DavidÂ H Mathews

List of Publications by Year
in descending order

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	A small RNA that cooperatively senses two stacked metabolites in one pocket for gene control. Nature Communications, 2022, 13, 199.	5.8	19
2	Secondary Structure of Influenza A Virus Genomic Segment 8 RNA Folded in a Cellular Environment. International Journal of Molecular Sciences, 2022, 23, 2452.	1.8	3
3	Specific length and structure rather than high thermodynamic stability enable regulatory mRNA stem-loops to pause translation. Nature Communications, 2022, 13, 988.	5.8	10
4	Secondary structure prediction for RNA sequences including N6-methyladenosine. Nature Communications, 2022, 13, 1271.	5.8	27
5	Pre-mRNA splicing factor U2AF2 recognizes distinct conformations of nucleotide variants at the center of the pre-mRNA splice site signal. Nucleic Acids Research, 2022, 50, 5299-5312.	6.5	8
6	Nearest neighbor rules for RNA helix folding thermodynamics: improved end effects. Nucleic Acids Research, 2022, 50, 5251-5262.	6.5	12
7	Computational Resources for Molecular Biology 2022. Journal of Molecular Biology, 2022, 434, 167625.	2.0	2
8	A Test and Refinement of Folding Free Energy Nearest Neighbor Parameters for RNA Including N6-Methyladenosine. Journal of Molecular Biology, 2022, 434, 167632.	2.0	8
9	Making ends meet: New functions of <scp>mRNA</scp> secondary structure. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1611.	3.2	21
10	Inverse RNA Folding Workflow to Design and Test Ribozymes that Include Pseudoknots. Methods in Molecular Biology, 2021, 2167, 113-143.	0.4	2
11	LinearTurboFold: Linear-time global prediction of conserved structures for RNA homologs with applications to SARS-CoV-2. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	14
12	Analysis of a preQ1-I riboswitch in effector-free and bound states reveals a metabolite-programmed nucleobase-stacking spine that controls gene regulation. Nucleic Acids Research, 2020, 48, 8146-8164.	6.5	21
13	LinearPartition: linear-time approximation of RNA folding partition function and base-pairing probabilities. Bioinformatics, 2020, 36, i258-i267.	1.8	44
14	Arginine Forks Are a Widespread Motif to Recognize Phosphate Backbones and Guanine Nucleobases in the RNA Major Groove. Journal of the American Chemical Society, 2020, 142, 19835-19839.	6.6	26
15	Design of highly active double-pseudoknotted ribozymes: a combined computational and experimental study. Nucleic Acids Research, 2019, 47, 29-42.	6.5	12
16	LinearFold: linear-time approximate RNA folding by 5'-to-3' dynamic programming and beam search. Bioinformatics, 2019, 35, i295-i304.	1.8	100
17	CRISPR-Cas9-based mutagenesis frequently provokes on-target mRNA misregulation. Nature Communications, 2019, 10, 4056.	5.8	139
18	Estimating uncertainty in predicted folding free energy changes of RNA secondary structures. Rna, 2019, 25, 747-754.	1.6	5

