

David H Mathews

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.

131
papers

11,402
citations

41
h-index

106
g-index

156
ext. papers

13,221
ext. citations

9.3
avg, IF

6.65
L-index

#	Paper	IF	Citations
131	A small RNA that cooperatively senses two stacked metabolites in one pocket for gene control.. <i>Nature Communications</i> , 2022 , 13, 199	17.4	4
130	Specific length and structure rather than high thermodynamic stability enable regulatory mRNA stem-loops to pause translation.. <i>Nature Communications</i> , 2022 , 13, 988	17.4	2
129	Secondary structure prediction for RNA sequences including N-methyladenosine.. <i>Nature Communications</i> , 2022 , 13, 1271	17.4	4
128	Nearest neighbor rules for RNA helix folding thermodynamics: improved end effects.. <i>Nucleic Acids Research</i> , 2022 ,	20.1	1
127	A Test and Refinement of Folding Free Energy Nearest Neighbor Parameters for RNA Including N-Methyladenosine.. <i>Journal of Molecular Biology</i> , 2022 , 167632	6.5	0
126	Inverse RNA Folding Workflow to Design and Test Ribozymes that Include Pseudoknots. <i>Methods in Molecular Biology</i> , 2021 , 2167, 113-143	1.4	
125	LinearTurboFold: Linear-Time Global Prediction of Conserved Structures for RNA Homologs with Applications to SARS-CoV-2 2021 ,		1
124	Improved and Linear-Time Stochastic Sampling of RNA Secondary Structure with Applications to SARS-CoV-2 2021 ,		3
123	Making ends meet: New functions of mRNA secondary structure. <i>Wiley Interdisciplinary Reviews RNA</i> , 2021 , 12, e1611	9.3	3
122	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,	11.5	3
121	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	20.1	11
120	LinearPartition: linear-time approximation of RNA folding partition function and base-pairing probabilities. <i>Bioinformatics</i> , 2020 , 36, i258-i267	7.2	13
119	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	16.4	6
118	CRISPR-Cas9-based mutagenesis frequently provokes on-target mRNA misregulation. <i>Nature Communications</i> , 2019 , 10, 4056	17.4	90
117	Estimating uncertainty in predicted folding free energy changes of RNA secondary structures. <i>Rna</i> , 2019 , 25, 747-754	5.8	5
116	How to benchmark RNA secondary structure prediction accuracy. <i>Methods</i> , 2019 , 162-163, 60-67	4.6	10
115	Determining parameters for non-linear models of multi-loop free energy change. <i>Bioinformatics</i> , 2019 , 35, 4298-4306	7.2	1

114	LinearFold: linear-time approximate RNA folding by 5' to 3' dynamic programming and beam search. <i>Bioinformatics</i> , 2019 , 35, i295-i304	7.2	29
113	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	20.1	6
112	Design of highly active double-pseudoknotted ribozymes: a combined computational and experimental study. <i>Nucleic Acids Research</i> , 2019 , 47, 29-42	20.1	3
111	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	5.8	7
110	Widespread temperature sensitivity and tRNA decay due to mutations in a yeast tRNA. <i>Rna</i> , 2018 , 24, 410-422	5.8	12
109	Modeling RNA secondary structure folding ensembles using SHAPE mapping data. <i>Nucleic Acids Research</i> , 2018 , 46, 314-323	20.1	47
108	Surprising Sequence Effects on GU Closure of Symmetric 2 \square Nucleotide RNA Internal Loops. <i>Biochemistry</i> , 2018 , 57, 2121-2131	3.2	4
107	Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. <i>Nucleic Acids Research</i> , 2018 , 46, 4883-4892	20.1	10
106	Analysis of RNA nearest neighbor parameters reveals interdependencies and quantifies the uncertainty in RNA secondary structure prediction. <i>Rna</i> , 2018 , 24, 1568-1582	5.8	18
105	Accelerated RNA secondary structure design using preselected sequences for helices and loops. <i>Rna</i> , 2018 , 24, 1555-1567	5.8	3
104	Gene architecture influences on the outcome of INDEL-based genome editing. <i>FASEB Journal</i> , 2018 , 32, 649.8	0.9	
103	Identification of new high affinity targets for Roquin based on structural conservation. <i>Nucleic Acids Research</i> , 2018 , 46, 12109-12125	20.1	9
102	Chemically Accurate Relative Folding Stability of RNA Hairpins from Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2018 , 14, 6598-6612	6.4	9
101	mRNAs and lncRNAs intrinsically form secondary structures with short end-to-end distances. <i>Nature Communications</i> , 2018 , 9, 4328	17.4	33
100	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	20.1	18
99	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	20.1	11
98	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	20.1	27
97	Revised RNA Dihedral Parameters for the Amber Force Field Improve RNA Molecular Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2017 , 13, 900-915	6.4	57

