

Chin Lung Lu

List of Publications by Year in descending order

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Version: 2024-02-01

16
papers

141
citations

1478505

6
h-index

1281871

11
g-index

16
all docs

16
docs citations

16
times ranked

201
citing authors

#	ARTICLE	IF	CITATIONS
1	Multi-CSAR: a web server for scaffolding contigs using multiple reference genomes. <i>Nucleic Acids Research</i> , 2022, 50, W500-W509.	14.5	3
2	Clover: a clustering-oriented de novo assembler for Illumina sequences. <i>BMC Bioinformatics</i> , 2020, 21, 528.	2.6	1
3	CSAR: a contig scaffolding tool using algebraic rearrangements. <i>Bioinformatics</i> , 2018, 34, 109-111.	4.1	26
4	Two-string consensus problem under non-overlapping inversion and transposition distance. <i>Information Processing Letters</i> , 2018, 130, 46-51.	0.6	0
5	Multi-CSAR: a multiple reference-based contig scaffolder using algebraic rearrangements. <i>BMC Systems Biology</i> , 2018, 12, 139.	3.0	11
6	CSAR-web: a web server of contig scaffolding using algebraic rearrangements. <i>Nucleic Acids Research</i> , 2018, 46, W55-W59.	14.5	18
7	R3D-BLAST2: an improved search tool for similar RNA 3D substructures. <i>BMC Bioinformatics</i> , 2017, 18, 574.	2.6	2
8	An efficient algorithm for computing non-overlapping inversion and transposition distance. <i>Information Processing Letters</i> , 2016, 116, 744-749.	0.6	5
9	Multi-CAR: a tool of contig scaffolding using multiple references. <i>BMC Bioinformatics</i> , 2016, 17, 469.	2.6	9
10	iPARTS2: an improved tool for pairwise alignment of RNA tertiary structures, version 2. <i>Nucleic Acids Research</i> , 2016, 44, W328-W332.	14.5	6
11	An efficient algorithm for one-sided block ordering problem under block-interchange distance. <i>Theoretical Computer Science</i> , 2016, 609, 296-305.	0.9	3
12	An Efficient Algorithm for the Contig Ordering Problem under Algebraic Rearrangement Distance. <i>Journal of Computational Biology</i> , 2015, 22, 975-987.	1.6	9
13	CAR: contig assembly of prokaryotic draft genomes using rearrangements. <i>BMC Bioinformatics</i> , 2014, 15, 381.	2.6	39
14	Assembling contigs in draft genomes using reversals and block-interchanges. <i>BMC Bioinformatics</i> , 2013, 14, S9.	2.6	6
15	A new filtration method and a hybrid strategy for approximate string matching. <i>Theoretical Computer Science</i> , 2013, 481, 9-17.	0.9	3
16	An Integer Linear Programming Approach for Scaffolding Based on Exemplar Breakpoint Distance. <i>Journal of Computational Biology</i> , 0, , .	1.6	0