

# Christian HÄjner zu Siederdisen

## List of Publications by Year in descending order

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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	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	1.2	3,719
2	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
3	Predicting RNA 3D structure using a coarse-grain helix-centered model. Rna, 2015, 21, 1110-1121.	3.5	69
4	A folding algorithm for extended RNA secondary structures. Bioinformatics, 2011, 27, i129-i136.	4.1	59
5	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
6	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	3.1	30
7	RNAlien – Unsupervised RNA family model construction. Nucleic Acids Research, 2016, 44, 8433-8441.	14.5	30
8	Deep sequencing of small RNAs confirms an annelid affinity of Myzostomida. Molecular Phylogenetics and Evolution, 2012, 64, 198-203.	2.7	28
9	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. Cellular and Molecular Life Sciences, 2017, 74, 747-760.	5.4	28
10	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	2.4	27
11	Towards a comprehensive picture of alloacceptor tRNA remodeling in metazoan mitochondrial genomes. Nucleic Acids Research, 2015, 43, 8044-8056.	14.5	22
12	Accurate annotation of protein-coding genes in mitochondrial genomes. Molecular Phylogenetics and Evolution, 2017, 106, 209-216.	2.7	22
13	Discriminatory power of RNA family models. Bioinformatics, 2010, 26, i453-i459.	4.1	17
14	flowEMMi: an automated model-based clustering tool for microbial cytometric data. BMC Bioinformatics, 2019, 20, 643.	2.6	16
15	Automated identification of RNA 3D modules with discriminative power in RNA structural alignments. Nucleic Acids Research, 2013, 41, 9999-10009.	14.5	14
16	Semantics and Ambiguity of Stochastic RNA Family Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 499-516.	3.0	13
17	Product Grammars for Alignment and Folding. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 507-519.	3.0	12
18	SSS-test: a novel test for detecting positive selection on RNA secondary structure. BMC Bioinformatics, 2019, 20, 151.	2.6	12

#	ARTICLE	IF	CITATIONS
19	Sneaking around concatMap. , 2012, , .		11
20	RNA 3D Modules in Genome-Wide Predictions of RNA 2D Structure. PLoS ONE, 2015, 10, e0139900.	2.5	11
21	Algebraic Dynamic Programming over general data structures. BMC Bioinformatics, 2015, 16, S2.	2.6	10
22	Coordinate systems for supergenomes. Algorithms for Molecular Biology, 2018, 13, 15.	1.2	10
23	Sneaking around concatMap. ACM SIGPLAN Notices, 2012, 47, 215-226.	0.2	9
24	Selection Pressures on RNA Sequences and Structures. Evolutionary Bioinformatics, 2019, 15, 117693431987191.	1.2	9
25	Algebraic dynamic programming for multiple context-free grammars. Theoretical Computer Science, 2016, 639, 91-109.	0.9	8
26	Partially local three-way alignments and the sequence signatures of mitochondrial genome rearrangements. Algorithms for Molecular Biology, 2017, 12, 22.	1.2	7
27	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
28	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.3	7
29	CMV: visualization for RNA and protein family models and their comparisons. Bioinformatics, 2018, 34, 2676-2678.	4.1	5
30	Algebraic Dynamic Programming on Trees. Algorithms, 2017, 10, 135.	2.1	4
31	Dynamic Programming for Set Data Types. Lecture Notes in Computer Science, 2014, , 57-64.	1.3	4
32	How to Multiply Dynamic Programming Algorithms. Lecture Notes in Computer Science, 2013, , 82-93.	1.3	4
33	Compositional Properties of Alignments. Mathematics in Computer Science, 2021, 15, 609.	0.4	3
34	Processed Small RNAs in Archaea and BHB Elements. Genomics and Computational Biology, 2015, 1, 18.	0.7	2
35	Expansion of gene clusters, circular orders, and the shortest Hamiltonian path problem. Journal of Mathematical Biology, 2018, 77, 313-341.	1.9	1
36	Discovering Biomarkers for Myocardial Infarction from SELDI-TOF Spectra. Studies in Classification, Data Analysis, and Knowledge Organization, 2007, , 569-576.	0.2	1

#	ARTICLE	IF	CITATIONS
37	Superbubbles as an empirical characteristic of directed networks. Network Science, 2021, 9, 49-58.	1.0	0