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19	How to benchmark RNA secondary structure prediction accuracy. Methods, 2019, 162-163, 60-67.	1.9	32
20	Determining parameters for non-linear models of multi-loop free energy change. Bioinformatics, 2019, 35, 4298-4306.	1.8	5
21	Conservation of location of several specific inhibitory codon pairs in the Saccharomyces sensu stricto yeasts reveals translational selection. Nucleic Acids Research, 2019, 47, 1164-1177.	6.5	15
22	Molecular dynamics correctly models the unusual major conformation of the GAGU RNA internal loop and with NMR reveals an unusual minor conformation. Rna, 2018, 24, 656-672.	1.6	9
23	Widespread temperature sensitivity and tRNA decay due to mutations in a yeast tRNA. Rna, 2018, 24, 410-422.	1.6	14
24	Modeling RNA secondary structure folding ensembles using SHAPE mapping data. Nucleic Acids Research, 2018, 46, 314-323.	6.5	72
25	Surprising Sequence Effects on GU Closure of Symmetric 2 Ã— 2 Nucleotide RNA Internal Loops. Biochemistry, 2018, 57, 2121-2131.	1.2	4
26	Identification of new high affinity targets for Roquin based on structural conservation. Nucleic Acids Research, 2018, 46, 12109-12125.	6.5	17
27	Chemically Accurate Relative Folding Stability of RNA Hairpins from Molecular Simulations. Journal of Chemical Theory and Computation, 2018, 14, 6598-6612.	2.3	17
28	mRNAs and lncRNAs intrinsically form secondary structures with short end-to-end distances. Nature Communications, 2018, 9, 4328.	5.8	62
29	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. Nucleic Acids Research, 2018, 46, 6401-6415.	6.5	27
30	Improving RNA nearest neighbor parameters for helices by going beyond the two-state model. Nucleic Acids Research, 2018, 46, 4883-4892.	6.5	22
31	Analysis of RNA nearest neighbor parameters reveals interdependencies and quantifies the uncertainty in RNA secondary structure prediction. Rna, 2018, 24, 1568-1582.	1.6	25
32	Accelerated RNA secondary structure design using preselected sequences for helices and loops. Rna, 2018, 24, 1555-1567.	1.6	14
33	Gene architecture influences on the outcome of INDELâ€based genome editing. FASEB Journal, 2018, 32, 649.8.	0.2	0
34	Advanced multi-loop algorithms for RNA secondary structure prediction reveal that the simplest model is best. Nucleic Acids Research, 2017, 45, 8541-8550.	6.5	29
35	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. Nucleic Acids Research, 2017, 45, 6168-6176.	6.5	34
36	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

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37	Modeling RNA Secondary Structure with Sequence Comparison and Experimental Mapping Data. Biophysical Journal, 2017, 113, 330-338.	0.2	14
38	Physicsâ€based allâ€atom modeling of <scp>RNA</scp> energetics and structure. Wiley Interdisciplinary Reviews RNA, 2017, 8, e1422.	3.2	32
39	Structure-Function Model for Kissing Loop Interactions That Initiate Dimerization of Ty1 RNA. Viruses, 2017, 9, 93.	1.5	7
40	TurboFold II: RNA structural alignment and secondary structure prediction informed by multiple homologs. Nucleic Acids Research, 2017, 45, 11570-11581.	6.5	100
41	Base pair probability estimates improve the prediction accuracy of RNA non-canonical base pairs. PLoS Computational Biology, 2017, 13, e1005827.	1.5	27
42	Bridging the gap betweenin vitroandin vivoRNA folding. Quarterly Reviews of Biophysics, 2016, 49, e10.	2.4	108
43	RNA Secondary Structure Prediction. Current Protocols in Nucleic Acid Chemistry, 2016, 67, 11.2.1-11.2.19.	0.5	32
44	Experiment-Assisted Secondary Structure Prediction with RNAstructure. Methods in Molecular Biology, 2016, 1490, 163-176.	0.4	20
45	Predicting RNAâ€“RNA Interactions Using RNAstructure. Methods in Molecular Biology, 2016, 1490, 51-62.	0.4	15
46	Secondary Structure Prediction of Single Sequences Using RNAstructure. Methods in Molecular Biology, 2016, 1490, 15-34.	0.4	21
47	Prediction of Secondary Structures Conserved in Multiple RNA Sequences. Methods in Molecular Biology, 2016, 1490, 35-50.	0.4	7
48	Exact calculation of loop formation probability identifies folding motifs in RNA secondary structures. Rna, 2016, 22, 1808-1818.	1.6	59
49	AccessFold: predicting RNAâ€“RNA interactions with consideration for competing self-structure. Bioinformatics, 2016, 32, 1033-1039.	1.8	26
50	Discovery of Novel ncRNA Sequences in Multiple Genome Alignments on the Basis of Conserved and Stable Secondary Structures. PLoS ONE, 2015, 10, e0130200.	1.1	26
51	Improving RNA Secondary Structure Prediction with Structure Mapping Data. Methods in Enzymology, 2015, 553, 91-114.	0.4	46
52	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
53	Structural analysis of a class III preQ ₁ riboswitch reveals an aptamer distant from a ribosome-binding site regulated by fast dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E3485-94.	3.3	62
54	Molecular mechanism for preQ₁-II riboswitch function revealed by molecular dynamics. Rna, 2015, 21, 1898-1907.	1.6	21

