

# David H Mathews

## List of Publications by Year in descending order

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128  
papers

14,576  
citations

57631

44  
h-index

20900

115  
g-index

156  
all docs

156  
docs citations

156  
times ranked

10171  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	RNAstructure: software for RNA secondary structure prediction and analysis. <i>BMC Bioinformatics</i> , 2010, 11, 129.	1.2	1,568
3	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
4	Accurate SHAPE-directed RNA structure determination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 97-102.	3.3	624
5	NNDB: the nearest neighbor parameter database for predicting stability of nucleic acid secondary structure. <i>Nucleic Acids Research</i> , 2010, 38, D280-D282.	6.5	444
6	Dynalign: an algorithm for finding the secondary structure common to two RNA sequences. <i>Journal of Molecular Biology</i> , 2002, 317, 191-203.	2.0	340
7	Prediction of RNA secondary structure by free energy minimization. <i>Current Opinion in Structural Biology</i> , 2006, 16, 270-278.	2.6	339
8	RNAstructure: web servers for RNA secondary structure prediction and analysis. <i>Nucleic Acids Research</i> , 2013, 41, W471-W474.	6.5	321
9	Using an RNA secondary structure partition function to determine confidence in base pairs predicted by free energy minimization. <i>Rna</i> , 2004, 10, 1178-1190.	1.6	315
10	FragSeq: transcriptome-wide RNA structure probing using high-throughput sequencing. <i>Nature Methods</i> , 2010, 7, 995-1001.	9.0	289
11	Accurate SHAPE-directed RNA secondary structure modeling, including pseudoknots. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 5498-5503.	3.3	286
12	Predicting oligonucleotide affinity to nucleic acid targets. <i>Rna</i> , 1999, 5, 1458-1469.	1.6	228
13	Improved RNA secondary structure prediction by maximizing expected pair accuracy. <i>Rna</i> , 2009, 15, 1805-1813.	1.6	194
14	Efficient parameter estimation for RNA secondary structure prediction. <i>Bioinformatics</i> , 2007, 23, i19-i28.	1.8	169
15	ProbKnot: Fast prediction of RNA secondary structure including pseudoknots. <i>Rna</i> , 2010, 16, 1870-1880.	1.6	169
16	Revolutions in RNA Secondary Structure Prediction. <i>Journal of Molecular Biology</i> , 2006, 359, 526-532.	2.0	167
17	Detection of non-coding RNAs on the basis of predicted secondary structure formation free energy change. <i>BMC Bioinformatics</i> , 2006, 7, 173.	1.2	150
18	CRISPR-Cas9-based mutagenesis frequently provokes on-target mRNA misregulation. <i>Nature Communications</i> , 2019, 10, 4056.	5.8	139

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19	Folding and Finding RNA Secondary Structure. Cold Spring Harbor Perspectives in Biology, 2010, 2, a003665-a003665.	2.3	136
20	RNA Structure Prediction: An Overview of Methods. Methods in Molecular Biology, 2012, 905, 99-122.	0.4	135
21	Efficient siRNA selection using hybridization thermodynamics. Nucleic Acids Research, 2007, 36, 640-647.	6.5	126
22	A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. Nucleic Acids Research, 2006, 34, 4912-4924.	6.5	121
23	Computational approaches for RNA energy parameter estimation. Rna, 2010, 16, 2304-2318.	1.6	110
24	Predicting a set of minimal free energy RNA secondary structures common to two sequences. Bioinformatics, 2005, 21, 2246-2253.	1.8	109
25	Bridging the gap between <i>in vitro</i> and <i>in vivo</i> RNA folding. Quarterly Reviews of Biophysics, 2016, 49, e10.	2.4	108
26	Revised RNA Dihedral Parameters for the Amber Force Field Improve RNA Molecular Dynamics. Journal of Chemical Theory and Computation, 2017, 13, 900-915.	2.3	103
27	TurboFold II: RNA structural alignment and secondary structure prediction informed by multiple homologs. Nucleic Acids Research, 2017, 45, 11570-11581.	6.5	100
28	LinearFold: linear-time approximate RNA folding by 5'-to-3' dynamic programming and beam search. Bioinformatics, 2019, 35, i295-i304.	1.8	100
29	Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign. BMC Bioinformatics, 2007, 8, 130.	1.2	94
30	OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. Nucleic Acids Research, 2008, 36, W104-W108.	6.5	93
31	RNA Secondary Structure Prediction. Current Protocols in Nucleic Acid Chemistry, 2007, 28, Unit 11.2.	0.5	91
32	Thermodynamics of Three-Way Multibranch Loops in RNA. Biochemistry, 2001, 40, 6971-6981.	1.2	88
33	Improved prediction of RNA secondary structure by integrating the free energy model with restraints derived from experimental probing data. Nucleic Acids Research, 2015, 43, 7247-7259.	6.5	87
34	TurboFold: Iterative probabilistic estimation of secondary structures for multiple RNA sequences. BMC Bioinformatics, 2011, 12, 108.	1.2	80
35	Experimentally Derived Nearest-Neighbor Parameters for the Stability of RNA Three- and Four-Way Multibranch Loops. Biochemistry, 2002, 41, 869-880.	1.2	73
36	RNA Secondary Structure Analysis Using RNAstructure. Current Protocols in Bioinformatics, 2006, 13, Unit 12.6.	25.8	73

