019, 786, 32-43.	0.5	0
168	Computing a Consensus Phylogeny via Leaf Removal. Journal of Computational Biology, 2020, 27, 175-188.	0.8	0
169	Space Efficient Algorithms for Ordered Tree Comparison. Lecture Notes in Computer Science, 2005, , 380-391.	1.0	0
170	VOTING ALGORITHMS FOR THE MOTIF FINDING PROBLEM. , 2008, , .		0
171	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.	1.0	0
172	Constant Time Approximation Scheme for Largest Well Predicted Subset. Lecture Notes in Computer Science, 2010, , 429-438.	1.0	0
173	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.	1.0	0
174	The Parameterized Complexity of the Shared Center Problem. Lecture Notes in Computer Science, 2012, , 439-452.	1.0	0
175	A Polynomial Time Approximation Scheme for the Closest Shared Center Problem. Lecture Notes in Computer Science, 2013, , 385-396.	1.0	0
176	Closest String and Substring Problems. , 2014, , 1-4.		0
177	Closest String and Substring Problems. , 2016, , 321-324.		0
178	Designing and Implementing Algorithms for the Closest String Problem. Lecture Notes in Computer Science, 2017, , 79-90.	1.0	0
179	A Randomized Approximation Algorithm for Metric Triangle Packing. Lecture Notes in Computer Science, 2019, , 119-129.	1.0	0
180	Identifying Duplications and Lateral Gene Transfers Simultaneously and Rapidly. Journal of Bioinformatics and Computational Biology, 2021, , 2150033.	0.3	0

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181	Identification of Distinguishing Motifs. , 0, , 1-14.		0
182	Proteoform identification based on top-down tandem mass spectra with peak error corrections. Briefings in Bioinformatics, 2022, , .	3.2	0
183	mzMD: visualization-oriented MS data storage and retrieval. Bioinformatics, 2022, 38, 2333-2340.	1.8	0