Peter Clote

List of Publications by Year
in descending order

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	Structural RNA has lower folding energy than random RNA of the same dinucleotide frequency. Rna, 2005, 11, 578-591.	3.5	178
2	RNAiFOLD: A CONSTRAINT PROGRAMMING ALGORITHM FOR RNA INVERSE FOLDING AND MOLECULAR DESIGN. Journal of Bioinformatics and Computational Biology, 2013, 11, 1350001.	0.8	70
3	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
4	Efficient Algorithms for Probing the RNA Mutation Landscape. PLoS Computational Biology, 2008, 4, e1000124.	3.2	38
5	Boltzmann probability of RNA structural neighbors and riboswitch detection. Bioinformatics, 2007, 23, 2054-2062.	4.1	37
6	Computing the Partition Function for Kinetically Trapped RNA Secondary Structures. PLoS ONE, 2011, 6, e16178.	2.5	37
7	Predicting transmembrane Î²-barrels and interstrand residue interactions from sequence. Proteins: Structure, Function and Bioinformatics, 2006, 65, 61-74.	2.6	36
8	An Efficient Algorithm to Compute the Landscape of Locally Optimal RNA Secondary Structures with Respect to the Nussinovâ€"Jacobson Energy Model. Journal of Computational Biology, 2005, 12, 83-101.	1.6	35
9	Computing folding pathways between RNA secondary structures. Nucleic Acids Research, 2010, 38, 1711-1722.	14.5	35
10	transFold: a web server for predicting the structure and residue contacts of transmembrane beta-barrels. Nucleic Acids Research, 2006, 34, W189-W193.	14.5	34
11	Asymptotics of RNA Shapes. Journal of Computational Biology, 2008, 15, 31-63.	1.6	30
12	Expected distance between terminal nucleotides of RNA secondary structures. Journal of Mathematical Biology, 2012, 65, 581-599.	1.9	30
13	Complete RNA inverse folding: computational design of functional hammerhead ribozymes. Nucleic Acids Research, 2014, 42, 11752-11762.	14.5	29
14	Modeling ensembles of transmembrane Î²â€"barrel proteins. Proteins: Structure, Function and Bioinformatics, 2008, 71, 1097-1112.	2.6	26
15	RNAiFold 2.0: a web server and software to design custom and Rfam-based RNA molecules. Nucleic Acids Research, 2015, 43, W513-W521.	14.5	26
16	Cutting planes, connectivity, and threshold logic. Archive for Mathematical Logic, 1996, 35, 33-62.	0.3	25
17	Computing the Partition Function and Sampling for Saturated Secondary Structures of RNA, with Respect to the Turner Energy Model. Journal of Computational Biology, 2007, 14, 190-215.	1.6	24
18	Using RNA inverse folding to identify IRES-like structural subdomains. RNA Biology, 2013, 10, 1842-1852.	3.1	20

#	Article	IF	Citations
19	RNAiFold: a web server for RNA inverse folding and molecular design. Nucleic Acids Research, 2013, 41, W465-W470.	14.5	20
20	RNAmutants: a web server to explore the mutational landscape of RNA secondary structures. Nucleic Acids Research, 2009, 37, W281-W286.	14.5	19
21	Using the Fast Fourier Transform to Accelerate the Computational Search for RNA Conformational Switches. PLoS ONE, 2012, 7, e50506.	2.5	19
22	RNAbor: a web server for RNA structural neighbors. Nucleic Acids Research, 2007, 35, W305-W309.	14.5	18
23	Combinatorics of Saturated Secondary Structures of RNA. Journal of Computational Biology, 2006, 13, 1640-1657.	1.6	17
24	RNA Thermodynamic Structural Entropy. PLoS ONE, 2015, 10, e0137859.	2.5	17
25	Energy landscape of k-point mutants of an RNA molecule. Bioinformatics, 2005, 21, 4140-4147.	4.1	16
26	On the page number of RNA secondary structures with pseudoknots. Journal of Mathematical Biology, 2012, 65, 1337-1357.	1.9	14
27	Maximum expected accuracy structural neighbors of an RNA secondary structure. BMC Bioinformatics, 2012, 13, S6.	2.6	14
28	ASYMPTOTICS OF CANONICAL AND SATURATED RNA SECONDARY STRUCTURES. Journal of Bioinformatics and Computational Biology, 2009, 07, 869-893.	0.8	13
29	RNALOSS: a web server for RNA locally optimal secondary structures. Nucleic Acids Research, 2005, 33, W600-W604.	14.5	12
30	Symmetric time warping, Boltzmann pair probabilities and functional genomics. Journal of Mathematical Biology, 2006, 53, 135-161.	1.9	10
31	RNA folding pathways and kinetics using 2D energy landscapes. Journal of Mathematical Biology, 2015, 70, 173-196.	1.9	10
32	RNAdualPF: software to compute the dual partition function with sample applications in molecular evolution theory. BMC Bioinformatics, 2016, 17, 424.	2.6	10
33	Thermodynamics of RNA structures by Wangâ€"Landau sampling. Bioinformatics, 2010, 26, i278-i286.	4.1	9
34	Combinatorics of locally optimal RNA secondary structures. Journal of Mathematical Biology, 2014, 68, 341-375.	1.9	9
35	RNAiFold2T: Constraint Programming design of thermo-IRES switches. Bioinformatics, 2016, 32, i360-i368.	4.1	8
36	Designing synthetic RNAs to determine the relevance of structural motifs in picornavirus IRES elements. Scientific Reports, 2016, 6, 24243.	3.3	8