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37	Modeling RNA secondary structure folding ensembles using SHAPE mapping data. <i>Nucleic Acids Research</i> , 2018, 46, 314-323.	6.5	72
38	Structural analysis of a class III preQ <sub>1</sub> riboswitch reveals an aptamer distant from a ribosome-binding site regulated by fast dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3485-94.	3.3	62
39	mRNAs and lncRNAs intrinsically form secondary structures with short end-to-end distances. <i>Nature Communications</i> , 2018, 9, 4328.	5.8	62
40	Predicting helical coaxial stacking in RNA multibranch loops. <i>Rna</i> , 2007, 13, 939-951.	1.6	60
41	Exact calculation of loop formation probability identifies folding motifs in RNA secondary structures. <i>Rna</i> , 2016, 22, 1808-1818.	1.6	59
42	Identification of the determinants of tRNA function and susceptibility to rapid tRNA decay by high-throughput in vivo analysis. <i>Genes and Development</i> , 2014, 28, 1721-1732.	2.7	58
43	Multalign: an algorithm to predict secondary structures conserved in multiple RNA sequences. <i>Bioinformatics</i> , 2011, 27, 626-632.	1.8	54
44	The Determination of RNA Folding Nearest Neighbor Parameters. <i>Methods in Molecular Biology</i> , 2014, 1097, 45-70.	0.4	52
45	RNA Secondary Structure Analysis Using RNAstructure. <i>Current Protocols in Bioinformatics</i> , 2014, 46, 12.6.1-25.	25.8	50
46	Nudged Elastic Band Calculation of Minimal Energy Paths for the Conformational Change of a GG Non-canonical Pair. <i>Journal of Molecular Biology</i> , 2006, 357, 1683-1693.	2.0	47
47	An RNA Molecular Switch: Intrinsic Flexibility of 23S rRNA Helices 40 and 68 5'-UAA/5'-GAN Internal Loops Studied by Molecular Dynamics Methods. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 910-929.	2.3	46
48	Improving RNA Secondary Structure Prediction with Structure Mapping Data. <i>Methods in Enzymology</i> , 2015, 553, 91-114.	0.4	46
49	NMR-Assisted Prediction of RNA Secondary Structure: Identification of a Probable Pseudoknot in the Coding Region of an R2 Retrotransposon. <i>Journal of the American Chemical Society</i> , 2008, 130, 10233-10239.	6.6	45
50	PARTS: Probabilistic Alignment for RNA joint Secondary structure prediction. <i>Nucleic Acids Research</i> , 2008, 36, 2406-2417.	6.5	44
51	LinearPartition: linear-time approximation of RNA folding partition function and base-pairing probabilities. <i>Bioinformatics</i> , 2020, 36, i258-i267.	1.8	44
52	Principles for Understanding the Accuracy of SHAPE-Directed RNA Structure Modeling. <i>Biochemistry</i> , 2013, 52, 588-595.	1.2	41
53	Dynalign II: common secondary structure prediction for RNA homologs with domain insertions. <i>Nucleic Acids Research</i> , 2014, 42, 13939-13948.	6.5	40
54	The Amber ff99 Force Field Predicts Relative Free Energy Changes for RNA Helix Formation. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 2497-2505.	2.3	39

