

# Michael Zuker

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43  
papers

21,736  
citations

27  
h-index

43  
g-index

43  
ext. papers

23,568  
ext. citations

7.3  
avg, IF

7.54  
L-index

#	Paper	IF	Citations
43	Combining temperature and force to study folding of an RNA hairpin. <i>Physical Chemistry Chemical Physics</i> , <b>2014</b> , 16, 906-17	3.6	15
42	Quantitative prediction of miRNA-mRNA interaction based on equilibrium concentrations. <i>PLoS Computational Biology</i> , <b>2011</b> , 7, e1001090	5	64
41	Comparing RNA secondary structures using a relaxed base-pair score. <i>Rna</i> , <b>2010</b> , 16, 865-78	5.8	15
40	Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH. <i>PLoS ONE</i> , <b>2009</b> , 4, e5745	3.7	20
39	Development of lead hammerhead ribozyme candidates against human rod opsin mRNA for retinal degeneration therapy. <i>Experimental Eye Research</i> , <b>2009</b> , 88, 859-79	3.7	11
38	UNAFold: software for nucleic acid folding and hybridization. <i>Methods in Molecular Biology</i> , <b>2008</b> , 453, 3-31	1.4	692
37	RNA secondary structure prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , <b>2007</b> , Chapter 11, Unit 11.2	0.5	52
36	DINAMelt web server for nucleic acid melting prediction. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W577-81	20.1	734
35	RNA secondary structure prediction <b>2005</b> ,		1
34	MicroRNA-responsive sensor transgenes uncover Hox-like and other developmentally regulated patterns of vertebrate microRNA expression. <i>Nature Genetics</i> , <b>2004</b> , 36, 1079-83	36.3	378
33	Prediction of hybridization and melting for double-stranded nucleic acids. <i>Biophysical Journal</i> , <b>2004</b> , 87, 215-26	2.9	173
32	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> , <b>2004</b> , 101, 7287-92	11.5	1090
31	Mfold web server for nucleic acid folding and hybridization prediction. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3406-15	20.1	9653
30	OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3057-62	20.1	308
29	RNAML: a standard syntax for exchanging RNA information. <i>Rna</i> , <b>2002</b> , 8, 707-17	5.8	68
28	OligoArray: genome-scale oligonucleotide design for microarrays. <i>Bioinformatics</i> , <b>2002</b> , 18, 486-7	7.2	137
27	RNA Secondary Structure Prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , <b>2000</b> , 2, 11.2.1	0.5	7

26	Calculating nucleic acid secondary structure. <i>Current Opinion in Structural Biology</i> , <b>2000</b> , 10, 303-10	8.1	189
25	Metrics on RNA secondary structures. <i>Journal of Computational Biology</i> , <b>2000</b> , 7, 277-92	1.7	68
24	The hepatitis B virus pregenome: prediction of RNA structure and implications for the emergence of deletions. <i>Intervirology</i> , <b>2000</b> , 43, 154-64	2.5	13
23	Internal loops in RNA secondary structure prediction <b>1999</b> ,		14
22	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. <i>Journal of Molecular Biology</i> , <b>1999</b> , 288, 911-40	6.5	3182
21	Using reliability information to annotate RNA secondary structures. <i>Rna</i> , <b>1998</b> , 4, 669-79	5.8	127
20	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. <i>ACS Symposium Series</i> , <b>1997</b> , 246-257	0.4	14
19	The Giardia lamblia actin gene and the phylogeny of eukaryotes. <i>Journal of Molecular Evolution</i> , <b>1995</b> , 41, 841-9	3.1	84
18	"Well-determined" regions in RNA secondary structure prediction: analysis of small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , <b>1995</b> , 23, 2791-8	20.1	90
17	Prediction of RNA secondary structure by energy minimization. <i>Methods in Molecular Biology</i> , <b>1994</b> , 25, 267-94	1.4	129
16	Structural analysis by energy dot plot of a large mRNA. <i>Journal of Molecular Biology</i> , <b>1993</b> , 233, 261-9	6.5	70
15	Predicting common foldings of homologous RNAs. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>1991</b> , 8, 1027-44	3.6	17
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> , <b>1991</b> , 19, 2707-14	20.1	171
13	Melting and chemical modification of a cyclized self-splicing group I intron: similarity of structures in 1 M Na <sup>+</sup> , in 10 mM Mg <sup>2+</sup> , and in the presence of substrate. <i>Biochemistry</i> , <b>1990</b> , 29, 10147-58	3.2	53
12	Common structures of the 5' non-coding RNA in enteroviruses and rhinoviruses. Thermodynamical stability and statistical significance. <i>Journal of Molecular Biology</i> , <b>1990</b> , 216, 729-41	6.5	92
11	Predicting optimal and suboptimal secondary structure for RNA. <i>Methods in Enzymology</i> , <b>1990</b> , 183, 281-306	3.6	306
10	Computer prediction of RNA structure. <i>Methods in Enzymology</i> , <b>1989</b> , 180, 262-88	1.7	286
9	The primary structure of the ribosomal A-protein (L12) from the halophilic eubacterium Haloanaerobium praevalens. <i>Biochimie</i> , <b>1987</b> , 69, 1013-20	4.6	12

8	Comparative Studies on the Secondary Structure of the RNAs of Related RNA Coliphages <b>1987</b> , 331-354		3
7	The primary structure of the ribosomal A-protein (L12) from the moderate halophile NRCC 41227. <i>Biochemistry and Cell Biology</i> , <b>1986</b> , 64, 675-80	3.6	16
6	Effect of spermidine on the conformation of bacteriophage MS2 RNA. Electron microscopy and computer modeling. <i>Journal of Molecular Biology</i> , <b>1985</b> , 181, 517-31	6.5	15
5	RNA secondary structures and their prediction. <i>Bulletin of Mathematical Biology</i> , <b>1984</b> , 46, 591-621	2.1	279
4	Signs of Terms in a Combinatorial Recursion. <i>SIAM Journal on Algebraic and Discrete Methods</i> , <b>1983</b> , 4, 437-441		
3	Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information. <i>Nucleic Acids Research</i> , <b>1981</b> , 9, 133-48	20.1	2984
2	Structural organization of the 16S ribosomal RNA from E. coli. Topography and secondary structure. <i>Nucleic Acids Research</i> , <b>1981</b> , 9, 2153-72	20.1	100
1	Analytic methods applied to a sequence of binomial coefficients. <i>Discrete Mathematics</i> , <b>1978</b> , 24, 299-310.7		4