

# Michael Zuker

## List of Publications by Year in descending order

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43  
papers

25,403  
citations

249298

26  
h-index

355658

38  
g-index

43  
all docs

43  
docs citations

43  
times ranked

26422  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mfold web server for nucleic acid folding and hybridization prediction. <i>Nucleic Acids Research</i> , 2003, 31, 3406-3415.	6.5	11,479
2	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. <i>Journal of Molecular Biology</i> , 1999, 288, 911-940.	2.0	3,486
3	Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information. <i>Nucleic Acids Research</i> , 1981, 9, 133-148.	6.5	3,462
4	Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 7287-7292.	3.3	1,332
5	UNAFold. <i>Methods in Molecular Biology</i> , 2008, 453, 3-31.	0.4	843
6	DINAMelt web server for nucleic acid melting prediction. <i>Nucleic Acids Research</i> , 2005, 33, W577-W581.	6.5	825
7	MicroRNA-responsive 'sensor' transgenes uncover Hox-like and other developmentally regulated patterns of vertebrate microRNA expression. <i>Nature Genetics</i> , 2004, 36, 1079-1083.	9.4	411
8	[17] Predicting optimal and suboptimal secondary structure for RNA. <i>Methods in Enzymology</i> , 1990, 183, 281-306.	0.4	376
9	OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach. <i>Nucleic Acids Research</i> , 2003, 31, 3057-3062.	6.5	349
10	[20] Computer prediction of RNA structure. <i>Methods in Enzymology</i> , 1989, 180, 262-288.	0.4	344
11	RNA secondary structures and their prediction. <i>Bulletin of Mathematical Biology</i> , 1984, 46, 591-621.	0.9	308
12	Calculating nucleic acid secondary structure. <i>Current Opinion in Structural Biology</i> , 2000, 10, 303-310.	2.6	218
13	Prediction of Hybridization and Melting for Double-Stranded Nucleic Acids. <i>Biophysical Journal</i> , 2004, 87, 215-226.	0.2	194
14	A comparison of optimal and suboptimal RNA secondary structures predicted by free energy minimization with structures determined by phylogenetic comparison. <i>Nucleic Acids Research</i> , 1991, 19, 2707-2714.	6.5	190
15	Using reliability information to annotate RNA secondary structures. <i>Rna</i> , 1998, 4, 669-679.	1.6	162
16	OligoArray: genome-scale oligonucleotide design for microarrays. <i>Bioinformatics</i> , 2002, 18, 486-487.	1.8	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. <i>Journal of Molecular Biology</i> , 1990, 216, 729-741.	2.0	115

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19	Structural organization of the 16S ribosomal RNA from E. coli. Topography and secondary structure. <i>Nucleic Acids Research</i> , 1981, 9, 2153-2172.	6.5	113
20	“Well-determined” regions in RNA secondary structure prediction: analysis of small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , 1995, 23, 2791-2798.	6.5	96
21	The <i>Giardia lamblia</i> actin gene and the phylogeny of eukaryotes. <i>Journal of Molecular Evolution</i> , 1995, 41, 841-849.	0.8	93
22	RNAML: A standard syntax for exchanging RNA information. <i>Rna</i> , 2002, 8, 707-717.	1.6	91
23	RNA Secondary Structure Prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2007, 28, Unit 11.2.	0.5	91
24	Metrics on RNA Secondary Structures. <i>Journal of Computational Biology</i> , 2000, 7, 277-292.	0.8	90
25	Structural Analysis by Energy Dot Plot of a Large mRNA. <i>Journal of Molecular Biology</i> , 1993, 233, 261-269.	2.0	73
26	Quantitative Prediction of miRNA-mRNA Interaction Based on Equilibrium Concentrations. <i>PLoS Computational Biology</i> , 2011, 7, e1001090.	1.5	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. <i>Biochemistry</i> , 1990, 29, 10147-10158.	1.2	55
28	Internal loops in RNA secondary structure prediction. , 1999, , .		28
29	Transcriptome-Wide Prediction of miRNA Targets in Human and Mouse Using FASTH. <i>PLoS ONE</i> , 2009, 4, e5745.	1.1	27
30	Combining temperature and force to study folding of an RNA hairpin. <i>Physical Chemistry Chemical Physics</i> , 2014, 16, 906-917.	1.3	22
31	Predicting Common Foldings of Homologous RNAs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991, 8, 1027-1044.	2.0	21
32	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. <i>ACS Symposium Series</i> , 1997, , 246-257.	0.5	21
33	The primary structure of the ribosomal A-protein (L12) from the moderate halophile NRCC 41227. <i>Biochemistry and Cell Biology</i> , 1986, 64, 675-680.	0.9	17
34	Effect of spermidine on the conformation of bacteriophage MS2 RNA. <i>Journal of Molecular Biology</i> , 1985, 181, 517-531.	2.0	16
35	Comparing RNA secondary structures using a relaxed base-pair score. <i>Rna</i> , 2010, 16, 865-878.	1.6	16
36	The primary structure of the ribosomal A-protein (L12) from the halophilic eubacterium <i>Haloanaerobium praevalens</i> . <i>Biochimie</i> , 1987, 69, 1013-1020.	1.3	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.	1.2	14
38	Development of lead hammerhead ribozyme candidates against human rod opsin mRNA for retinal degeneration therapy. Experimental Eye Research, 2009, 88, 859-879.	1.2	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.	0.4	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