Christoph Flamm

List of Publications by Year
in descending order

72 papers	11,217 citations	218592 26 h-index	98753 67 g-index
76 all docs	76 docs citations	76 times ranked	16908 citing authors

#	Article	IF	Citations
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	13.7	4,709
2	ViennaRNA Package 2.0. Algorithms for Molecular Biology, 2011, 6, 26.	0.3	3,719
3	The expansion of the metazoan microRNA repertoire. BMC Genomics, 2006, 7, 25.	1.2	304
4	RNA folding at elementary step resolution. Rna, 2000, 6, 325-338.	1.6	266
5	Partition function and base pairing probabilities of RNA heterodimers. Algorithms for Molecular Biology, 2006, 1, 3.	0.3	239
6	Noisy: Identification of problematic columns in multiple sequence alignments. Algorithms for Molecular Biology, 2008, 3, 7.	0.3	154
7	Design of multistable RNA molecules. Rna, 2001, 7, 254-265.	1.6	138
8	Barrier Trees of Degenerate Landscapes. Zeitschrift Fur Physikalische Chemie, 2002, 216, .	1.4	130
9	Automatic detection of conserved RNA structure elements in complete RNA virus genomes. Nucleic Acids Research, 1998, 26, 3825-3836.	6.5	115
10	Efficient computation of RNA folding dynamics. Journal of Physics A, 2004, 37, 4731-4741.	1.6	99
11	Inverse problems in systems biology. Inverse Problems, 2009, 25, 123014.	1.0	94
12	The SBML ODE Solver Library: a native API for symbolic and fast numerical analysis of reaction networks. Bioinformatics, 2006, 22, 1406-1407.	1.8	88
13	A generalized model of the repressilator. Journal of Mathematical Biology, 2006, 53, 905-937.	0.8	86
14	A Graph-Based Toy Model of Chemistry. Journal of Chemical Information and Computer Sciences, 2003, 43, 1085-1093.	2.8	82
15	Folding Kinetics of Large RNAs. Journal of Molecular Biology, 2008, 379, 160-173.	2.0	77
16	Evolutionary patterns of non-coding RNAs. Theory in Biosciences, 2005, 123, 301-369.	0.6	64
17	BarMap: RNA folding on dynamic energy landscapes. Rna, 2010, 16, 1308-1316.	1.6	53
18	Determination of thermodynamic parameters for HIV DIS type loop-loop kissing complexes. Nucleic Acids Research, 2004, 32, 5126-5133.	6.5	50

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19	Beyond energy minimization: approaches to the kinetic folding of RNA. Monatshefte FÃ¼r Chemie, 2008, 139, 447-457.	0.9	49
20	RNAs everywhere: genome-wide annotation of structured RNAs. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2007, 308B, 1-25.	0.6	46
21	Surveying phylogenetic footprints in large gene clusters: applications to Hox cluster duplications. Molecular Phylogenetics and Evolution, 2004, 31, 581-604.	1.2	45
22	Maximizing output and recognizing autocatalysis in chemical reaction networks is NP-complete. Journal of Systems Chemistry, 2012, 3, .	1.7	39
23	Navigating the Chemical Space of HCN Polymerization and Hydrolysis: Guiding Graph Grammars by Mass Spectrometry Data. Entropy, 2013, 15, 4066-4083.	1.1	38
24	Algebraic comparison of metabolic networks, phylogenetic inference, and metabolic innovation. BMC Bioinformatics, 2006, 7, 67.	1.2	33
25	A Software Package for Chemically Inspired Graph Transformation. Lecture Notes in Computer Science, 2016, , 73-88.	1.0	31
26	Chemical Transformation Motifsâ€"Modelling Pathways as Integer Hyperflows. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 510-523.	1.9	31
27	Inferring chemical reaction patterns using rule composition in graph grammars. Journal of Systems Chemistry, 2013, 4, .	1.7	28
28	Computational design of RNAs with complex energy landscapes. Biopolymers, 2013, 99, n/a-n/a.	1.2	27
29	Generic strategies for chemical space exploration. International Journal of Computational Biology and Drug Design, 2014, 7, 225.	0.3	26
30	Barrier Trees on Poset-Valued Landscapes. Genetic Programming and Evolvable Machines, 2003, 4, 7-20.	1.5	19
31	Thermodynamic and Kinetic Folding of Riboswitches. Methods in Enzymology, 2015, 553, 193-213.	0.4	19
32	Sequence-controlled RNA self-processing: computational design, biochemical analysis, and visualization by AFM. Rna, 2015, 21, 1249-1260.	1.6	18
33	RNAblueprint: flexible multiple target nucleic acid sequence design. Bioinformatics, 2017, 33, 2850-2858.	1.8	17
34	A Topological Approach to Chemical Organizations. Artificial Life, 2009, 15, 71-88.	1.0	15
35	Evolution of metabolic networks: a computational frame-work. Journal of Systems Chemistry, 2010, 1, 4.	1.7	15
36	Atom mapping with constraint programming. Algorithms for Molecular Biology, 2014, 9, 23.	0.3	14

