

Kaizhong Zhang

List of Publications by Year in descending order

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81
papers

4,980
citations

218677

26
h-index

106344

65
g-index

86
all docs

86
docs citations

86
times ranked

3809
citing authors

#	ARTICLE	IF	CITATIONS
1	NBPMF. Advances in Computational Intelligence and Robotics Book Series, 2020, , 228-258.	0.4	0
2	An Improved Approach for N-Linked Glycan Structure Identification from HCD MS/MS Spectra. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 388-395.	3.0	4
3	An approach for N-linked glycan identification from MS/MS spectra by target-decoy strategy. Computational Biology and Chemistry, 2018, 74, 391-398.	2.3	7
4	An Approach for Peptide Identification by De Novo Sequencing of Mixture Spectra. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 326-336.	3.0	4
5	DISC: DISulfide linkage Characterization from tandem mass spectra. Bioinformatics, 2017, 33, 3861-3870.	4.1	3
6	NBPMF. International Journal of Cognitive Informatics and Natural Intelligence, 2017, 11, 41-65.	0.4	1
7	Similarity metric induced metrics with application in machine learning and bioinformatics. , 2016, , .		0
8	Spectra library assisted de novo peptide sequencing for HCD and ETD spectra pairs. BMC Bioinformatics, 2016, 17, 538.	2.6	2
9	De Novo Sequencing Assisted Approach for Characterizing Mixture MS/MS Spectra. IEEE Transactions on Nanobioscience, 2016, 15, 166-176.	3.3	2
10	An Approach for Matching Mixture MS/MS Spectra with a Pair of Peptide Sequences in a Protein Database. Lecture Notes in Computer Science, 2015, , 223-234.	1.3	0
11	Algorithms for local similarity between forests. Journal of Combinatorial Optimization, 2014, 27, 14-31.	1.3	1
12	An improved algorithm for tree edit distance with applications for RNA secondary structure comparison. Journal of Combinatorial Optimization, 2014, 27, 778-797.	1.3	6
13	A METHOD FOR DISCOVERING COMMON PATTERNS FROM TWO RNA SECONDARY STRUCTURES AND ITS APPLICATION TO STRUCTURAL REPEAT DETECTION. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250001.	0.8	2
14	Efficient filtration for similarity search with spaced k-mer neighbors. , 2012, , .		1
15	Algorithms for Forest Local Similarity. Lecture Notes in Computer Science, 2012, , 163-175.	1.3	1
16	On the Longest Common Rigid Subsequence Problem. Algorithmica, 2010, 56, 270-280.	1.3	6
17	ON COMPARING TWO STRUCTURED RNA MULTIPLE ALIGNMENTS. Journal of Bioinformatics and Computational Biology, 2010, 08, 967-980.	0.8	3
18	On the similarity metric and the distance metric. Theoretical Computer Science, 2009, 410, 2365-2376.	0.9	82

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19	A new quartet approach for reconstructing phylogenetic trees: quartet joining method. Journal of Combinatorial Optimization, 2008, 16, 293-306.	1.3	7
20	Space Efficient Algorithms for Ordered Tree Comparison. Algorithmica, 2008, 51, 283-297.	1.3	7
21	COMPLEXITIES AND ALGORITHMS FOR GLYCAN SEQUENCING USING TANDEM MASS SPECTROMETRY. Journal of Bioinformatics and Computational Biology, 2008, 06, 77-91.	0.8	23
22	Locality and Gaps in RNA Comparison. Journal of Computational Biology, 2007, 14, 1074-1087.	1.6	8
23	Deploying Wireless Sensor Networks under Limited Mobility Constraints. IEEE Transactions on Mobile Computing, 2007, 6, 1142-1157.	5.8	86
24	The Normalized Similarity Metric and Its Applications. , 2007, , .		5
25	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
26	RADAR: An InteractiveWeb-Based Toolkit for RNA Data Analysis and Research. , 2006, , .		4
27	RNA-RNA Interaction Prediction and Antisense RNA Target Search. Journal of Computational Biology, 2006, 13, 267-282.	1.6	106
28	An effective algorithm for peptide de novo sequencing from MS/MS spectra. Journal of Computer and System Sciences, 2005, 70, 418-430.	1.2	44
29	MULTIPLE RNA STRUCTURE ALIGNMENT. Journal of Bioinformatics and Computational Biology, 2005, 03, 609-626.	0.8	5
30	AN AUTOMATA APPROACH TO MATCH GAPPED SEQUENCE TAGS AGAINST PROTEIN DATABASE. International Journal of Foundations of Computer Science, 2005, 16, 487-497.	1.1	1
31	SPIDER: SOFTWARE FOR PROTEIN IDENTIFICATION FROM SEQUENCE TAGS WITH DE NOVO SEQUENCING ERROR. Journal of Bioinformatics and Computational Biology, 2005, 03, 697-716.	0.8	202
32	Space Efficient Algorithms for Ordered Tree Comparison. Lecture Notes in Computer Science, 2005, , 380-391.	1.3	0
33	An Automata Approach to Match Gapped Sequence Tags Against Protein Database. Lecture Notes in Computer Science, 2005, , 167-177.	1.3	0
34	Multiple RNA structure alignment. , 2004, , 246-54.		1
35	WORD COMPLEXITY AND REPETITIONS IN WORDS. International Journal of Foundations of Computer Science, 2004, 15, 41-55.	1.1	11
36	FINDING CONSERVED WELL-ORDERED RNA STRUCTURES IN GENOMIC SEQUENCES. International Journal of Computational Intelligence and Applications, 2004, 04, 417-430.	0.8	5

