

# Robert Giegerich

## List of Publications by Year in descending order

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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	The BRaliBase dentâ€™a tale of benchmark design and interpretation. Briefings in Bioinformatics, 2017, 18, bbw022.	6.5	8
2	Integrating Pareto Optimization into Dynamic Programming. Algorithms, 2016, 9, 12.	2.1	5
3	Pareto optimization in algebraic dynamic programming. Algorithms for Molecular Biology, 2015, 10, 22.	1.2	13
4	Thermodynamic matchers for the construction of the cuckoo RNA family. RNA Biology, 2015, 12, 197-207.	3.1	13
5	Ambivalent covariance models. BMC Bioinformatics, 2015, 16, 178.	2.6	4
6	The RNA shapes studio. Bioinformatics, 2015, 31, 423-425.	4.1	113
7	Modeling Dynamic Programming Problems over Sequences and Trees with Inverse Coupled Rewrite Systems. Algorithms, 2014, 7, 62-144.	2.1	11
8	Riboregulation in plant-associated Î±-proteobacteria. RNA Biology, 2014, 11, 550-562.	3.1	43
9	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
10	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
11	Abstract Shape Analysis of RNA. Methods in Molecular Biology, 2014, 1097, 215-245.	0.9	3
12	Introduction to RNA Secondary Structure Comparison. Methods in Molecular Biology, 2014, 1097, 247-273.	0.9	7
13	Introduction to Stochastic Context Free Grammars. Methods in Molecular Biology, 2014, 1097, 85-106.	0.9	9
14	Bellmanâ€™s GAPâ€™a language and compiler for dynamic programming in sequence analysis. Bioinformatics, 2013, 29, 551-560.	4.1	15
15	Forest alignment with affine gaps and anchors, applied in RNA structure comparison. Theoretical Computer Science, 2013, 483, 51-67.	0.9	10
16	Global mapping of transcription start sites and promoter motifs in the symbiotic Î±-proteobacterium <i>Sinorhizobium meliloti</i> 1021. BMC Genomics, 2013, 14, 156.	2.8	163
17	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
18	Personalized cloud-based bioinformatics services for research and education: use cases and the elasticHPC package. BMC Bioinformatics, 2012, 13, S22.	2.6	20

#	ARTICLE	IF	CITATIONS
19	Semantics and Ambiguity of Stochastic RNA Family Models. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 499-516.	3.0	13
20	Conservation and Occurrence of Trans-Encoded sRNAs in the Rhizobiales. Genes, 2011, 2, 925-956.	2.4	29
21	Lost in folding space? Comparing four variants of the thermodynamic model for RNA secondary structure prediction. BMC Bioinformatics, 2011, 12, 429.	2.6	24
22	Bellman's GAP. , 2011, , .		13
23	Forest Alignment with Affine Gaps and Anchors. Lecture Notes in Computer Science, 2011, , 104-117.	1.3	8
24	Fine-tuning structural RNA alignments in the twilight zone. BMC Bioinformatics, 2010, 11, 222.	2.6	12
25	A genome-wide survey of sRNAs in the symbiotic nitrogen-fixing alpha-proteobacterium Sinorhizobium meliloti. BMC Genomics, 2010, 11, 245.	2.8	104
26	Analyzing ambiguity of context-free grammars. Science of Computer Programming, 2010, 75, 176-191.	1.9	24
27	Faster computation of exact RNA shape probabilities. Bioinformatics, 2010, 26, 632-639.	4.1	21
28	GPU Parallelization of Algebraic Dynamic Programming. Lecture Notes in Computer Science, 2010, , 290-299.	1.3	12
29	Prediction of RNA Secondary Structure Including Kissing Hairpin Motifs. Lecture Notes in Computer Science, 2010, , 52-64.	1.3	16
30	RNA Secondary Structure Analysis Using The RNASHAPES Package. Current Protocols in Bioinformatics, 2009, 26, Unit12.8.	25.8	5
31	Shape based indexing for faster search of RNA family databases. BMC Bioinformatics, 2008, 9, 131.	2.6	23
32	GeneFisher-P: variations of GeneFisher as processes in Bio-jETI. BMC Bioinformatics, 2008, 9, S13.	2.6	34
33	KnotInFrame: prediction of $\pm 1$ ribosomal frameshift events. Nucleic Acids Research, 2008, 36, 6013-6020.	14.5	61
34	The BREW workshop series: a stimulating experience in PhD education. Briefings in Bioinformatics, 2008, 9, 250-253.	6.5	0
35	Locomotif: from graphical motif description to RNA motif search. Bioinformatics, 2007, 23, i392-i400.	4.1	36
36	Analyzing Ambiguity of Context-Free Grammars. , 2007, , 214-225.		7

