

Michael Zuker

List of Publications by Citations

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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	Mfold web server for nucleic acid folding and hybridization prediction. <i>Nucleic Acids Research</i> , 2003 , 31, 3406-15	20.1	9653
42	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. <i>Journal of Molecular Biology</i> , 1999 , 288, 911-40	6.5	3182
41	Optimal computer folding of large RNA sequences using thermodynamics and auxiliary information. <i>Nucleic Acids Research</i> , 1981 , 9, 133-48	20.1	2984
40	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, 7287-92	11.5	1090
39	DINAMelt web server for nucleic acid melting prediction. <i>Nucleic Acids Research</i> , 2005 , 33, W577-81	20.1	734
38	UNAFold: software for nucleic acid folding and hybridization. <i>Methods in Molecular Biology</i> , 2008 , 453, 3-31	1.4	692
37	MicroRNA-responsive sensor transgenes uncover Hox-like and other developmentally regulated patterns of vertebrate microRNA expression. <i>Nature Genetics</i> , 2004 , 36, 1079-83	36.3	378
36	OligoArray 2.0: design of oligonucleotide probes for DNA microarrays using a thermodynamic approach. <i>Nucleic Acids Research</i> , 2003 , 31, 3057-62	20.1	308
35	Predicting optimal and suboptimal secondary structure for RNA. <i>Methods in Enzymology</i> , 1990 , 183, 281-306	30.6	306
34	Computer prediction of RNA structure. <i>Methods in Enzymology</i> , 1989 , 180, 262-88	1.7	286
33	RNA secondary structures and their prediction. <i>Bulletin of Mathematical Biology</i> , 1984 , 46, 591-621	2.1	279
32	Calculating nucleic acid secondary structure. <i>Current Opinion in Structural Biology</i> , 2000 , 10, 303-10	8.1	189
31	Prediction of hybridization and melting for double-stranded nucleic acids. <i>Biophysical Journal</i> , 2004 , 87, 215-26	2.9	173
30	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, 2707-14	20.1	171
29	OligoArray: genome-scale oligonucleotide design for microarrays. <i>Bioinformatics</i> , 2002 , 18, 486-7	7.2	137
28	Prediction of RNA secondary structure by energy minimization. <i>Methods in Molecular Biology</i> , 1994 , 25, 267-94	1.4	129
27	Using reliability information to annotate RNA secondary structures. <i>Rna</i> , 1998 , 4, 669-79	5.8	127

26	Structural organization of the 16S ribosomal RNA from E. coli. Topography and secondary structure. <i>Nucleic Acids Research</i> , 1981 , 9, 2153-72	20.1	100
25	Common structures of the 5' non-coding RNA in enteroviruses and rhinoviruses. Thermodynamical stability and statistical significance. <i>Journal of Molecular Biology</i> , 1990 , 216, 729-41	6.5	92
24	"Well-determined" regions in RNA secondary structure prediction: analysis of small subunit ribosomal RNA. <i>Nucleic Acids Research</i> , 1995 , 23, 2791-8	20.1	90
23	The Giardia lamblia actin gene and the phylogeny of eukaryotes. <i>Journal of Molecular Evolution</i> , 1995 , 41, 841-9	3.1	84
22	Structural analysis by energy dot plot of a large mRNA. <i>Journal of Molecular Biology</i> , 1993 , 233, 261-9	6.5	70
21	RNAML: a standard syntax for exchanging RNA information. <i>Rna</i> , 2002 , 8, 707-17	5.8	68
20	Metrics on RNA secondary structures. <i>Journal of Computational Biology</i> , 2000 , 7, 277-92	1.7	68
19	Quantitative prediction of miRNA-mRNA interaction based on equilibrium concentrations. <i>PLoS Computational Biology</i> , 2011 , 7, e1001090	5	64
18	Melting and chemical modification of a cyclized self-splicing group I intron: similarity of structures in 1 M Na ⁺ , in 10 mM Mg ²⁺ , and in the presence of substrate. <i>Biochemistry</i> , 1990 , 29, 10147-58	3.2	53
17	RNA secondary structure prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2007 , Chapter 11, Unit 11.2	0.5	52
16	Transcriptome-wide prediction of miRNA targets in human and mouse using FASTH. <i>PLoS ONE</i> , 2009 , 4, e5745	3.7	20
15	Predicting common foldings of homologous RNAs. <i>Journal of Biomolecular Structure and Dynamics</i> , 1991 , 8, 1027-44	3.6	17
14	The primary structure of the ribosomal A-protein (L12) from the moderate halophile NRCC 41227. <i>Biochemistry and Cell Biology</i> , 1986 , 64, 675-80	3.6	16
13	Combining temperature and force to study folding of an RNA hairpin. <i>Physical Chemistry Chemical Physics</i> , 2014 , 16, 906-17	3.6	15
12	Comparing RNA secondary structures using a relaxed base-pair score. <i>Rna</i> , 2010 , 16, 865-78	5.8	15
11	Effect of spermidine on the conformation of bacteriophage MS2 RNA. Electron microscopy and computer modeling. <i>Journal of Molecular Biology</i> , 1985 , 181, 517-31	6.5	15
10	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. <i>ACS Symposium Series</i> , 1997 , 246-257	0.4	14
9	Internal loops in RNA secondary structure prediction 1999 ,		14

8	The hepatitis B virus pregenome: prediction of RNA structure and implications for the emergence of deletions. <i>Intervirology</i> , 2000 , 43, 154-64	2.5	13
7	The primary structure of the ribosomal A-protein (L12) from the halophilic eubacterium <i>Haloanaerobium praevalens</i> . <i>Biochimie</i> , 1987 , 69, 1013-20	4.6	12
6	Development of lead hammerhead ribozyme candidates against human rod opsin mRNA for retinal degeneration therapy. <i>Experimental Eye Research</i> , 2009 , 88, 859-79	3.7	11
5	RNA Secondary Structure Prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2000 , 2, 11.2.1	0.5	7
4	Analytic methods applied to a sequence of binomial coefficients. <i>Discrete Mathematics</i> , 1978 , 24, 299-310.7		4
3	Comparative Studies on the Secondary Structure of the RNAs of Related RNA Coliphages 1987 , 331-354		3
2	RNA secondary structure prediction 2005 ,		1
1	Signs of Terms in a Combinatorial Recursion. <i>SIAM Journal on Algebraic and Discrete Methods</i> , 1983 , 4, 437-441		