Christian HÃ¶ner zu Siederdissen

List of Publications by Year
in descending order

37 papers	4,370 citations	623734 14 h-index	377865 34 g-index
38 all docs	38 docs citations	38 times ranked	7601 citing authors

#	Article	IF	Citations
1	Superbubbles as an empirical characteristic of directed networks. Network Science, 2021, 9, 49-58.	1.0	0
2	Compositional Properties of Alignments. Mathematics in Computer Science, 2021, 15, 609.	0.4	3
3	Selection Pressures on RNA Sequences and Structures. Evolutionary Bioinformatics, 2019, 15, 117693431987191.	1.2	9
4	SSS-test: a novel test for detecting positive selection on RNA secondary structure. BMC Bioinformatics, 2019, 20, 151.	2.6	12
5	flowEMMi: an automated model-based clustering tool for microbial cytometric data. BMC Bioinformatics, 2019, 20, 643.	2.6	16
6	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. Journal of Mathematical Biology, 2018, 77, 313-341.	1.9	1
7	CMV: visualization for RNA and protein family models and their comparisons. Bioinformatics, 2018, 34, 2676-2678.	4.1	5
8	Temporal ordering of substitutions in RNA evolution: Uncovering the structural evolution of the Human Accelerated Region 1. Journal of Theoretical Biology, 2018, 438, 143-150.	1.7	7
9	Coordinate systems for supergenomes. Algorithms for Molecular Biology, 2018, 13, 15.	1.2	10
10	microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3â€² untranslated region: function in replication and influence of RNA secondary structure. Cellular and Molecular Life Sciences, 2017, 74, 747-760.	5.4	28
11	Accurate annotation of protein-coding genes in mitochondrial genomes. Molecular Phylogenetics and Evolution, 2017, 106, 209-216.	2.7	22
12	Algebraic Dynamic Programming on Trees. Algorithms, 2017, 10, 135.	2.1	4
13	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. Algorithms for Molecular Biology, 2017, 12, 22.	1.2	7
14	RNAlien â€“ Unsupervised RNA family model construction. Nucleic Acids Research, 2016, 44, 8433-8441.	14.5	30
15	Algebraic dynamic programming for multiple context-free grammars. Theoretical Computer Science, 2016, 639, 91-109.	0.9	8
16	Algebraic Dynamic Programming over general data structures. BMC Bioinformatics, 2015, 16, S2.	2.6	10
17	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. PLoS ONE, 2015, 10, e0139900.	2.5	11
18	Product Grammars for Alignment and Folding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 507-519.	3.0	12

#	ARTICLE	IF	CITATIONS
19	Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. Nucleic Acids Research, 2015, 43, 8044-8056.	14.5	22
20	Predicting RNA 3D structure using a coarse-grain helix-centered model. Rna, 2015, 21, 1110-1121.	3.5	69
21	Processed Small RNAs in Archaea and BHB Elements. Genomics and Computational Biology, 2015, 1, 18.	0.7	2
22	Dynamic Programming for Set Data Types. Lecture Notes in Computer Science, 2014, , 57-64.	1.3	4
23	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 832-844.	3.0	37
24	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. Nucleic Acids Research, 2013, 41, 9999-10009.	14.5	14
25	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	2.4	27
26	How to Multiply Dynamic Programming Algorithms. Lecture Notes in Computer Science, 2013, , 82-93.	1.3	4
27	Sneaking around concatMap. , 2012, , .		11
28	Sneaking around concatMap. ACM SIGPLAN Notices, 2012, 47, 215-226.	0.2	9
29	Deep sequencing of small RNAs confirms an annelid affinity of Myzostomida. Molecular Phylogenetics and Evolution, 2012, 64, 198-203.	2.7	28
30	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.3	7
31	Semantics and Ambiguity of Stochastic RNA Family Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 499-516.	3.0	13
32	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	1.2	3,719
33	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. Journal of Biotechnology, 2011, 153, 62-75.	3.8	102
34	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	3.1	30
35	A folding algorithm for extended RNA secondary structures. Bioinformatics, 2011, 27, i129-i136.	4.1	59
36	Discriminatory power of RNA family models. Bioinformatics, 2010, 26, i453-i459.	4.1	17

#	Article	IF	Citations
37	Discovering Biomarkers for Myocardial Infarction from SELDI-TOF Spectra. Studies in Classification, Data Analysis, and Knowledge Organization, 2007, , 569-576.	0.2	1