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55	Nearest neighbor parameters for Watson-Crick complementary heteroduplexes formed between 2'-O-methyl RNA and RNA oligonucleotides. <i>Nucleic Acids Research</i> , 2006, 34, 3609-3614.	6.5	36
56	Automated RNA tertiary structure prediction from secondary structure and low-resolution restraints. <i>Journal of Computational Chemistry</i> , 2011, 32, 2232-2244.	1.5	35
57	A sensitivity analysis of RNA folding nearest neighbor parameters identifies a subset of free energy parameters with the greatest impact on RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2017, 45, 6168-6176.	6.5	34
58	RNA Secondary Structure Prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2016, 67, 11.2.1-11.2.19.	0.5	32
59	Physics-based all-atom modeling of RNA energetics and structure. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017, 8, e1422.	3.2	32
60	How to benchmark RNA secondary structure prediction accuracy. <i>Methods</i> , 2019, 162-163, 60-67.	1.9	32
61	Using the RNAstructure Software Package to Predict Conserved RNA Structures. <i>Current Protocols in Bioinformatics</i> , 2014, 46, 12.4.1-22.	25.8	31
62	RNA pseudoknots: folding and finding. <i>F1000 Biology Reports</i> , 2010, 2, 8.	4.0	30
63	Advanced multi-loop algorithms for RNA secondary structure prediction reveal that the simplest model is best. <i>Nucleic Acids Research</i> , 2017, 45, 8541-8550.	6.5	29
64	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	1.6	28
65	A sequence similar to tRNA <sup>Lys</sup> gene is embedded in HIV-1 U3 and promotes minus-strand transfer. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 83-89.	3.6	27
66	Base pair probability estimates improve the prediction accuracy of RNA non-canonical base pairs. <i>PLoS Computational Biology</i> , 2017, 13, e1005827.	1.5	27
67	Structure of HIV TAR in complex with a Lab-Evolved RRM provides insight into duplex RNA recognition and synthesis of a constrained peptide that impairs transcription. <i>Nucleic Acids Research</i> , 2018, 46, 6401-6415.	6.5	27
68	Secondary structure prediction for RNA sequences including N6-methyladenosine. <i>Nature Communications</i> , 2022, 13, 1271.	5.8	27
69	Pyvinium pamoate changes alternative splicing of the serotonin receptor 2C by influencing its RNA structure. <i>Nucleic Acids Research</i> , 2013, 41, 3819-3832.	6.5	26
70	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. <i>PLoS ONE</i> , 2015, 10, e0130200.	1.1	26
71	AccessFold: predicting RNA-RNA interactions with consideration for competing self-structure. <i>Bioinformatics</i> , 2016, 32, 1033-1039.	1.8	26
72	Arginine Forks Are a Widespread Motif to Recognize Phosphate Backbones and Guanine Nucleobases in the RNA Major Groove. <i>Journal of the American Chemical Society</i> , 2020, 142, 19835-19839.	6.6	26