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37	An algorithm for detecting homologues of known structured rnas in genomes. , 2004, , 300-10.		5
38	PEAKS: powerful software for peptide <i>de novo</i> sequencing by tandem mass spectrometry. Rapid Communications in Mass Spectrometry, 2003, 17, 2337-2342.	1.5	1,156
39	Finding patterns in three-dimensional graphs: algorithms and applications to scientific data mining. IEEE Transactions on Knowledge and Data Engineering, 2002, 14, 731-749.	5.7	30
40	A General Edit Distance between RNA Structures. Journal of Computational Biology, 2002, 9, 371-388.	1.6	175
41	Computing similarity between RNA structures. Theoretical Computer Science, 2002, 276, 111-132.	0.9	34
42	Finding approximate patterns in undirected acyclic graphs. Pattern Recognition, 2002, 35, 473-483.	8.1	21
43	A new algorithm for computing similarity between RNA structures. Information Sciences, 2001, 139, 59-77.	6.9	7
44	Finding similar consensus between trees: an algorithm and a distance hierarchy. Pattern Recognition, 2001, 34, 127-137.	8.1	47
45	Perfect Phylogenetic Networks with Recombination. Journal of Computational Biology, 2001, 8, 69-78.	1.6	187
46	Identifying consensus of trees through alignment. Information Sciences, 2000, 126, 165-189.	6.9	9
47	An Index Structure for Data Mining and Clustering. Knowledge and Information Systems, 2000, 2, 161-184.	3.2	46
48	An approximate search engine for structural databases. SIGMOD Record, 2000, 29, 584.	1.2	0
49	Identifying approximately common substructures in trees based on a restricted edit distance. Information Sciences, 1999, 121, 367-386.	6.9	10
50	Computing Similarity between RNA Structures. Lecture Notes in Computer Science, 1999, , 281-293.	1.3	25
51	Efficient parallel algorithm for the editing distance between ordered trees. Lecture Notes in Computer Science, 1998, , 80-90.	1.3	0
52	Structural matching and discovery in document databases. , 1997, , .		18
53	Structural matching and discovery in document databases. SIGMOD Record, 1997, 26, 560-563.	1.2	2
54	A constrained edit distance between unordered labeled trees. Algorithmica, 1996, 15, 205-222.	1.3	155

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55	Fast algorithms for minimum matrix norm with application in computer graphics. <i>Algorithmica</i> , 1996, 15, 68-81.	1.3	0
56	On the complexity of comparing evolutionary trees. <i>Discrete Applied Mathematics</i> , 1996, 71, 153-169.	0.9	188
57	Linear Cartographic Data Acquisition from Scanned Topographic Maps. <i>Annals of GIS</i> , 1996, 2, 12-23.	3.1	0
58	ON THE EDITING DISTANCE BETWEEN UNDIRECTED ACYCLIC GRAPHS. <i>International Journal of Foundations of Computer Science</i> , 1996, 07, 43-57.	1.1	75
59	Efficient parallel algorithms for tree editing problems. <i>Lecture Notes in Computer Science</i> , 1996, , 361-372.	1.3	7
60	A Constrained Edit Distance Between Unordered Labeled Trees. <i>Algorithmica</i> , 1996, 15, 205.	1.3	1
61	Algorithms for approximate graph matching. <i>Information Sciences</i> , 1995, 82, 45-74.	6.9	30
62	Alignment of trees "an alternative to tree edit. <i>Theoretical Computer Science</i> , 1995, 143, 137-148.	0.9	152
63	Algorithms for the constrained editing distance between ordered labeled trees and related problems. <i>Pattern Recognition</i> , 1995, 28, 463-474.	8.1	94
64	On the editing distance between undirected acyclic graphs and related problems. <i>Lecture Notes in Computer Science</i> , 1995, , 395-407.	1.3	33
65	Pattern matching and pattern discovery in scientific, program, and document databases. <i>SIGMOD Record</i> , 1995, 24, 487.	1.2	1
66	A system for approximate tree matching. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 1994, 6, 559-571.	5.7	97
67	Some MAX SNP-hard results concerning unordered labeled trees. <i>Information Processing Letters</i> , 1994, 49, 249-254.	0.6	109
68	Exact and approximate algorithms for unordered tree matching. <i>IEEE Transactions on Systems, Man, and Cybernetics</i> , 1994, 24, 668-678.	0.9	90
69	A new algorithm for multispectral remotely sensed data clustering. <i>International Journal of Remote Sensing</i> , 1994, 9, 115-134.	1.0	1
70	Combinatorial pattern discovery for scientific data. <i>SIGMOD Record</i> , 1994, 23, 115-125.	1.2	43
71	Alignment of trees "An alternative to tree edit. <i>Lecture Notes in Computer Science</i> , 1994, , 75-86.	1.3	65
72	A new editing based distance between unordered labeled trees. , 1993, , 254-265.		26

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73	On the editing distance between unordered labeled trees. Information Processing Letters, 1992, 42, 133-139.	0.6	257
74	Fast serial and parallel algorithms for approximate tree matching with VLDC's (Extended Abstract). Lecture Notes in Computer Science, 1992, , 151-161.	1.3	8
75	Fast algorithms for the unit cost editing distance between trees. Journal of Algorithms, 1990, 11, 581-621.	0.9	89
76	Simple Fast Algorithms for the Editing Distance between Trees and Related Problems. SIAM Journal on Computing, 1989, 18, 1245-1262.	1.0	956
77	An algorithm for constrained optimal band ordering of multispectral remote sensing images in lossless data compression. , 0, , .		2
78	Computing similarity between RNA secondary structures. , 0, , .		17
79	ATreeGrep: approximate searching in unordered trees. , 0, , .		25
80	A wavelet transform based method for road extraction from high-resolution remotely sensed data. , 0, , .		3
81	Algorithms for new distance measures between histograms. , 0, , .		1