Ronny Lorenz

List of Publications by Year
in descending order

27 papers	6,631 citations	567144 15 h-index	642610 23 g-index
31 all docs	31 docs citations	31 times ranked	11012 citing authors

#	Article	IF	Citations
1	Efficient Algorithms for Co-folding of Multiple RNAs. Communications in Computer and Information Science, 2021, , 193-214.	0.4	0
2	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. Bioinformatics, 2021, 37, 2126-2133.	1.8	3
3	RNA Secondary Structures with Limited Base Pair Span: Exact Backtracking and an Application. Genes, 2021, 12, 14.	1.0	7
4	Efficient Computation of Base-pairing Probabilities in Multi-strand RNA Folding. , 2020, , .		4
5	RNA modifications in structure prediction â€" Status quo and future challenges. Methods, 2019, 156, 32-39.	1.9	31
6	Evolving AVX512 Parallel C Code Using GP. Lecture Notes in Computer Science, 2019, , 245-261.	1.0	3
7	Evolving Better RNAfold Structure Prediction. Lecture Notes in Computer Science, 2018, , 220-236.	1.0	14
8	Improving SSE parallel code with grow and graft genetic programming. , 2017, , .		8
9	SHAPE directed RNA folding. Bioinformatics, 2016, 32, 145-147.	1.8	91
10	Predicting RNA secondary structures from sequence and probing data. Methods, 2016, 103, 86-98.	1.9	110
11	RNA folding with hard and soft constraints. Algorithms for Molecular Biology, 2016, 11, 8.	0.3	89
12	Model-Free RNA Sequence and Structure Alignment Informed by SHAPE Probing Reveals a Conserved Alternate Secondary Structure for 16S rRNA. PLoS Computational Biology, 2015, 11, e1004126.	1.5	45
13	Design criteria for synthetic riboswitches acting on transcription. RNA Biology, 2015, 12, 221-231.	1.5	41
14	The ViennaRNA Web Services. Methods in Molecular Biology, 2015, 1269, 307-326.	0.4	135
15	Predicting RNA Structure: Advances and Limitations. Methods in Molecular Biology, 2014, 1086, 1-19.	0.4	18
16	TSSAR: TSS annotation regime for dRNA-seq data. BMC Bioinformatics, 2014, 15, 89.	1.2	73
17	2D Meets 4G: G-Quadruplexes in RNA Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 832-844.	1.9	37
18	Folding RNA/DNA hybrid duplexes. Bioinformatics, 2012, 28, 2530-2531.	1.8	17

#	Article	IF	Citations
19	RNA Folding Algorithms with G-Quadruplexes. Lecture Notes in Computer Science, 2012, , 49-60.	1.0	7
20	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
21	Animal snoRNAs and scaRNAs with exceptional structures. RNA Biology, 2011, 8, 938-946.	1.5	30
22	Nematode sbRNAs: Homologs of Vertebrate Y RNAs. Journal of Molecular Evolution, 2010, 70, 346-358.	0.8	32
23	A novel view on stem cell development: analysing the shape of cellular genealogies. Cell Proliferation, 2009, 42, 248-263.	2.4	28
24	The Vienna RNA Websuite. Nucleic Acids Research, 2008, 36, W70-W74.	6.5	2,012
25	Stem Cell Fate Analysis Revisited: Interpretation of Individual Clone Dynamics in the Light of a New Paradigm of Stem Cell Organization. Journal of Biomedicine and Biotechnology, 2007, 2007, 1-9.	3.0	15
26	Asymmetry of stem cell fate and the potential impact of the niche. Stem Cell Reviews and Reports, 2006, 2, 171-180.	5.6	44
27	Caveats to Deep Learning Approaches to RNA Secondary Structure Prediction. Frontiers in Bioinformatics, 0, 2, .	1.0	11