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73	Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. <i>Nucleic Acids Research</i> , 2008, 36, 3738-3745.	6.5	25
74	Fluorescence Competition and Optical Melting Measurements of RNA Three-Way Multibranch Loops Provide a Revised Model for Thermodynamic Parameters. <i>Biochemistry</i> , 2011, 50, 640-653.	1.2	25
75	Analysis of RNA nearest neighbor parameters reveals interdependencies and quantifies the uncertainty in RNA secondary structure prediction. <i>Rna</i> , 2018, 24, 1568-1582.	1.6	25
76	Secondary structure models of the 3' untranslated regions of diverse R2 RNAs. <i>Rna</i> , 2004, 10, 978-987.	1.6	23
77	Statistical evaluation of improvement in RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2012, 40, e26-e26.	6.5	23
78	Influence of Sequence and Covalent Modifications on Yeast tRNA Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 3473-3483.	2.3	22
79	Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. <i>Nucleic Acids Research</i> , 2018, 46, 4883-4892.	6.5	22
80	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. <i>ACS Symposium Series</i> , 1997, , 246-257.	0.5	21
81	NMR Reveals the Absence of Hydrogen Bonding in Adjacent UUU and AG Mismatches in an Isolated Internal Loop from Ribosomal RNA. <i>Biochemistry</i> , 2007, 46, 12665-12678.	1.2	21
82	Molecular mechanism for preQ1-III riboswitch function revealed by molecular dynamics. <i>Rna</i> , 2015, 21, 1898-1907.	1.6	21
83	Secondary Structure Prediction of Single Sequences Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016, 1490, 15-34.	0.4	21
84	Analysis of a preQ1-I riboswitch in effector-free and bound states reveals a metabolite-programmed nucleobase-stacking spine that controls gene regulation. <i>Nucleic Acids Research</i> , 2020, 48, 8146-8164.	6.5	21
85	Making ends meet: New functions of mRNA secondary structure. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021, 12, e1611.	3.2	21
86	Predicting RNA secondary structure by free energy minimization. <i>Theoretical Chemistry Accounts</i> , 2006, 116, 160-168.	0.5	20
87	Experiment-Assisted Secondary Structure Prediction with RNAstructure. <i>Methods in Molecular Biology</i> , 2016, 1490, 163-176.	0.4	20
88	Stochastic sampling of the RNA structural alignment space. <i>Nucleic Acids Research</i> , 2009, 37, 4063-4075.	6.5	19
89	TurboKnot: rapid prediction of conserved RNA secondary structures including pseudoknots. <i>Bioinformatics</i> , 2012, 28, 792-798.	1.8	19
90	A small RNA that cooperatively senses two stacked metabolites in one pocket for gene control. <i>Nature Communications</i> , 2022, 13, 199.	5.8	19

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91	Identification of new high affinity targets for Roquin based on structural conservation. <i>Nucleic Acids Research</i> , 2018, 46, 12109-12125.	6.5	17
92	Chemically Accurate Relative Folding Stability of RNA Hairpins from Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 6598-6612.	2.3	17
93	An RNA molecular switch: Intrinsic flexibility of 23S rRNA Helices 40 and 68 5'-UAA/5'-GAN internal loops studied by molecular dynamics methods. <i>Journal of Chemical Theory and Computation</i> , 2010, 10, 910-929.	2.3	17
94	Modified Amber Force Field Correctly Models the Conformational Preference for Tandem GA pairs in RNA. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 1292-1301.	2.3	16
95	Predicting RNA-RNA Interactions Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016, 1490, 51-62.	0.4	15
96	Conservation of location of several specific inhibitory codon pairs in the <i>Saccharomyces sensu stricto</i> yeasts reveals translational selection. <i>Nucleic Acids Research</i> , 2019, 47, 1164-1177.	6.5	15
97	Molecular Mechanics Investigation of an Adenine-Adenine Non-Canonical Pair Conformational Change. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 3779-3792.	2.3	14
98	Modeling RNA Secondary Structure with Sequence Comparison and Experimental Mapping Data. <i>Biophysical Journal</i> , 2017, 113, 330-338.	0.2	14
99	Widespread temperature sensitivity and tRNA decay due to mutations in a yeast tRNA. <i>Rna</i> , 2018, 24, 410-422.	1.6	14
100	Accelerated RNA secondary structure design using preselected sequences for helices and loops. <i>Rna</i> , 2018, 24, 1555-1567.	1.6	14
101	LinearTurboFold: Linear-time global prediction of conserved structures for RNA homologs with applications to SARS-CoV-2. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	14
102	Nuclear Magnetic Resonance-Assisted Prediction of Secondary Structure for RNA: Incorporation of Direction-Dependent Chemical Shift Constraints. <i>Biochemistry</i> , 2015, 54, 6769-6782.	1.2	13
103	Using OligoWalk to Identify Efficient siRNA Sequences. <i>Methods in Molecular Biology</i> , 2010, 629, 107-119.	0.4	13
104	Design of highly active double-pseudoknotted ribozymes: a combined computational and experimental study. <i>Nucleic Acids Research</i> , 2019, 47, 29-42.	6.5	12
105	Nearest neighbor rules for RNA helix folding thermodynamics: improved end effects. <i>Nucleic Acids Research</i> , 2022, 50, 5251-5262.	6.5	12
106	Specific length and structure rather than high thermodynamic stability enable regulatory mRNA stem-loops to pause translation. <i>Nature Communications</i> , 2022, 13, 988.	5.8	10
107	Molecular dynamics correctly models the unusual major conformation of the GAGU RNA internal loop and with NMR reveals an unusual minor conformation. <i>Rna</i> , 2018, 24, 656-672.	1.6	9
108	Pre-mRNA splicing factor U2AF2 recognizes distinct conformations of nucleotide variants at the center of the pre-mRNA splice site signal. <i>Nucleic Acids Research</i> , 2022, 50, 5299-5312.	6.5	8

