

# Peter Clote

## List of Publications by Year in descending order

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60  
papers

1,083  
citations

430874

18  
h-index

454955

30  
g-index

63  
all docs

63  
docs citations

63  
times ranked

891  
citing authors

#	ARTICLE	IF	CITATIONS
1	Are RNA networks scale-free?. <i>Journal of Mathematical Biology</i> , 2020, 80, 1291-1321.	1.9	4
2	RNAmountAlign: Efficient software for local, global, semiglobal pairwise and multiple RNA sequence/structure alignment. <i>PLoS ONE</i> , 2020, 15, e0227177.	2.5	3
3	Small-World Networks and RNA Secondary Structures. <i>Journal of Computational Biology</i> , 2019, 26, 16-26.	1.6	2
4	RNA folding kinetics using Monte Carlo and Gillespie algorithms. <i>Journal of Mathematical Biology</i> , 2018, 76, 1195-1227.	1.9	2
5	RNAiFold2T: Constraint Programming design of thermo-IRES switches. <i>Bioinformatics</i> , 2016, 32, i360-i368.	4.1	8
6	RNA DualPF: software to compute the dual partition function with sample applications in molecular evolution theory. <i>BMC Bioinformatics</i> , 2016, 17, 424.	2.6	10
7	Designing synthetic RNAs to determine the relevance of structural motifs in picornavirus IRES elements. <i>Scientific Reports</i> , 2016, 6, 24243.	3.3	8
8	New tools to analyze overlapping coding regions. <i>BMC Bioinformatics</i> , 2016, 17, 530.	2.6	1
9	Structural diversity measures for RNA. , 2015, , .		0
10	RNA Thermodynamic Structural Entropy. <i>PLoS ONE</i> , 2015, 10, e0137859.	2.5	17
11	Network Properties of the Ensemble of RNA Structures. <i>PLoS ONE</i> , 2015, 10, e0139476.	2.5	3
12	RNAiFold 2.0: a web server and software to design custom and Rfam-based RNA molecules. <i>Nucleic Acids Research</i> , 2015, 43, W513-W521.	14.5	26
13	Computational Prediction of Riboswitches. <i>Methods in Enzymology</i> , 2015, 553, 287-312.	1.0	7
14	Expected degree for RNA secondary structure networks. <i>Journal of Computational Chemistry</i> , 2015, 36, 103-117.	3.3	4
15	Fast, Approximate Kinetics of RNA Folding. <i>Journal of Computational Biology</i> , 2015, 22, 124-144.	1.6	6
16	RNA folding pathways and kinetics using 2D energy landscapes. <i>Journal of Mathematical Biology</i> , 2015, 70, 173-196.	1.9	10
17	Energy Parameters and Novel Algorithms for an Extended Nearest Neighbor Energy Model of RNA. <i>PLoS ONE</i> , 2014, 9, e85412.	2.5	2
18	Complete RNA inverse folding: computational design of functional hammerhead ribozymes. <i>Nucleic Acids Research</i> , 2014, 42, 11752-11762.	14.5	29

#	ARTICLE	IF	CITATIONS
19	Combinatorics of locally optimal RNA secondary structures. <i>Journal of Mathematical Biology</i> , 2014, 68, 341-375.	1.9	9
20	Computing the Probability of RNA Hairpin and Multiloop Formation. <i>Journal of Computational Biology</i> , 2014, 21, 201-218.	1.6	0
21	Asymptotic Number of Hairpins of Saturated RNA Secondary Structures. <i>Bulletin of Mathematical Biology</i> , 2013, 75, 2410-2430.	1.9	0
22	Asymptotic structural properties of quasi-random saturated structures of RNA. <i>Algorithms for Molecular Biology</i> , 2013, 8, 24.	1.2	1
23	Using RNA inverse folding to identify IRES-like structural subdomains. <i>RNA Biology</i> , 2013, 10, 1842-1852.	3.1	20
24	RNAiFOLD: A CONSTRAINT PROGRAMMING ALGORITHM FOR RNA INVERSE FOLDING AND MOLECULAR DESIGN. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1350001.	0.8	70
25	RNAiFold: a web server for RNA inverse folding and molecular design. <i>Nucleic Acids Research</i> , 2013, 41, W465-W470.	14.5	20
26	On the page number of RNA secondary structures with pseudoknots. <i>Journal of Mathematical Biology</i> , 2012, 65, 1337-1357.	1.9	14
27	Expected distance between terminal nucleotides of RNA secondary structures. <i>Journal of Mathematical Biology</i> , 2012, 65, 581-599.	1.9	30
28	Using the Fast Fourier Transform to Accelerate the Computational Search for RNA Conformational Switches. <i>PLoS ONE</i> , 2012, 7, e50506.	2.5	19
29	Maximum expected accuracy structural neighbors of an RNA secondary structure. <i>BMC Bioinformatics</i> , 2012, 13, S6.	2.6	14
30	Maximum expected accurate structural neighbors of an RNA secondary structure. , 2011, , .		3
31	Computing the Partition Function for Kinetically Trapped RNA Secondary Structures. <i>PLoS ONE</i> , 2011, 6, e16178.	2.5	37
32	Computing folding pathways between RNA secondary structures. <i>Nucleic Acids Research</i> , 2010, 38, 1711-1722.	14.5	35
33	Thermodynamics of RNA structures by Wang's Landau sampling. <i>Bioinformatics</i> , 2010, 26, i278-i286.	4.1	9
34	Asymptotics of Canonical RNA Secondary Structures. , 2009, , .		0
35	ASYMPTOTICS OF CANONICAL AND SATURATED RNA SECONDARY STRUCTURES. <i>Journal of Bioinformatics and Computational Biology</i> , 2009, 07, 869-893.	0.8	13
36	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. <i>Nucleic Acids Research</i> , 2009, 37, W281-W286.	14.5	19

