Christian Hner zu Siederdissen

List of Publications by Citations

37 papers	2,880 citations	13 h-index	38 g-index
38 ext. papers	3,789 ext. citations	4.4 avg, IF	4.83 L-index

#	Paper	IF	Citations
37	ViennaRNA Package 2.0. *Algorithms for Molecular Biology*, **2011**, 6, 26	1.8	2351
36	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	3.7	95
35	Predicting RNA 3D structure using a coarse-grain helix-centered model. *Rna*, **2015**, 21, 1110-21	5.8	52
34	A folding algorithm for extended RNA secondary structures. *Bioinformatics*, **2011**, 27, i129-36	7.2	46
33	2D meets 4G: G-quadruplexes in RNA secondary structure prediction. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2013**, 10, 832-44	3	31
32	Animal snoRNAs and scaRNAs with exceptional structures. *RNA Biology*, **2011**, 8, 938-46	4.8	27
31	microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3buntranslated region: function in replication and influence of RNA secondary structure. *Cellular and Molecular Life Sciences*, **2017**, 74, 747-760	10.3	25
30	Deep sequencing of small RNAs confirms an annelid affinity of Myzostomida. *Molecular Phylogenetics and Evolution*, **2012**, 64, 198-203	4.1	23
29	RNAlien - Unsupervised RNA family model construction. *Nucleic Acids Research*, **2016**, 44, 8433-41	20.1	23
28	Computational design of RNAs with complex energy landscapes. *Biopolymers*, **2013**, 99, 1124-36	2.2	22
27	Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. *Nucleic Acids Research*, **2015**, 43, 8044-56	20.1	16
26	Discriminatory power of RNA family models. *Bioinformatics*, **2010**, 26, i453-9	7.2	16
25	Accurate annotation of protein-coding genes in mitochondrial genomes. *Molecular Phylogenetics and Evolution*, **2017**, 106, 209-216	4.1	13
24	Semantics and ambiguity of stochastic RNA family models. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2011**, 8, 499-516	3	12
23	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. *Nucleic Acids Research*, **2013**, 41, 9999-10009	20.1	11
22	Algebraic Dynamic Programming over general data structures. *BMC Bioinformatics*, **2015**, 16 Suppl 19, S2	3.6	10
21	flowEMMi: an automated model-based clustering tool for microbial cytometric data. *BMC Bioinformatics*, **2019**, 20, 643	3.6	10

#	Title		
20	Product Grammars for Alignment and Folding. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2015**, 12, 507-19	3	9
19	Sneaking around concatMap **2012**,		9
18	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. *PLoS ONE*, **2015**, 10, e0139900	3.7	8
17	Coordinate systems for supergenomes. *Algorithms for Molecular Biology*, **2018**, 13, 15	1.8	8
16	SSS-test: a novel test for detecting positive selection on RNA secondary structure. *BMC Bioinformatics*, **2019**, 20, 151	3.6	7
15	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	2.3	7
14	Algebraic dynamic programming for multiple context-free grammars. *Theoretical Computer Science*, **2016**, 639, 91-109	1.1	6
13	Sneaking around concatMap. *ACM SIGPLAN Notices*, **2012**, 47, 215-226	0.2	6
12	RNA Folding Algorithms with G-Quadruplexes. *Lecture Notes in Computer Science*, **2012**, 49-60	0.9	6
11	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. *Algorithms for Molecular Biology*, **2017**, 12, 22	1.8	5
10	CMV: visualization for RNA and protein family models and their comparisons. *Bioinformatics*, **2018**, 34, 2676-2678	7.2	5
9	Selection Pressures on RNA Sequences and Structures. *Evolutionary Bioinformatics*, **2019**, 15, 1176934319871919	2.5	5
8	Dynamic Programming for Set Data Types. *Lecture Notes in Computer Science*, **2014**, 57-64	0.9	4
7	Algebraic Dynamic Programming on Trees. *Algorithms*, **2017**, 10, 135	1.8	3
6	How to Multiply Dynamic Programming Algorithms. *Lecture Notes in Computer Science*, **2013**, 82-93	0.9	3
5	Processed Small RNAs in Archaea and BHB Elements. *Genomics and Computational Biology*, **2015**, 1, 18		2
4	Compositional Properties of Alignments. *Mathematics in Computer Science*, **2021**, 15, 609	0.5	2
3	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. *Journal of Mathematical Biology*, **2018**, 77, 313-341	2	1

2   Discovering Biomarkers for Myocardial Infarction from SELDI-TOF Spectra. *Studies in Classification, Data Analysis, and Knowledge Organization*, **2007**, 569-576   0.2   1

1   Superbubbles as an empirical characteristic of directed networks. *Network Science*, **2021**, 9, 49-58   2.9