

# Christian Hner zu Siederdisen

## List of Publications by Year in Descending Order

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**Version:** 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Compositional Properties of Alignments. <i>Mathematics in Computer Science</i> , <b>2021</b> , 15, 609	0.5	2
36	Superbubbles as an empirical characteristic of directed networks. <i>Network Science</i> , <b>2021</b> , 9, 49-58	2.9	
35	SSS-test: a novel test for detecting positive selection on RNA secondary structure. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 151	3.6	7
34	Selection Pressures on RNA Sequences and Structures. <i>Evolutionary Bioinformatics</i> , <b>2019</b> , 15, 1176934319371919	10.7	19
33	flowEMMi: an automated model-based clustering tool for microbial cytometric data. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 643	3.6	10
32	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. <i>Journal of Mathematical Biology</i> , <b>2018</b> , 77, 313-341	2	1
31	CMV: visualization for RNA and protein family models and their comparisons. <i>Bioinformatics</i> , <b>2018</b> , 34, 2676-2678	7.2	5
30	Temporal ordering of substitutions in RNA evolution: Uncovering the structural evolution of the Human Accelerated Region 1. <i>Journal of Theoretical Biology</i> , <b>2018</b> , 438, 143-150	2.3	7
29	Coordinate systems for supergenomes. <i>Algorithms for Molecular Biology</i> , <b>2018</b> , 13, 15	1.8	8
28	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. <i>Algorithms for Molecular Biology</i> , <b>2017</b> , 12, 22	1.8	5
27	microRNA-122 target sites in the hepatitis C virus RNA NS5B coding region and 3'untranslated region: function in replication and influence of RNA secondary structure. <i>Cellular and Molecular Life Sciences</i> , <b>2017</b> , 74, 747-760	10.3	25
26	Accurate annotation of protein-coding genes in mitochondrial genomes. <i>Molecular Phylogenetics and Evolution</i> , <b>2017</b> , 106, 209-216	4.1	13
25	Algebraic Dynamic Programming on Trees. <i>Algorithms</i> , <b>2017</b> , 10, 135	1.8	3
24	Algebraic dynamic programming for multiple context-free grammars. <i>Theoretical Computer Science</i> , <b>2016</b> , 639, 91-109	1.1	6
23	RNAlien - Unsupervised RNA family model construction. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, 8433-41	20.1	23
22	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 8044-56	20.1	16
21	Predicting RNA 3D structure using a coarse-grain helix-centered model. <i>Rna</i> , <b>2015</b> , 21, 1110-21	5.8	52

20	Algebraic Dynamic Programming over general data structures. <i>BMC Bioinformatics</i> , <b>2015</b> , 16 Suppl 19, S2	3.6	10
19	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. <i>PLoS ONE</i> , <b>2015</b> , 10, e0139900	3.7	8
18	Product Grammars for Alignment and Folding. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2015</b> , 12, 507-19	3	9
17	Processed Small RNAs in Archaea and BHB Elements. <i>Genomics and Computational Biology</i> , <b>2015</b> , 1, 18		2
16	Dynamic Programming for Set Data Types. <i>Lecture Notes in Computer Science</i> , <b>2014</b> , 57-64	0.9	4
15	2D meets 4G: G-quadruplexes in RNA secondary structure prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2013</b> , 10, 832-44	3	31
14	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 9999-10009	20.1	11
13	Computational design of RNAs with complex energy landscapes. <i>Biopolymers</i> , <b>2013</b> , 99, 1124-36	2.2	22
12	How to Multiply Dynamic Programming Algorithms. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 82-93	0.9	3
11	Deep sequencing of small RNAs confirms an annelid affinity of Myzostomida. <i>Molecular Phylogenetics and Evolution</i> , <b>2012</b> , 64, 198-203	4.1	23
10	Sneaking around concatMap <b>2012</b> ,		9
9	Sneaking around concatMap. <i>ACM SIGPLAN Notices</i> , <b>2012</b> , 47, 215-226	0.2	6
8	RNA Folding Algorithms with G-Quadruplexes. <i>Lecture Notes in Computer Science</i> , <b>2012</b> , 49-60	0.9	6
7	ViennaRNA Package 2.0. <i>Algorithms for Molecular Biology</i> , <b>2011</b> , 6, 26	1.8	2351
6	Semantics and ambiguity of stochastic RNA Family models. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2011</b> , 8, 499-516	3	12
5	Next-generation sequencing of the Chinese hamster ovary microRNA transcriptome: Identification, annotation and profiling of microRNAs as targets for cellular engineering. <i>Journal of Biotechnology</i> , <b>2011</b> , 153, 62-75	3.7	95
4	Animal snoRNAs and scaRNAs with exceptional structures. <i>RNA Biology</i> , <b>2011</b> , 8, 938-46	4.8	27
3	A folding algorithm for extended RNA secondary structures. <i>Bioinformatics</i> , <b>2011</b> , 27, i129-36	7.2	46

2	Discriminatory power of RNA family models. <i>Bioinformatics</i> , <b>2010</b> , 26, i453-9	7.2	16
1	Discovering Biomarkers for Myocardial Infarction from SELDI-TOF Spectra. <i>Studies in Classification, Data Analysis, and Knowledge Organization</i> , <b>2007</b> , 569-576	0.2	1