#	Article	IF	Citations
37	On realizing shapes in the theory of RNA neutral networks. Journal of Theoretical Biology, 2005, 236, 216-227.	1.7	7
38	Asymptotic expected number of base pairs in optimal secondary structure for random RNA using the Nussinovâ€"Jacobson energy model. Discrete Applied Mathematics, 2007, 155, 759-787.	0.9	7
39	Computational Prediction of Riboswitches. Methods in Enzymology, 2015, 553, 287-312.	1.0	7
40	BTW: a web server for Boltzmann time warping of gene expression time series. Nucleic Acids Research, 2006, 34, W482-W485.	14.5	6
41	Fast, Approximate Kinetics of RNA Folding. Journal of Computational Biology, 2015, 22, 124-144.	1.6	6
42	Expected degree for RNA secondary structure networks. Journal of Computational Chemistry, 2015, 36, 103-117.	3.3	4
43	Are RNA networks scale-free?. Journal of Mathematical Biology, 2020, 80, 1291-1321.	1.9	4
44	Maximum expected accurate structural neighbors of an RNA secondary structure. , 2011, , .		3
45	Network Properties of the Ensemble of RNA Structures. PLoS ONE, 2015, 10, e0139476.	2.5	3
46	RNAmountAlign: Efficient software for local, global, semiglobal pairwise and multiple RNA sequence/structure alignment. PLoS ONE, 2020, 15, e0227177.	2.5	3
47	Cutting planes, connectivity, and threshold logic. Archive for Mathematical Logic, 1996, 35, 33-62.	0.3	3
48	A generalization of the limit lemma and clopen games. Journal of Symbolic Logic, 1986, 51, 273-291.	0.5	2
49	Performance comparison of generalized PSSM in in signal peptide cleavage site and disulfide bond recognition. , 0, , .		2
50	Energy Parameters and Novel Algorithms for an Extended Nearest Neighbor Energy Model of RNA. PLoS ONE, 2014, 9, e85412.	2.5	2
51	RNA folding kinetics using Monte Carlo and Gillespie algorithms. Journal of Mathematical Biology, 2018, 76, 1195-1227.	1.9	2
52	Small-World Networks and RNA Secondary Structures. Journal of Computational Biology, 2019, 26, 16-26.	1.6	2
53	Asymptotic structural properties of quasi-random saturated structures of RNA. Algorithms for Molecular Biology, 2013, 8, 24.	1.2	1
54	New tools to analyze overlapping coding regions. BMC Bioinformatics, 2016, 17, 530.	2.6	1

#	ARTICLE	IF	CITATIONS
55	Introduction to special issue on RNA. Journal of Mathematical Biology, 2007, 56, 3-13.	1.9	0
56	Asymptotics of Canonical RNA Secondary Structures. , 2009, , .		0
57	Asymptotic Number of Hairpins of Saturated RNA Secondary Structures. Bulletin of Mathematical Biology, 2013, 75, 2410-2430.	1.9	0
58	Computing the Probability of RNA Hairpin and Multiloop Formation. Journal of Computational Biology, 2014, 21, 201-218.	1.6	0
59	Structural diversity measures for RNA. , 2015, , .		0
60	Proteins: Structure, Function and Evolution. , 2001, , .		0