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109	A Test and Refinement of Folding Free Energy Nearest Neighbor Parameters for RNA Including N6-Methyladenosine. <i>Journal of Molecular Biology</i> , 2022, 434, 167632.	2.0	8
110	Thermodynamics of RNA Secondary Structure Formation. , 1999, , 21-47.		7
111	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. <i>Methods in Molecular Biology</i> , 2016, 1490, 35-50.	0.4	7
112	Structure-Function Model for Kissing Loop Interactions That Initiate Dimerization of Ty1 RNA. <i>Viruses</i> , 2017, 9, 93.	1.5	7
113	Accelerating calculations of RNA secondary structure partition functions using GPUs. <i>Algorithms for Molecular Biology</i> , 2013, 8, 29.	0.3	6
114	Quantitative prediction of variant effects on alternative splicing in MAPT using endogenous pre-messenger RNA structure probing. <i>ELife</i> , 0, 11, .	2.8	6
115	Estimating uncertainty in predicted folding free energy changes of RNA secondary structures. <i>Rna</i> , 2019, 25, 747-754.	1.6	5
116	Determining parameters for non-linear models of multi-loop free energy change. <i>Bioinformatics</i> , 2019, 35, 4298-4306.	1.8	5
117	RNA secondary structure prediction. , 2005, , .		4
118	Toward Turbo Decoding of RNA Secondary Structure. , 2007, , .		4
119	Surprising Sequence Effects on GU Closure of Symmetric 2 Å— 2 Nucleotide RNA Internal Loops. <i>Biochemistry</i> , 2018, 57, 2121-2131.	1.2	4
120	Secondary Structure of Influenza A Virus Genomic Segment 8 RNA Folded in a Cellular Environment. <i>International Journal of Molecular Sciences</i> , 2022, 23, 2452.	1.8	3
121	Probabilistic structural alignment of RNA sequences. <i>Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing</i> , 2008, , .	1.8	2
122	Inverse RNA Folding Workflow to Design and Test Ribozymes that Include Pseudoknots. <i>Methods in Molecular Biology</i> , 2021, 2167, 113-143.	0.4	2
123	Computational Resources for Molecular Biology 2022. <i>Journal of Molecular Biology</i> , 2022, 434, 167625.	2.0	2
124	Probabilistic Methods for Improving Efficiency of RNA Secondary Structure Prediction across Multiple Sequences. <i>Conference Record of the Asilomar Conference on Signals, Systems and Computers</i> , 2007, , .	0.0	1
125	Iterative estimation of structures of multiple RNA homologs: Turbofold. , 2011, , .		1
126	Joint stochastic sampling for RNA secondary structure prediction. , 2009, , .		0



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127	Accurate SHAPE-directed RNA structure prediction. FASEB Journal, 2009, 23, 843.2.	0.2	0
128	Gene architecture influences on the outcome of INDEL-based genome editing. FASEB Journal, 2018, 32, 649.8.	0.2	0