

# Yann Ponty

## List of Publications by Year in descending order

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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	Tree diet: reducing the treewidth to unlock FPT algorithms in RNA bioinformatics. Algorithms for Molecular Biology, 2022, 17, 8.	1.2	2
2	RNAXplorer: harnessing the power of guiding potentials to sample RNA landscapes. Bioinformatics, 2021, 37, 2126-2133.	4.1	3
3	Reference-free transcriptome signatures for prostate cancer prognosis. BMC Cancer, 2021, 21, 394.	2.6	6
4	The SARS-CoV-2 subgenome landscape and its novel regulatory features. Molecular Cell, 2021, 81, 2135-2147.e5.	9.7	72
5	Sequence Graphs Realizations and Ambiguity in Language Models. Lecture Notes in Computer Science, 2021, , 153-163.	1.3	0
6	Advanced Design of Structural RNAs Using RNARedPrint. Methods in Molecular Biology, 2021, 2284, 1-15.	0.9	0
7	Progress toward SHAPE Constrained Computational Prediction of Tertiary Interactions in RNA Structure. Non-coding RNA, 2021, 7, 71.	2.6	6
8	IPANEMAP: integrative probing analysis of nucleic acids empowered by multiple accessibility profiles. Nucleic Acids Research, 2020, 48, 8276-8289.	14.5	9
9	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
10	<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
11	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
12	Fixed-parameter tractable sampling for RNA design with multiple target structures. BMC Bioinformatics, 2019, 20, 209.	2.6	13
13	Effective Rotation-Invariant Point CNN with Spherical Harmonics Kernels. , 2019, , .		53
14	Small-World Networks and RNA Secondary Structures. Journal of Computational Biology, 2019, 26, 16-26.	1.6	2
15	Exponentially Few RNA Structures are Designable. , 2019, , .		0
16	Design of RNAs: comparing programs for inverse RNA folding. Briefings in Bioinformatics, 2018, 19, bbw120.	6.5	35
17	Counting, Generating, Analyzing and Sampling Tree Alignments. International Journal of Foundations of Computer Science, 2018, 29, 741-767.	1.1	3
18	Meet-U: Educating through research immersion. PLoS Computational Biology, 2018, 14, e1005992.	3.2	4

#	ARTICLE	IF	CITATIONS
19	The BRaliBase dentâ€”a tale of benchmark design and interpretation. Briefings in Bioinformatics, 2017, 18, bbw022.	6.5	8
20	DeCoSTAR: Reconstructing the Ancestral Organization of Genes or Genomes Using Reconciled Phylogenies. Genome Biology and Evolution, 2017, 9, 1312-1319.	2.5	32
21	Two ribosome recruitment sites direct multiple translation events within HIV1 Gag open reading frame. Nucleic Acids Research, 2017, 45, 7382-7400.	14.5	28
22	Combinatorial RNA Design: Designability and Structure-Approximating Algorithm in Watsonâ€”Crick and Nussinovâ€”Jacobson Energy Models. Algorithmica, 2017, 79, 835-856.	1.3	11
23	Taming reluctant random walks in the positive quadrant. Electronic Notes in Discrete Mathematics, 2017, 59, 99-114.	0.4	1
24	Efficient approximations of RNA kinetics landscape using non-redundant sampling. Bioinformatics, 2017, 33, i283-i292.	4.1	14
25	ecceTERA: comprehensive gene tree-species tree reconciliation using parsimony. Bioinformatics, 2016, 32, 2056-2058.	4.1	98
26	Combining structure probing data on RNA mutants with evolutionary information reveals RNA-binding interfaces. Nucleic Acids Research, 2016, 44, e104-e104.	14.5	5
27	<tt>incaRNAfbiny</tt>: a web server for the fragment-based design of RNA sequences. Nucleic Acids Research, 2016, 44, W308-W314.	14.5	10
28	Counting, Generating and Sampling Tree Alignments. Lecture Notes in Computer Science, 2016, , 53-64.	1.3	1
29	Evolution of genes neighborhood within reconciled phylogenies: an ensemble approach. BMC Bioinformatics, 2015, 16, S6.	2.6	10
30	Preface. Journal of Computational Biology, 2015, 22, 189-189.	1.6	0
31	Drawing and Editing the Secondary Structure(s) of RNA. Methods in Molecular Biology, 2015, 1269, 63-100.	0.9	12
32	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
33	Combinatorial RNA Design: Designability and Structure-Approximating Algorithm. Lecture Notes in Computer Science, 2015, , 231-246.	1.3	3
34	Introduction to RNA Secondary Structure Comparison. Methods in Molecular Biology, 2014, 1097, 247-273.	0.9	7
35	Evolution of Genes Neighborhood within Reconciled Phylogenies: An Ensemble Approach. Lecture Notes in Computer Science, 2014, , 49-56.	1.3	2
36	Non-redundant random generation algorithms for weighted context-free grammars. Theoretical Computer Science, 2013, 502, 177-194.	0.9	3