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37	Modeling ensembles of transmembrane $\beta$ -barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 71, 1097-1112.	2.6	26
38	Asymptotics of RNA Shapes. <i>Journal of Computational Biology</i> , 2008, 15, 31-63.	1.6	30
39	Efficient Algorithms for Probing the RNA Mutation Landscape. <i>PLoS Computational Biology</i> , 2008, 4, e1000124.	3.2	38
40	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
41	Computing the Partition Function and Sampling for Saturated Secondary Structures of RNA, with Respect to the Turner Energy Model. <i>Journal of Computational Biology</i> , 2007, 14, 190-215.	1.6	24
42	Boltzmann probability of RNA structural neighbors and riboswitch detection. <i>Bioinformatics</i> , 2007, 23, 2054-2062.	4.1	37
43	RNAbor: a web server for RNA structural neighbors. <i>Nucleic Acids Research</i> , 2007, 35, W305-W309.	14.5	18
44	Asymptotic expected number of base pairs in optimal secondary structure for random RNA using the Nussinov-Jacobson energy model. <i>Discrete Applied Mathematics</i> , 2007, 155, 759-787.	0.9	7
45	Introduction to special issue on RNA. <i>Journal of Mathematical Biology</i> , 2007, 56, 3-13.	1.9	0
46	Predicting transmembrane $\beta$ -barrels and interstrand residue interactions from sequence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 65, 61-74.	2.6	36
47	Symmetric time warping, Boltzmann pair probabilities and functional genomics. <i>Journal of Mathematical Biology</i> , 2006, 53, 135-161.	1.9	10
48	transFold: a web server for predicting the structure and residue contacts of transmembrane beta-barrels. <i>Nucleic Acids Research</i> , 2006, 34, W189-W193.	14.5	34
49	BTW: a web server for Boltzmann time warping of gene expression time series. <i>Nucleic Acids Research</i> , 2006, 34, W482-W485.	14.5	6
50	Combinatorics of Saturated Secondary Structures of RNA. <i>Journal of Computational Biology</i> , 2006, 13, 1640-1657.	1.6	17
51	On realizing shapes in the theory of RNA neutral networks. <i>Journal of Theoretical Biology</i> , 2005, 236, 216-227.	1.7	7
52	Energy landscape of k-point mutants of an RNA molecule. <i>Bioinformatics</i> , 2005, 21, 4140-4147.	4.1	16
53	Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency. <i>Rna</i> , 2005, 11, 578-591.	3.5	178
54	An Efficient Algorithm to Compute the Landscape of Locally Optimal RNA Secondary Structures with Respect to the Nussinov-Jacobson Energy Model. <i>Journal of Computational Biology</i> , 2005, 12, 83-101.	1.6	35

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55	RNALOSS: a web server for RNA locally optimal secondary structures. Nucleic Acids Research, 2005, 33, W600-W604.	14.5	12
56	Proteins: Structure, Function and Evolution. , 2001, , .		0
57	Cutting planes, connectivity, and threshold logic. Archive for Mathematical Logic, 1996, 35, 33-62.	0.3	25
58	Cutting planes, connectivity, and threshold logic. Archive for Mathematical Logic, 1996, 35, 33-62.	0.3	3
59	A generalization of the limit lemma and clopen games. Journal of Symbolic Logic, 1986, 51, 273-291.	0.5	2
60	Performance comparison of generalized PSSM in in signal peptide cleavage site and disulfide bond recognition. , 0, , .		2