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37	In silico design of ligand triggered RNA switches. Methods, 2018, 143, 90-101.	1.9	14
38	Visualization of Barrier Tree Sequences. IEEE Transactions on Visualization and Computer Graphics, 2006, 12, 781-788.	2.9	13
39	An intermediate level of abstraction for computational systems chemistry. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2017, 375, 20160354.	1.6	13
40	RNA structure prediction: from 2D to 3D. Emerging Topics in Life Sciences, 2017, 1, 275-285.	1.1	13
41	Efficient computation of co-transcriptional RNA-ligand interaction dynamics. Methods, 2018, 143, 70-76.	1.9	13
42	Physiological environment induces quick response â€“ slow exhaustion reactions. Frontiers in Physiology, 2011, 2, 50.	1.3	12
43	â€œMinimal metabolismâ€: A key concept to investigate the origins and nature of biological systems. BioEssays, 2021, 43, e2100103.	1.2	11
44	Caveats to Deep Learning Approaches to RNA Secondary Structure Prediction. Frontiers in Bioinformatics, 0, 2, .	1.0	11
45	In Silico Evolution of Early Metabolism. Artificial Life, 2011, 17, 87-108.	1.0	10
46	Memory-efficient RNA energy landscape exploration. Bioinformatics, 2014, 30, 2584-2591.	1.8	10
47	In silico Support for Eschenmoserâ€™s Glyoxylate Scenario. Israel Journal of Chemistry, 2015, 55, 919-933.	1.0	10
48	Saddles and Barrier in Landscapes of Generalized Search Operators. Lecture Notes in Computer Science, 2007, , 194-212.	1.0	10
49	Modelling Translation Initiation under the Influence of sRNA. International Journal of Molecular Sciences, 2012, 13, 16223-16240.	1.8	9
50	Finding the K best synthesis plans. Journal of Cheminformatics, 2018, 10, 19.	2.8	9
51	50 Shades of Rule Composition. Lecture Notes in Computer Science, 2014, , 117-135.	1.0	9
52	The Graph Grammar Library - A Generic Framework for Chemical Graph Rewrite Systems. Lecture Notes in Computer Science, 2013, , 52-53.	1.0	8
53	A minimal and self-consistent in silico cell model based on macromolecular interactions. Philosophical Transactions of the Royal Society B: Biological Sciences, 2007, 362, 1831-1839.	1.8	7
54	EHreact: Extended Hasse Diagrams for the Extraction and Scoring of Enzymatic Reaction Templates. Journal of Chemical Information and Modeling, 2021, 61, 4949-4961.	2.5	7

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55	Chemical Graph Transformation with Stereo-Information. Lecture Notes in Computer Science, 2017, , 54-69.	1.0	7
56	Graph transformation for enzymatic mechanisms. Bioinformatics, 2021, 37, i392-i400.	1.8	5
57	Exploring Plant Sesquiterpene Diversity by Generating Chemical Networks. Processes, 2019, 7, 240.	1.3	4
58	Efficient Computation of Base-pairing Probabilities in Multi-strand RNA Folding. , 2020, , .		4
59	Computational Design of a Circular RNA with Prionlike Behavior. Artificial Life, 2016, 22, 172-184.	1.0	3
60	Practical Guidelines for Incorporating Knowledge-Based and Data-Driven Strategies into the Inference of Gene Regulatory Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 64-75.	1.9	3
61	Exploring Chemistry Using SMT. Lecture Notes in Computer Science, 2012, , 900-915.	1.0	3
62	On the Complexity of Reconstructing Chemical Reaction Networks. Mathematics in Computer Science, 2013, 7, 275-292.	0.2	2
63	Automatic Inference of Graph Transformation Rules Using the Cyclic Nature of Chemical Reactions. Lecture Notes in Computer Science, 2016, , 206-222.	1.0	2
64	Atom Mapping with Constraint Programming. Lecture Notes in Computer Science, 2013, , 805-822.	1.0	2
65	Functional Evolution of Ribozyme-Catalyzed Metabolisms in a Graph-Based Toy-Universe. Lecture Notes in Computer Science, 2008, , 28-43.	1.0	2
66	Generic Context-Aware Group Contributions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 429-442.	1.9	1
67	CelloS: A Multi-level Approach to Evolutionary Dynamics. Lecture Notes in Computer Science, 2005, , 500-509.	1.0	1
68	Visualization of Barrier Tree Sequences Revisited. Mathematics and Visualization, 2008, , 275-290.	0.4	1
69	Towards an Optimal DNA-Templated Molecular Assembler. , 0, , .		1
70	Efficient Algorithms for Co-folding of Multiple RNAs. Communications in Computer and Information Science, 2021, , 193-214.	0.4	0
71	A Sequence-to-Function Map for Ribozyme-Catalyzed Metabolisms. Lecture Notes in Computer Science, 2011, , 19-26.	1.0	0
72	Computational Simulations for Cyclizations Catalyzed by Plant Monoterpene Synthases. Lecture Notes in Computer Science, 2020, , 247-258.	1.0	0