## Michael Zuker

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Mfold web server for nucleic acid folding and hybridization prediction. Nucleic Acids Research, 2003, 31, 3406-3415.	14.5	11,479
2	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. Journal of Molecular Biology, 1999, 288, 911-940.	4.2	3,486
3	Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information. Nucleic Acids Research, 1981, 9, 133-148.	14.5	3,462
4	Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7287-7292.	7.1	1,332
5	UNAFold. Methods in Molecular Biology, 2008, 453, 3-31.	0.9	843
6	DINAMelt web server for nucleic acid melting prediction. Nucleic Acids Research, 2005, 33, W577-W581.	14.5	825
7	MicroRNA-responsive 'sensor' transgenes uncover Hox-like and other developmentally regulated patterns of vertebrate microRNA expression. Nature Genetics, 2004, 36, 1079-1083.	21.4	411
8	[17] Predicting optimal and suboptimal secondary structure for RNA. Methods in Enzymology, 1990, 183, 281-306.	1.0	376
9	OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach. Nucleic Acids Research, 2003, 31, 3057-3062.	14.5	349
10	[20] Computer prediction of RNA structure. Methods in Enzymology, 1989, 180, 262-288.	1.0	344
11	RNA secondary structures and their prediction. Bulletin of Mathematical Biology, 1984, 46, 591-621.	1.9	308
12	Calculating nucleic acid secondary structure. Current Opinion in Structural Biology, 2000, 10, 303-310.	5.7	218
13	Prediction of Hybridization and Melting for Double-Stranded Nucleic Acids. Biophysical Journal, 2004, 87, 215-226.	0.5	194
14	A comparison of optimal and suboptimal RNA secondary structures predicted by free energy minimization with structures determined by phylogenetic comparison. Nucleic Acids Research, 1991, 19, 2707-2714.	14.5	190
15	Using reliability information to annotate RNA secondary structures. Rna, 1998, 4, 669-679.	3.5	162
16	OligoArray: genome-scale oligonucleotide design for microarrays. Bioinformatics, 2002, 18, 486-487.	4.1	156
17	Prediction of RNA Secondary Structure by Energy Minimization. , 1994, 25, 267-294.		150
18	Common structures of the 5′ non-coding RNA in enteroviruses and rhinoviruses. Journal of Molecular Biology, 1990, 216, 729-741.	4.2	115

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19	Structural organization of the 16S ribosomal RNA from E. coli. Topography and secondary structure. Nucleic Acids Research, 1981, 9, 2153-2172.	14.5	113
20	â€~Well-determined' regions in RNA secondary structure prediction: analysis of small subunit ribosomal RNA. Nucleic Acids Research, 1995, 23, 2791-2798.	14.5	96
21	The Giardia lamblia actin gene and the phylogeny of eukaryotes. Journal of Molecular Evolution, 1995, 41, 841-849.	1.8	93
22	RNAML: A standard syntax for exchanging RNA information. Rna, 2002, 8, 707-717.	3.5	91
23	RNA Secondary Structure Prediction. Current Protocols in Nucleic Acid Chemistry, 2007, 28, Unit 11.2.	0.5	91
24	Metrics on RNA Secondary Structures. Journal of Computational Biology, 2000, 7, 277-292.	1.6	90
25	Structural Analysis by Energy Dot Plot of a Large mRNA. Journal of Molecular Biology, 1993, 233, 261-269.	4.2	73
26	Quantitative Prediction of miRNA-mRNA Interaction Based on Equilibrium Concentrations. PLoS Computational Biology, 2011, 7, e1001090.	3.2	72
27	Melting and chemical modification of a cyclized self-splicing group I intron: similarity of structures in 1 M sodium, in 10 mM magnesium and in the presence of substrate. Biochemistry, 1990, 29, 10147-10158.	2.5	55
28	Internal loops in RNA secondary structure prediction. , 1999, , .		28
29	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. PLoS ONE, 2009, 4, e5745.	2.5	27
30	Combining temperature and force to study folding of an RNA hairpin. Physical Chemistry Chemical Physics, 2014, 16, 906-917.	2.8	22
31	Predicting Common Foldings of Homologous RNAs. Journal of Biomolecular Structure and Dynamics, 1991, 8, 1027-1044.	3.5	21
32	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. ACS Symposium Series, 1997, , 246-257.	0.5	21
33	The primary structure of the ribosomal A-protein (L12) from the moderate halophile NRCC 41227. Biochemistry and Cell Biology, 1986, 64, 675-680.	2.0	17
34	Effect of spermidine on the conformation of bacteriophage MS2 RNA. Journal of Molecular Biology, 1985, 181, 517-531.	4.2	16
35	Comparing RNA secondary structures using a relaxed base-pair score. Rna, 2010, 16, 865-878.	3.5	16
36	The primary structure of the ribosomal A-protein (L12) from the halophilic eubacterium Haloanaerobium praevalens. Biochimie, 1987, 69, 1013-1020.	2.6	14

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37	The Hepatitis B Virus Pregenome: Prediction of RNA Structure and Implications for the Emergence of Deletions. Intervirology, 2000, 43, 154-164.	2.8	14
38	Development of lead hammerhead ribozyme candidates against human rod opsin mRNA for retinal degeneration therapy. Experimental Eye Research, 2009, 88, 859-879.	2.6	14
39	RNA Secondary Structure Prediction. Current Protocols in Nucleic Acid Chemistry, 2000, 2, 11.2.1.	0.5	7
40	Analytic methods applied to a sequence of binomial coefficients. Discrete Mathematics, 1978, 24, 299-310.	0.7	5
41	RNA secondary structure prediction. , 2005, , .		4
42	Comparative Studies on the Secondary Structure of the RNAs of Related RNA Coliphages. , 1987, , 331-354.		3
43	Signs of Terms in a Combinatorial Recursion. SIAM Journal on Algebraic and Discrete Methods, 1983, 4, 437-441.	0.8	0