Yann Ponty

List of Publications by Year
in descending order

61 papers	2,035 citations	567281 15 h-index	276875 41 g-index
70 all docs	70 docs citations	70 times ranked	2814 citing authors

#	Article	IF	Citations
1	VARNA: Interactive drawing and editing of the RNA secondary structure. Bioinformatics, 2009, 25, 1974-1975.	4.1	1,094
2	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. Bioinformatics, 2016, 32, 2056-2058.	4.1	98
3	The SARS-CoV-2 subgenome landscape and its novel regulatory features. Molecular Cell, 2021, 81, 2135-2147.e5.	9.7	72
4	GenRGenS: software for generating random genomic sequences and structures. Bioinformatics, 2006, 22, 1534-1535.	4.1	62
5	DIAL: a web server for the pairwise alignment of two RNA three-dimensional structures using nucleotide, dihedral angle and base-pairing similarities. Nucleic Acids Research, 2007, 35, W659-W668.	14.5	55
6	Effective Rotation-Invariant Point CNN with Spherical Harmonics Kernels. , 2019, , .		53
7	Protein-Protein Interactions in a Crowded Environment: An Analysis via Cross-Docking Simulations and Evolutionary Information. PLoS Computational Biology, 2013, 9, e1003369.	3.2	48
8	A weighted sampling algorithm for the design of RNA sequences with targeted secondary structure and nucleotide distribution. Bioinformatics, 2013, 29, i308-i315.	4.1	38
9	Design of RNAs: comparing programs for inverse RNA folding. Briefings in Bioinformatics, 2018, 19, bbw120.	6.5	35
10	A global sampling approach to designing and reengineering RNA secondary structures. Nucleic Acids Research, 2012, 40, 10041-10052.	14.5	32
11	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. Genome Biology and Evolution, 2017, 9, 1312-1319.	2.5	32
12	Asymptotics of RNA Shapes. Journal of Computational Biology, 2008, 15, 31-63.	1.6	30
13	Expected distance between terminal nucleotides of RNA secondary structures. Journal of Mathematical Biology, 2012, 65, 581-599.	1.9	30
14	Efficient sampling of RNA secondary structures from the Boltzmann ensemble of low-energy. Journal of Mathematical Biology, 2007, 56, 107-127.	1.9	29
15	Two ribosome recruitment sites direct multiple translation events within HIV1 Gag open reading frame. Nucleic Acids Research, 2017, 45, 7382-7400.	14.5	28
16	Using the Fast Fourier Transform to Accelerate the Computational Search for RNA Conformational Switches. PLoS ONE, 2012, 7, e50506.	2.5	19
17	Controlled non-uniform random generation of decomposable structures. Theoretical Computer Science, 2010, 411, 3527-3552.	0.9	15
18	Estimating seed sensitivity on homogeneous alignments. , 0, , .		14

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19	Efficient approximations of RNA kinetics landscape using non-redundant sampling. Bioinformatics, 2017, 33, i283-i292.	4.1	14
20	An Unbiased Adaptive Sampling Algorithm for the Exploration of RNA Mutational Landscapes Under Evolutionary Pressure. Journal of Computational Biology, 2011, 18, 1465-1479.	1.6	13
21	Impact of the Energy Model on the Complexity of RNA Folding with Pseudoknots. Lecture Notes in Computer Science, 2012, , 321-333.	1.3	13
22	SPARCS: a web server to analyze (un)structured regions in coding RNA sequences. Nucleic Acids Research, 2013, 41, W480-W485.	14.5	13
23	Fixed-parameter tractable sampling for RNA design with multiple target structures. BMC Bioinformatics, 2019, 20, 209.	2.6	13
24	Drawing and Editing the Secondary Structure(s) of RNA. Methods in Molecular Biology, 2015, 1269, 63-100.	0.9	12
25	Multi-dimensional Boltzmann Sampling of Languages. Discrete Mathematics and Theoretical Computer Science, 2010, DMTCS Proceedings vol. AM,..., .	0.1	12
26	Combinatorial RNA Design: Designability and Structure-Approximating Algorithm in Watson–Crick and Nussinov–Jacobson Energy Models. Algorithmica, 2017, 79, 835-856.	1.3	11
27	A Combinatorial Framework for Designing (Pseudoknotted) RNA Algorithms. Lecture Notes in Computer Science, 2011, , 250-269.	1.3	11
28	Evolution of genes neighborhood within reconciled phylogenies: an ensemble approach. BMC Bioinformatics, 2015, 16, S6.	2.6	10
29	<tt>incaRNAfbinv</tt>: a web server for the fragment-based design of RNA sequences. Nucleic Acids Research, 2016, 44, W308-W314.	14.5	10
30	IPANEMAP: integrative probing analysis of nucleic acids empowered by multiple accessibility profiles. Nucleic Acids Research, 2020, 48, 8276-8289.	14.5	9
31	LocalMove: computing on-lattice fits for biopolymers. Nucleic Acids Research, 2008, 36, W216-W222.	14.5	8
32	The BRaliBase dent—a tale of benchmark design and interpretation. Briefings in Bioinformatics, 2017, 18, bbw022.	6.5	8
33	Tree Decomposition and Parameterized Algorithms for RNA Structure-Sequence Alignment Including Tertiary Interactions and Pseudoknots. Lecture Notes in Computer Science, 2012, , 149-164.	1.3	8
34	Introduction to RNA Secondary Structure Comparison. Methods in Molecular Biology, 2014, 1097, 247-273.	0.9	7
35	Reference-free transcriptome signatures for prostate cancer prognosis. BMC Cancer, 2021, 21, 394.	2.6	6
36	Progress toward SHAPE Constrained Computational Prediction of Tertiary Interactions in RNA Structure. Non-coding RNA, 2021, 7, 71.	2.6	6