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55	Nuclear Magnetic Resonance-Assisted Prediction of Secondary Structure for RNA: Incorporation of Direction-Dependent Chemical Shift Constraints. Biochemistry, 2015, 54, 6769-6782.	1.2	13
56	Dynalign II: common secondary structure prediction for RNA homologs with domain insertions. Nucleic Acids Research, 2014, 42, 13939-13948.	6.5	40
57	RNA Secondary Structure Analysis Using RNAstructure. Current Protocols in Bioinformatics, 2014, 46, 12.6.1-25.	25.8	50
58	Identification of the determinants of tRNA function and susceptibility to rapid tRNA decay by high-throughput in vivo analysis. Genes and Development, 2014, 28, 1721-1732.	2.7	58
59	Influence of Sequence and Covalent Modifications on Yeast tRNA Dynamics. Journal of Chemical Theory and Computation, 2014, 10, 3473-3483.	2.3	22
60	Modified Amber Force Field Correctly Models the Conformational Preference for Tandem GA pairs in RNA. Journal of Chemical Theory and Computation, 2014, 10, 1292-1301.	2.3	16
61	Using the RNA<scp>structure</scp> Software Package to Predict Conserved RNA Structures. Current Protocols in Bioinformatics, 2014, 46, 12.4.1-22.	25.8	31
62	The Determination of RNA Folding Nearest Neighbor Parameters. Methods in Molecular Biology, 2014, 1097, 45-70.	0.4	52
63	Accelerating calculations of RNA secondary structure partition functions using GPUs. Algorithms for Molecular Biology, 2013, 8, 29.	0.3	6
64	Principles for Understanding the Accuracy of SHAPE-Directed RNA Structure Modeling. Biochemistry, 2013, 52, 588-595.	1.2	41
65	RNAstructure: web servers for RNA secondary structure prediction and analysis. Nucleic Acids Research, 2013, 41, W471-W474.	6.5	321
66	Pyrvinium pamoate changes alternative splicing of the serotonin receptor 2C by influencing its RNA structure. Nucleic Acids Research, 2013, 41, 3819-3832.	6.5	26
67	Accurate SHAPE-directed RNA secondary structure modeling, including pseudoknots. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5498-5503.	3.3	286
68	Statistical evaluation of improvement in RNA secondary structure prediction. Nucleic Acids Research, 2012, 40, e26-e26.	6.5	23
69	TurboKnot: rapid prediction of conserved RNA secondary structures including pseudoknots. Bioinformatics, 2012, 28, 792-798.	1.8	19
70	RNA Structure Prediction: An Overview of Methods. Methods in Molecular Biology, 2012, 905, 99-122.	0.4	135
71	The Amber ff99 Force Field Predicts Relative Free Energy Changes for RNA Helix Formation. Journal of Chemical Theory and Computation, 2012, 8, 2497-2505.	2.3	39
72	Iterative estimation of structures of multiple RNA homologs: Turbofold. , 2011, , .		1

