HÃ©lÃ¨ne Touzet

List of Publications by Year
in descending order

22 papers	484 citations	840776 11 h-index	713466 21 g-index
24 all docs	24 docs citations	24 times ranked	1110 citing authors

#	Article	IF	Citations
1	Efficient and accurate P-value computation for Position Weight Matrices. Algorithms for Molecular Biology, 2007, 2, 15.	1.2	109
2	Assessment of Common and Emerging Bioinformatics Pipelines for Targeted Metagenomics. PLoS ONE, 2017, 12, e0169563.	2.5	80
3	CARNAC: folding families of related RNAs. Nucleic Acids Research, 2004, 32, W142-W145.	14.5	54
4	Comparative assessment of long-read error correction software applied to Nanopore RNA-sequencing data. Briefings in Bioinformatics, 2020, 21, 1164-1181.	6.5	33
5	A complete protocol for whole-genome sequencing of virus from clinical samples: Application to coronavirus OC43. Virology, 2019, 531, 141-148.	2.4	28
6	RNAspace.org: An integrated environment for the prediction, annotation, and analysis of ncRNA. Rna, 2011, 17, 1947-1956.	3.5	25
7	Decomposition algorithms for the tree edit distance problem. Journal of Discrete Algorithms, 2005, 3, 448-471.	0.7	22
8	Large Scale Matching for Position Weight Matrices. Lecture Notes in Computer Science, 2006, , 401-412.	1.3	17
9	Efficient approximations of RNA kinetics landscape using non-redundant sampling. Bioinformatics, 2017, 33, i283-i292.	4.1	14
10	miRkwood: a tool for the reliable identification of microRNAs in plant genomes. BMC Genomics, 2019, 20, 532.	2.8	14
11	Comparing similar ordered trees in linear-time. Journal of Discrete Algorithms, 2007, 5, 696-705.	0.7	13
12	Tree edit distance with gaps. Information Processing Letters, 2003, 85, 123-129.	0.6	11
13	Does Hybridization Increase Evolutionary Rate? Data from the 28S-rDNA D8 Domain in Echinoderms. Journal of Molecular Evolution, 2008, 67, 539-550.	1.8	11
14	Modeling Dynamic Programming Problems over Sequences and Trees with Inverse Coupled Rewrite Systems. Algorithms, 2014, 7, 62-144.	2.1	11
15	Self-overlapping Occurrences and Knuth-Morris-Pratt Algorithm for Weighted Matching. Lecture Notes in Computer Science, 2009, , 481-492.	1.3	7
16	Computational identification of protein-coding sequences by comparative analysis. International Journal of Data Mining and Bioinformatics, 2009, 3, 160.	0.1	6
17	RNA Locally Optimal Secondary Structures. Journal of Computational Biology, 2012, 19, 1120-1133.	1.6	6
18	A Characterisation of Multiply Recursive Functions with Higman's Lemma. Information and Computation, 2002, 178, 534-544.	0.7	5

#	Article	IF	Citations
19	Approximate search of short patterns with high error rates using the 01ǎ0 lossless seeds. Journal of Discrete Algorithms, 2016, 37, 3-16.	0.7	5
20	Use of whole-genome sequencing in the molecular investigation of care-associated HCoV-OC43 infections in a hematopoietic stem cell transplant unit. Journal of Clinical Virology, 2020, 122, 104206.	3.1	5
21	Modeling Alternate RNA Structures in Genomic Sequences. Journal of Computational Biology, 2015, 22, 190-204.	1.6	3
22	On the Levenshtein Automaton and the Size of the Neighbourhood of a Word. Lecture Notes in Computer Science, 2016, , 207-218.	1.3	1