Robert Giegerich

List of Publications by Year
in descending order

66 papers	5,678 citations	218677 26 h-index	123424 61 g-index
67 all docs	67 docs citations	67 times ranked	7149 citing authors

#	Article	IF	Citations
1	Fast and effective prediction of microRNA/target duplexes. Rna, 2004, 10, 1507-1517.	3.5	2,157
2	GenDB--an open source genome annotation system for prokaryote genomes. Nucleic Acids Research, 2003, 31, 2187-2195.	14.5	644
3	A comprehensive comparison of comparative RNA structure prediction approaches. BMC Bioinformatics, 2004, 5, 140.	2.6	291
4	RNAshapes: an integrated RNA analysis package based on abstract shapes. Bioinformatics, 2006, 22, 500-503.	4.1	272
5	Design, implementation and evaluation of a practical pseudoknot folding algorithm based on thermodynamics. BMC Bioinformatics, 2004, 5, 104.	2.6	248
6	Abstract shapes of RNA. Nucleic Acids Research, 2004, 32, 4843-4851.	14.5	179
7	Global mapping of transcription start sites and promoter motifs in the symbiotic Î±-proteobacterium Sinorhizobium meliloti1021. BMC Genomics, 2013, 14, 156.	2.8	163
8	Pure multiple RNA secondary structure alignments: a progressive profile approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2004, 1, 53-62.	3.0	122
9	The RNA shapes studio. Bioinformatics, 2015, 31, 423-425.	4.1	113
10	A genome-wide survey of sRNAs in the symbiotic nitrogen-fixing alpha-proteobacterium Sinorhizobium meliloti. BMC Genomics, 2010, 11, 245.	2.8	104
11	Consensus shapes: an alternative to the Sankoff algorithm for RNA consensus structure prediction. Bioinformatics, 2005, 21, 3516-3523.	4.1	88
12	A discipline of dynamic programming over sequence data. Science of Computer Programming, 2004, 51, 215-263.	1.9	75
13	PathFinder: reconstruction and dynamic visualization of metabolic pathways. Bioinformatics, 2002, 18, 124-129.	4.1	66
14	Complete probabilistic analysis of RNA shapes. BMC Biology, 2006, 4, 5.	3.8	66
15	Genome-wide profiling of Hfq-binding RNAs uncovers extensive post-transcriptional rewiring of major stress response and symbiotic regulons in<i>Sinorhizobium meliloti</i>. RNA Biology, 2014, 11, 563-579.	3.1	65
16	Table design in dynamic programming. Information and Computation, 2006, 204, 1325-1345.	0.7	63
17	KnotInFrame: prediction of â˜'1 ribosomal frameshift events. Nucleic Acids Research, 2008, 36, 6013-6020.	14.5	61
18	Beyond Mfold: Recent advances in RNA bioinformatics. Journal of Biotechnology, 2006, 124, 41-55.	3.8	59

#	ARTICLE	IF	CITATIONS
19	GUUGle: a utility for fast exact matching under RNA complementary rules including G-U base pairing. Bioinformatics, 2006, 22, 762-764.	4.1	54
20	Evaluating the predictability of conformational switching in RNA. Bioinformatics, 2004, 20, 1573-1582.	4.1	49
21	Composition and evaluation of attribute coupled grammars. Acta Informatica, 1988, 25, 355-423.	0.5	47
22	Riboregulation in plant-associated Î±-proteobacteria. RNA Biology, 2014, 11, 550-562.	3.1	43
23	Attribute coupled grammars. ACM SIGPLAN Notices, 1984, 19, 157-170.	0.2	37
24	Locomotif: from graphical motif description to RNA motif search. Bioinformatics, 2007, 23, i392-i400.	4.1	36
25	A truly generative semantics-directed compiler generator. , 1982, , .		34
26	GeneFisher-P: variations of GeneFisher as processes in Bio-jETI. BMC Bioinformatics, 2008, 9, S13.	2.6	34
27	Conservation and Occurrence of Trans-Encoded sRNAs in the Rhizobiales. Genes, 2011, 2, 925-956.	2.4	29
28	Versatile and declarative dynamic programming using pair algebras. BMC Bioinformatics, 2005, 6, 224.	2.6	25
29	XML schemas for common bioinformatic data types and their application in workflow systems. BMC Bioinformatics, 2006, 7, 490.	2.6	25
30	Analyzing ambiguity of context-free grammars. Science of Computer Programming, 2010, 75, 176-191.	1.9	24
31	Lost in folding space? Comparing four variants of the thermodynamic model for RNA secondary structure prediction. BMC Bioinformatics, 2011, 12, 429.	2.6	24
32	Shape based indexing for faster search of RNA family databases. BMC Bioinformatics, 2008, 9, 131.	2.6	23
33	A Formal Framework for the Derivation of Machine-Specific Optimizers. ACM Transactions on Programming Languages and Systems, 1983, 5, 478-498.	2.1	22
34	Faster computation of exact RNA shape probabilities. Bioinformatics, 2010, 26, 632-639.	4.1	21
35	Code selection techniques: Pattern matching, tree parsing, and inversion of derivors. Lecture Notes in Computer Science, 1988, , 247-268.	1.3	21
36	Personalized cloud-based bioinformatics services for research and education: use cases and the elasticHPC package. BMC Bioinformatics, 2012, 13, S22.	2.6	20

