

HÃ©lÃ¨ne Touzet

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

484
citations

840776

11
h-index

713466

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24
all docs

24
docs citations

24
times ranked

1110
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1164-1181.	6.5	33
2	Use of whole-genome sequencing in the molecular investigation of care-associated HCoV-OC43 infections in a hematopoietic stem cell transplant unit. <i>Journal of Clinical Virology</i> , 2020, 122, 104206.	3.1	5
3	miRkwood: a tool for the reliable identification of microRNAs in plant genomes. <i>BMC Genomics</i> , 2019, 20, 532.	2.8	14
4	A complete protocol for whole-genome sequencing of virus from clinical samples: Application to coronavirus OC43. <i>Virology</i> , 2019, 531, 141-148.	2.4	28
5	Assessment of Common and Emerging Bioinformatics Pipelines for Targeted Metagenomics. <i>PLoS ONE</i> , 2017, 12, e0169563.	2.5	80
6	Efficient approximations of RNA kinetics landscape using non-redundant sampling. <i>Bioinformatics</i> , 2017, 33, i283-i292.	4.1	14
7	On the Levenshtein Automaton and the Size of the Neighbourhood of a Word. <i>Lecture Notes in Computer Science</i> , 2016, , 207-218.	1.3	1
8	Approximate search of short patterns with high error rates using the 01-lossless seeds. <i>Journal of Discrete Algorithms</i> , 2016, 37, 3-16.	0.7	5
9	Modeling Alternate RNA Structures in Genomic Sequences. <i>Journal of Computational Biology</i> , 2015, 22, 190-204.	1.6	3
10	Modeling Dynamic Programming Problems over Sequences and Trees with Inverse Coupled Rewrite Systems. <i>Algorithms</i> , 2014, 7, 62-144.	2.1	11
11	RNA Locally Optimal Secondary Structures. <i>Journal of Computational Biology</i> , 2012, 19, 1120-1133.	1.6	6
12	RNAspace.org: An integrated environment for the prediction, annotation, and analysis of ncRNA. <i>Rna</i> , 2011, 17, 1947-1956.	3.5	25
13	Computational identification of protein-coding sequences by comparative analysis. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 160.	0.1	6
14	Self-overlapping Occurrences and Knuth-Morris-Pratt Algorithm for Weighted Matching. <i>Lecture Notes in Computer Science</i> , 2009, , 481-492.	1.3	7
15	Does Hybridization Increase Evolutionary Rate? Data from the 28S-rDNA D8 Domain in Echinoderms. <i>Journal of Molecular Evolution</i> , 2008, 67, 539-550.	1.8	11
16	Efficient and accurate P-value computation for Position Weight Matrices. <i>Algorithms for Molecular Biology</i> , 2007, 2, 15.	1.2	109
17	Comparing similar ordered trees in linear-time. <i>Journal of Discrete Algorithms</i> , 2007, 5, 696-705.	0.7	13
18	Large Scale Matching for Position Weight Matrices. <i>Lecture Notes in Computer Science</i> , 2006, , 401-412.	1.3	17

#	ARTICLE	IF	CITATIONS
19	Decomposition algorithms for the tree edit distance problem. Journal of Discrete Algorithms, 2005, 3, 448-471.	0.7	22
20	CARNAC: folding families of related RNAs. Nucleic Acids Research, 2004, 32, W142-W145.	14.5	54
21	Tree edit distance with gaps. Information Processing Letters, 2003, 85, 123-129.	0.6	11
22	A Characterisation of Multiply Recursive Functions with Higman's Lemma. Information and Computation, 2002, 178, 534-544.	0.7	5