96	Base pair probability estimates improve the prediction accuracy of RNA non-canonical base pairs. <i>PLoS Computational Biology</i> , 2017 , 13, e1005827	5	16
95	Modeling RNA Secondary Structure with Sequence Comparison and Experimental Mapping Data. <i>Biophysical Journal</i> , 2017 , 113, 330-338	2.9	9
94	Physics-based all-atom modeling of RNA energetics and structure. <i>Wiley Interdisciplinary Reviews RNA</i> , 2017 , 8, e1422	9.3	25
93	Structure-Function Model for Kissing Loop Interactions That Initiate Dimerization of Ty1 RNA. <i>Viruses</i> , 2017 , 9,	6.2	3
92	TurboFold II: RNA structural alignment and secondary structure prediction informed by multiple homologs. <i>Nucleic Acids Research</i> , 2017 , 45, 11570-11581	20.1	38
91	Exact calculation of loop formation probability identifies folding motifs in RNA secondary structures. <i>Rna</i> , 2016 , 22, 1808-1818	5.8	22
90	AccessFold: predicting RNA-RNA interactions with consideration for competing self-structure. <i>Bioinformatics</i> , 2016 , 32, 1033-9	7.2	14
89	Bridging the gap between in vitro and in vivo RNA folding. <i>Quarterly Reviews of Biophysics</i> , 2016 , 49, e10	7	70
88	RNA Secondary Structure Prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2016 , 67, 11.2.1-11.2.19	0.5	18
87	Experiment-Assisted Secondary Structure Prediction with RNAstructure. <i>Methods in Molecular Biology</i> , 2016 , 1490, 163-76	1.4	17
86	Predicting RNA-RNA Interactions Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016 , 1490, 51-62	1.4	8
85	Secondary Structure Prediction of Single Sequences Using RNAstructure. <i>Methods in Molecular Biology</i> , 2016 , 1490, 15-34	1.4	13
84	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. <i>Methods in Molecular Biology</i> , 2016 , 1490, 35-50	1.4	3
83	Improved prediction of RNA secondary structure by integrating the free energy model with restraints derived from experimental probing data. <i>Nucleic Acids Research</i> , 2015 , 43, 7247-59	20.1	55
82	Structural analysis of a class III preQ1 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	11.5	44
81	Molecular mechanism for preQ1-II riboswitch function revealed by molecular dynamics. <i>Rna</i> , 2015 , 21, 1898-907	5.8	20
80	Nuclear Magnetic Resonance-Assisted Prediction of Secondary Structure for RNA: Incorporation of Direction-Dependent Chemical Shift Constraints. <i>Biochemistry</i> , 2015 , 54, 6769-82	3.2	13
79	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	3.7	21

78	Improving RNA secondary structure prediction with structure mapping data. <i>Methods in Enzymology</i> , 2015 , 553, 91-114	1.7	37
77	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, 1721-32	12.6	45
76	Influence of Sequence and Covalent Modifications on Yeast tRNA Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2014 , 10, 3473-3483	6.4	15
75	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	6.4	15
74	Using the RNAstructure Software Package to Predict Conserved RNA Structures. <i>Current Protocols in Bioinformatics</i> , 2014 , 46, 12.4.1-22	24.2	21
73	Dynalign II: common secondary structure prediction for RNA homologs with domain insertions. <i>Nucleic Acids Research</i> , 2014 , 42, 13939-48	20.1	30
72	RNA Secondary Structure Analysis Using RNAstructure. <i>Current Protocols in Bioinformatics</i> , 2014 , 46, 12.6.1-25	24.2	41
71	The determination of RNA folding nearest neighbor parameters. <i>Methods in Molecular Biology</i> , 2014 , 1097, 45-70	1.4	34
70	Accelerating calculations of RNA secondary structure partition functions using GPUs. <i>Algorithms for Molecular Biology</i> , 2013 , 8, 29	1.8	5
69	Principles for understanding the accuracy of SHAPE-directed RNA structure modeling. <i>Biochemistry</i> , 2013 , 52, 588-95	3.2	35
68	RNAstructure: Web servers for RNA secondary structure prediction and analysis. <i>Nucleic Acids Research</i> , 2013 , 41, W471-4	20.1	220
67	Pyrvinium pamoate changes alternative splicing of the serotonin receptor 2C by influencing its RNA structure. <i>Nucleic Acids Research</i> , 2013 , 41, 3819-32	20.1	26
66	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, 5498-503	11.5	210
65	RNA structure prediction: an overview of methods. <i>Methods in Molecular Biology</i> , 2012 , 905, 99-122	1.4	97
64	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	6.4	30
63	Statistical evaluation of improvement in RNA secondary structure prediction. <i>Nucleic Acids Research</i> , 2012 , 40, e26	20.1	22
62	TurboKnot: rapid prediction of conserved RNA secondary structures including pseudoknots. <i>Bioinformatics</i> , 2012 , 28, 792-8	7.2	18
61	Fluorescence competition and optical melting measurements of RNA three-way multibranch loops provide a revised model for thermodynamic parameters. <i>Biochemistry</i> , 2011 , 50, 640-53	3.2	15