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37	Flexible RNA design under structure and sequence constraints using formal languages. , 2013, , .		5
38	Combining structure probing data on RNA mutants with evolutionary information reveals RNA-binding interfaces. Nucleic Acids Research, 2016, 44, e104-e104.	14.5	5
39	Stochastic Sampling of Structural Contexts Improves the Scalability and Accuracy of RNA 3D Module Identification. Lecture Notes in Computer Science, 2020, , 186-201.	1.3	4
40	Meet-U: Educating through research immersion. PLoS Computational Biology, 2018, 14, e1005992.	3.2	4
41	The weighted words collector. Discrete Mathematics and Theoretical Computer Science, 2012, DMTCS Proceedings vol. AQ,..., .	0.1	4
42	Non-redundant random generation algorithms for weighted context-free grammars. Theoretical Computer Science, 2013, 502, 177-194.	0.9	3
43	Counting, Generating, Analyzing and Sampling Tree Alignments. International Journal of Foundations of Computer Science, 2018, 29, 741-767.	1.1	3
44	RNAxplorer: harnessing the power of guiding potentials to sample RNA landscapes. Bioinformatics, 2021, 37, 2126-2133.	4.1	3
45	Combinatorial RNA Design: Designability and Structure-Approximating Algorithm. Lecture Notes in Computer Science, 2015, , 231-246.	1.3	3
46	Small-World Networks and RNA Secondary Structures. Journal of Computational Biology, 2019, 26, 16-26.	1.6	2
47	Counting and sampling gene family evolutionary histories in the duplication-loss and duplication-loss-transfer models. Journal of Mathematical Biology, 2020, 80, 1353-1388.	1.9	2
48	<tt>incaRNAfbinv 2.0</tt>: a webserver and software with motif control for fragment-based design of RNAs. Bioinformatics, 2020, 36, 2920-2922.	4.1	2
49	Evolution of Genes Neighborhood within Reconciled Phylogenies: An Ensemble Approach. Lecture Notes in Computer Science, 2014, , 49-56.	1.3	2
50	On the diversity of pattern distributions in rational language.. , 2012, , .		2
51	Tree diet: reducing the treewidth to unlock FPT algorithms in RNA bioinformatics. Algorithms for Molecular Biology, 2022, 17, 8.	1.2	2
52	Using Structural and Evolutionary Information to Detect and Correct Pyrosequencing Errors in Noncoding RNAs. Journal of Computational Biology, 2013, 20, 905-919.	1.6	1
53	Taming reluctant random walks in the positive quadrant. Electronic Notes in Discrete Mathematics, 2017, 59, 99-114.	0.4	1
54	Assessing the Robustness of Parsimonious Predictions for Gene Neighborhoods from Reconciled Phylogenies: Supplementary Material. Lecture Notes in Computer Science, 2015, , 260-271.	1.3	1

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55	Culminating paths. Discrete Mathematics and Theoretical Computer Science, 0, Vol. 10 no. 2, .	0.1	1
56	An Unbiased Adaptive Sampling Algorithm for the Exploration of RNA Mutational Landscapes under Evolutionary Pressure. Lecture Notes in Computer Science, 2011, , 501-515.	1.3	1
57	Counting, Generating and Sampling Tree Alignments. Lecture Notes in Computer Science, 2016, , 53-64.	1.3	1
58	Preface. Journal of Computational Biology, 2015, 22, 189-189.	1.6	0
59	Sequence Graphs Realizations and Ambiguity in Language Models. Lecture Notes in Computer Science, 2021, , 153-163.	1.3	0
60	Advanced Design of Structural RNAs Using RNARedPrint. Methods in Molecular Biology, 2021, 2284, 1-15.	0.9	0
61	Exponentially Few RNA Structures are Designable. , 2019, , .		0