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37	Effective ambiguity checking in biosequence analysis. BMC Bioinformatics, 2005, 6, 153.	2.6	19
38	RNA-related tools on the Bielefeld Bioinformatics Server. Nucleic Acids Research, 2003, 31, 3767-3770.	14.5	17
39	Algebraic Dynamic Programming. Lecture Notes in Computer Science, 2002, , 349-364.	1.3	17
40	Prediction of RNA Secondary Structure Including Kissing Hairpin Motifs. Lecture Notes in Computer Science, 2010, , 52-64.	1.3	16
41	Bellman's GAP—a language and compiler for dynamic programming in sequence analysis. Bioinformatics, 2013, 29, 551-560.	4.1	15
42	Explaining and Controlling Ambiguity in Dynamic Programming. Lecture Notes in Computer Science, 2000, , 46-59.	1.3	14
43	Semantics and Ambiguity of Stochastic RNA Family Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 499-516.	3.0	13
44	Bellman's GAP. , 2011, , .		13
45	Pareto optimization in algebraic dynamic programming. Algorithms for Molecular Biology, 2015, 10, 22.	1.2	13
46	Thermodynamic matchers for the construction of the cuckoo RNA family. RNA Biology, 2015, 12, 197-207.	3.1	13
47	Fine-tuning structural RNA alignments in the twilight zone. BMC Bioinformatics, 2010, 11, 222.	2.6	12
48	GPU Parallelization of Algebraic Dynamic Programming. Lecture Notes in Computer Science, 2010, , 290-299.	1.3	12
49	Modeling Dynamic Programming Problems over Sequences and Trees with Inverse Coupled Rewrite Systems. Algorithms, 2014, 7, 62-144.	2.1	11
50	Forest alignment with affine gaps and anchors, applied in RNA structure comparison. Theoretical Computer Science, 2013, 483, 51-67.	0.9	10
51	Introduction to Stochastic Context Free Grammars. Methods in Molecular Biology, 2014, 1097, 85-106.	0.9	9
52	The BRaliBase dent—a tale of benchmark design and interpretation. Briefings in Bioinformatics, 2017, 18, bbw022.	6.5	8
53	Forest Alignment with Affine Gaps and Anchors. Lecture Notes in Computer Science, 2011, , 104-117.	1.3	8
54	Introduction to RNA Secondary Structure Comparison. Methods in Molecular Biology, 2014, 1097, 247-273.	0.9	7

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55	Analyzing Ambiguity of Context-Free Grammars. , 2007, , 214-225.		7
56	Matching and Significance Evaluation of Combined Sequence-Structure Motifs in RNA. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	2.8	6
57	Implementing Algebraic Dynamic Programming in the Functional and the Imperative Programming Paradigm. Lecture Notes in Computer Science, 2002, , 1-20.	1.3	6
58	R NA Secondary Structure Analysis Using The RNAshapes Package. Current Protocols in Bioinformatics, 2009, 26, Unit12.8.	25.8	5
59	Integrating Pareto Optimization into Dynamic Programming. Algorithms, 2016, 9, 12.	2.1	5
60	Ambivalent covariance models. BMC Bioinformatics, 2015, 16, 178.	2.6	4
61	A graphical programming system for molecular motif search. , 2006, , .		3
62	Yield grammar analysis and product optimization in a domain-specific language for dynamic programming. Science of Computer Programming, 2014, 87, 2-22.	1.9	3
63	Considerate Code Selection. Workshops in Computing, 1992, , 51-65.	0.4	3
64	Abstract Shape Analysis of RNA. Methods in Molecular Biology, 2014, 1097, 215-245.	0.9	3
65	A Silent Exonic SNP in Kdm3a Affects Nucleic Acids Structure but Does Not Regulate Experimental Autoimmune Encephalomyelitis. PLoS ONE, 2013, 8, e81912.	2.5	1
66	The BREW workshop series: a stimulating experience in PhD education. Briefings in Bioinformatics, 2008, 9, 250-253.	6.5	0