

Chin Lung Lu

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4322982/publications.pdf>

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