60	TurboFold: iterative probabilistic estimation of secondary structures for multiple RNA sequences. <i>BMC Bioinformatics</i> , 2011 , 12, 108	3.6	66
59	Automated RNA tertiary structure prediction from secondary structure and low-resolution restraints. <i>Journal of Computational Chemistry</i> , 2011 , 32, 2232-44	3.5	29
58	Molecular Mechanics Investigation of an Adenine-Adenine Non-Canonical Pair Conformational Change. <i>Journal of Chemical Theory and Computation</i> , 2011 , 7, 3779-3792	6.4	12
57	Multilign: an algorithm to predict secondary structures conserved in multiple RNA sequences. <i>Bioinformatics</i> , 2011 , 27, 626-32	7.2	42
56	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011 , 17, 1204-12	5.8	27
55	A sequence similar to tRNA 3 Lys gene is embedded in HIV-1 U3-R and promotes minus-strand transfer. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 83-9	17.6	22
54	FragSeq: transcriptome-wide RNA structure probing using high-throughput sequencing. <i>Nature Methods</i> , 2010 , 7, 995-1001	21.6	254
53	Folding and finding RNA secondary structure. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010 , 2, a003665	5.2	107
52	ProbKnot: fast prediction of RNA secondary structure including pseudoknots. <i>Rna</i> , 2010 , 16, 1870-80	5.8	128
51	Computational approaches for RNA energy parameter estimation. <i>Rna</i> , 2010 , 16, 2304-18	5.8	78
50	NNDB: the nearest neighbor parameter database for predicting stability of nucleic acid secondary structure. <i>Nucleic Acids Research</i> , 2010 , 38, D280-2	20.1	316
49	RNAstructure: software for RNA secondary structure prediction and analysis. <i>BMC Bioinformatics</i> , 2010 , 11, 129	3.6	1095
48	An RNA Molecular Switch: Intrinsic Flexibility of 23S rRNA Helices 40 and 68 5WUAA/5WGAN Internal Loops Studied by Molecular Dynamics Methods. <i>Journal of Chemical Theory and Computation</i> , 2010 , 6, 910-29	6.4	41
47	An RNA molecular switch: Intrinsic flexibility of 23S rRNA Helices 40 and 68 5WUAA/5WGAN internal loops studied by molecular dynamics methods. <i>Journal of Chemical Theory and Computation</i> , 2010 , 2010, 910-929	6.4	16
46	RNA pseudoknots: folding and finding. <i>F1000 Biology Reports</i> , 2010 , 2, 8		28
45	Using OligoWalk to identify efficient siRNA sequences. <i>Methods in Molecular Biology</i> , 2010 , 629, 109-21	1.4	7
44	Improved RNA secondary structure prediction by maximizing expected pair accuracy. <i>Rna</i> , 2009 , 15, 1805-13	5.8	146
43	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	11.5	493