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37	Beyond Mfold: Recent advances in RNA bioinformatics. <i>Journal of Biotechnology</i> , 2006, 124, 41-55.	3.8	59
38	Complete probabilistic analysis of RNA shapes. <i>BMC Biology</i> , 2006, 4, 5.	3.8	66
39	Table design in dynamic programming. <i>Information and Computation</i> , 2006, 204, 1325-1345.	0.7	63
40	XML schemas for common bioinformatic data types and their application in workflow systems. <i>BMC Bioinformatics</i> , 2006, 7, 490.	2.6	25
41	GUUGle: a utility for fast exact matching under RNA complementary rules including G-U base pairing. <i>Bioinformatics</i> , 2006, 22, 762-764.	4.1	54
42	A graphical programming system for molecular motif search. , 2006, , .		3
43	RNASHAPES: an integrated RNA analysis package based on abstract shapes. <i>Bioinformatics</i> , 2006, 22, 500-503.	4.1	272
44	Effective ambiguity checking in biosequence analysis. <i>BMC Bioinformatics</i> , 2005, 6, 153.	2.6	19
45	Versatile and declarative dynamic programming using pair algebras. <i>BMC Bioinformatics</i> , 2005, 6, 224.	2.6	25
46	Consensus shapes: an alternative to the Sankoff algorithm for RNA consensus structure prediction. <i>Bioinformatics</i> , 2005, 21, 3516-3523.	4.1	88
47	Abstract shapes of RNA. <i>Nucleic Acids Research</i> , 2004, 32, 4843-4851.	14.5	179
48	Fast and effective prediction of microRNA/target duplexes. <i>Rna</i> , 2004, 10, 1507-1517.	3.5	2,157
49	Evaluating the predictability of conformational switching in RNA. <i>Bioinformatics</i> , 2004, 20, 1573-1582.	4.1	49
50	Design, implementation and evaluation of a practical pseudoknot folding algorithm based on thermodynamics. <i>BMC Bioinformatics</i> , 2004, 5, 104.	2.6	248
51	A comprehensive comparison of comparative RNA structure prediction approaches. <i>BMC Bioinformatics</i> , 2004, 5, 140.	2.6	291
52	A discipline of dynamic programming over sequence data. <i>Science of Computer Programming</i> , 2004, 51, 215-263.	1.9	75
53	Pure multiple RNA secondary structure alignments: a progressive profile approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2004, 1, 53-62.	3.0	122
54	GenDB--an open source genome annotation system for prokaryote genomes. <i>Nucleic Acids Research</i> , 2003, 31, 2187-2195.	14.5	644

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55	RNA-related tools on the Bielefeld Bioinformatics Server. Nucleic Acids Research, 2003, 31, 3767-3770.	14.5	17
56	PathFinder: reconstruction and dynamic visualization of metabolic pathways. Bioinformatics, 2002, 18, 124-129.	4.1	66
57	Matching and Significance Evaluation of Combined Sequence-Structure Motifs in RNA. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	2.8	6
58	Implementing Algebraic Dynamic Programming in the Functional and the Imperative Programming Paradigm. Lecture Notes in Computer Science, 2002, , 1-20.	1.3	6
59	Algebraic Dynamic Programming. Lecture Notes in Computer Science, 2002, , 349-364.	1.3	17
60	Explaining and Controlling Ambiguity in Dynamic Programming. Lecture Notes in Computer Science, 2000, , 46-59.	1.3	14
61	Considerate Code Selection. Workshops in Computing, 1992, , 51-65.	0.4	3
62	Composition and evaluation of attribute coupled grammars. Acta Informatica, 1988, 25, 355-423.	0.5	47
63	Code selection techniques: Pattern matching, tree parsing, and inversion of derivors. Lecture Notes in Computer Science, 1988, , 247-268.	1.3	21
64	Attribute coupled grammars. ACM SIGPLAN Notices, 1984, 19, 157-170.	0.2	37
65	A Formal Framework for the Derivation of Machine-Specific Optimizers. ACM Transactions on Programming Languages and Systems, 1983, 5, 478-498.	2.1	22
66	A truly generative semantics-directed compiler generator. , 1982, , .		34