#	ARTICLE	IF	CITATIONS
37	Flexible RNA design under structure and sequence constraints using formal languages. , 2013, , .		5
38	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
39	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
40	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
41	SPARCS: a web server to analyze (un)structured regions in coding RNA sequences. Nucleic Acids Research, 2013, 41, W480-W485.	14.5	13
42	A global sampling approach to designing and reengineering RNA secondary structures. Nucleic Acids Research, 2012, 40, 10041-10052.	14.5	32
43	Expected distance between terminal nucleotides of RNA secondary structures. Journal of Mathematical Biology, 2012, 65, 581-599.	1.9	30
44	Impact of the Energy Model on the Complexity of RNA Folding with Pseudoknots. Lecture Notes in Computer Science, 2012, , 321-333.	1.3	13
45	Using the Fast Fourier Transform to Accelerate the Computational Search for RNA Conformational Switches. PLoS ONE, 2012, 7, e50506.	2.5	19
46	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
47	On the diversity of pattern distributions in rational language.. , 2012, , .		2
48	The weighted words collector. Discrete Mathematics and Theoretical Computer Science, 2012, DMTCS Proceedings vol. AQ,...., .	0.1	4
49	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
50	A Combinatorial Framework for Designing (Pseudoknotted) RNA Algorithms. Lecture Notes in Computer Science, 2011, , 250-269.	1.3	11
51	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
52	Controlled non-uniform random generation of decomposable structures. Theoretical Computer Science, 2010, 411, 3527-3552.	0.9	15
53	Multi-dimensional Boltzmann Sampling of Languages. Discrete Mathematics and Theoretical Computer Science, 2010, DMTCS Proceedings vol. AM,...., .	0.1	12
54	VARNA: Interactive drawing and editing of the RNA secondary structure. Bioinformatics, 2009, 25, 1974-1975.	4.1	1,094

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55	Asymptotics of RNA Shapes. <i>Journal of Computational Biology</i> , 2008, 15, 31-63.	1.6	30
56	LocalMove: computing on-lattice fits for biopolymers. <i>Nucleic Acids Research</i> , 2008, 36, W216-W222.	14.5	8
57	DIAL: a web server for the pairwise alignment of two RNA three-dimensional structures using nucleotide, dihedral angle and base-pairing similarities. <i>Nucleic Acids Research</i> , 2007, 35, W659-W668.	14.5	55
58	Efficient sampling of RNA secondary structures from the Boltzmann ensemble of low-energy. <i>Journal of Mathematical Biology</i> , 2007, 56, 107-127.	1.9	29
59	GenRGenS: software for generating random genomic sequences and structures. <i>Bioinformatics</i> , 2006, 22, 1534-1535.	4.1	62
60	Estimating seed sensitivity on homogeneous alignments. , 0, , .		14
61	Culminating paths. <i>Discrete Mathematics and Theoretical Computer Science</i> , 0, Vol. 10 no. 2, .	0.1	1