42	Stochastic sampling of the RNA structural alignment space. <i>Nucleic Acids Research</i> , 2009 , 37, 4063-75	20.1	14
41	Accurate SHAPE-directed RNA structure prediction. <i>FASEB Journal</i> , 2009 , 23, 843.2	0.9	
40	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, 10233-9	16.4	37
39	OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2008 , 36, W104-8	20.1	66
38	Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. <i>Nucleic Acids Research</i> , 2008 , 36, 3738-45	20.1	20
37	PARTS: probabilistic alignment for RNA joint secondary structure prediction. <i>Nucleic Acids Research</i> , 2008 , 36, 2406-17	20.1	39
36	Probabilistic structural alignment of RNA sequences. <i>Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing</i> , 2008 ,	1.6	1
35	Efficient siRNA selection using hybridization thermodynamics. <i>Nucleic Acids Research</i> , 2008 , 36, 640-7	20.1	105
34	NMR reveals the absence of hydrogen bonding in adjacent UU and AG mismatches in an isolated internal loop from ribosomal RNA. <i>Biochemistry</i> , 2007 , 46, 12665-78	3.2	20
33	Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign. <i>BMC Bioinformatics</i> , 2007 , 8, 130	3.6	82
32	Predicting helical coaxial stacking in RNA multibranch loops. <i>Rna</i> , 2007 , 13, 939-51	5.8	52
31	Toward Turbo Decoding of RNA Secondary Structure 2007 ,		1
30	Efficient parameter estimation for RNA secondary structure prediction. <i>Bioinformatics</i> , 2007 , 23, i19-28	7.2	124
29	RNA secondary structure prediction. <i>Current Protocols in Nucleic Acid Chemistry</i> , 2007 , Chapter 11, Unit 11.2	0.5	52
28	Predicting RNA secondary structure by free energy minimization. <i>Theoretical Chemistry Accounts</i> , 2006 , 116, 160-168	1.9	16
27	Prediction of RNA secondary structure by free energy minimization. <i>Current Opinion in Structural Biology</i> , 2006 , 16, 270-8	8.1	283
26	Detection of non-coding RNAs on the basis of predicted secondary structure formation free energy change. <i>BMC Bioinformatics</i> , 2006 , 7, 173	3.6	125
25	A set of nearest neighbor parameters for predicting the enthalpy change of RNA secondary structure formation. <i>Nucleic Acids Research</i> , 2006 , 34, 4912-24	20.1	100

24	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, 1683-93	6.5	37
23	Revolutions in RNA secondary structure prediction. <i>Journal of Molecular Biology</i> , 2006 , 359, 526-32	6.5	134
22	Nearest neighbor parameters for Watson-Crick complementary heteroduplexes formed between 2MO-methyl RNA and RNA oligonucleotides. <i>Nucleic Acids Research</i> , 2006 , 34, 3609-14	20.1	33
21	RNA secondary structure analysis using RNAstructure. <i>Current Protocols in Bioinformatics</i> , 2006 , Chapter 12, Unit 12.6	24.2	51
20	RNA secondary structure prediction 2005 ,		1
19	Predicting a set of minimal free energy RNA secondary structures common to two sequences. <i>Bioinformatics</i> , 2005 , 21, 2246-53	7.2	95
18	Using an RNA secondary structure partition function to determine confidence in base pairs predicted by free energy minimization. <i>Rna</i> , 2004 , 10, 1178-90	5.8	249
17	Secondary structure models of the 3Wntranslated regions of diverse R2 RNAs. <i>Rna</i> , 2004 , 10, 978-87	5.8	20
16	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
15	Experimentally derived nearest-neighbor parameters for the stability of RNA three- and four-way multibranch loops. <i>Biochemistry</i> , 2002 , 41, 869-80	3.2	66
14	Dynalign: an algorithm for finding the secondary structure common to two RNA sequences. <i>Journal of Molecular Biology</i> , 2002 , 317, 191-203	6.5	302
13	Thermodynamics of three-way multibranch loops in RNA. <i>Biochemistry</i> , 2001 , 40, 6971-81	3.2	76
12	Thermodynamics of RNA Secondary Structure Formation 1999 , 21-47		6
11	Predicting oligonucleotide affinity to nucleic acid targets. <i>Rna</i> , 1999 , 5, 1458-69	5.8	199
10	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
9	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. <i>ACS Symposium Series</i> , 1997 , 246-257	0.4	14
8	RNA Helix Thermodynamics: The End Game		2
7	LinearFold: Linear-Time Prediction of RNA Secondary Structures		1

6	The formation of intramolecular secondary structure brings mRNA ends in close proximity	1
5	Chemically Accurate Relative Folding Stability of RNA Hairpins from Molecular Simulations	1
4	CRISPR/Cas9-based mutagenesis frequently provokes on-target mRNA misregulation	1
3	Secondary Structure Prediction for RNA Sequences Including N6-methyladenosine	1
2	Specific length and structure rather than high thermodynamic stability enable regulatory mRNA stem-loops to pause translation	2
1	Quantitative prediction of variant effects on alternative splicing using endogenous pre-messenger RNA structure probing	1