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73	Molecular Mechanics Investigation of an Adenineâ€“Adenine Non-Canonical Pair Conformational Change. Journal of Chemical Theory and Computation, 2011, 7, 3779-3792.	2.3	14
74	Fluorescence Competition and Optical Melting Measurements of RNA Three-Way Multibranch Loops Provide a Revised Model for Thermodynamic Parameters. Biochemistry, 2011, 50, 640-653.	1.2	25
75	TurboFold: Iterative probabilistic estimation of secondary structures for multiple RNA sequences. BMC Bioinformatics, 2011, 12, 108.	1.2	80
76	Automated RNA tertiary structure prediction from secondary structure and lowâ€resolution restraints. Journal of Computational Chemistry, 2011, 32, 2232-2244.	1.5	35
77	Multilign: an algorithm to predict secondary structures conserved in multiple RNA sequences. Bioinformatics, 2011, 27, 626-632.	1.8	54
78	Sharing and archiving nucleic acid structure mapping data. Rna, 2011, 17, 1204-1212.	1.6	28
79	A sequence similar to tRNA3Lys gene is embedded in HIV-1 U3â€“R and promotes minus-strand transfer. Nature Structural and Molecular Biology, 2010, 17, 83-89.	3.6	27
80	FragSeq: transcriptome-wide RNA structure probing using high-throughput sequencing. Nature Methods, 2010, 7, 995-1001.	9.0	289
81	Folding and Finding RNA Secondary Structure. Cold Spring Harbor Perspectives in Biology, 2010, 2, a003665-a003665.	2.3	136
82	ProbKnot: Fast prediction of RNA secondary structure including pseudoknots. Rna, 2010, 16, 1870-1880.	1.6	169
83	Computational approaches for RNA energy parameter estimation. Rna, 2010, 16, 2304-2318.	1.6	110
84	NNDB: the nearest neighbor parameter database for predicting stability of nucleic acid secondary structure. Nucleic Acids Research, 2010, 38, D280-D282.	6.5	444
85	RNAstructure: software for RNA secondary structure prediction and analysis. BMC Bioinformatics, 2010, 11, 129.	1.2	1,568
86	An RNA Molecular Switch: Intrinsic Flexibility of 23S rRNA Helices 40 and 68 5â€²-UAA/5â€²-GAN Internal Loops Studied by Molecular Dynamics Methods. Journal of Chemical Theory and Computation, 2010, 6, 910-929.	2.3	46
87	Using OligoWalk to Identify Efficient siRNA Sequences. Methods in Molecular Biology, 2010, 629, 107-119.	0.4	13
88	RNA pseudoknots: folding and finding. F1000 Biology Reports, 2010, 2, 8.	4.0	30
89	An RNA molecular switch: Intrinsic flexibility of 23S rRNA Helices 40 and 68 5'-UAA/5'-GAN internal loops studied by molecular dynamics methods. Journal of Chemical Theory and Computation, 2010, 2010, 910-929.	2.3	17
90	Improved RNA secondary structure prediction by maximizing expected pair accuracy. Rna, 2009, 15, 1805-1813.	1.6	194

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91	Accurate SHAPE-directed RNA structure determination. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 97-102.	3.3	624
92	Stochastic sampling of the RNA structural alignment space. Nucleic Acids Research, 2009, 37, 4063-4075.	6.5	19
93	Joint stochastic sampling for RNA secondary structure prediction. , 2009, , .		0
94	Accurate SHAPEâ€directed RNA structure prediction. FASEB Journal, 2009, 23, 843.2.	0.2	0
95	NMR-Assisted Prediction of RNA Secondary Structure: Identification of a Probable Pseudoknot in the Coding Region of an R2 Retrotransposon. Journal of the American Chemical Society, 2008, 130, 10233-10239.	6.6	45
96	OligoWalk: an online siRNA design tool utilizing hybridization thermodynamics. Nucleic Acids Research, 2008, 36, W104-W108.	6.5	93
97	Fundamental differences in the equilibrium considerations for siRNA and antisense oligodeoxynucleotide design. Nucleic Acids Research, 2008, 36, 3738-3745.	6.5	25
98	PARTS: Probabilistic Alignment for RNA joinT Secondary structure prediction. Nucleic Acids Research, 2008, 36, 2406-2417.	6.5	44
99	Probabilistic structural alignment of RNA sequences. Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing, 2008, , .	1.8	2
100	Predicting helical coaxial stacking in RNA multibranch loops. Rna, 2007, 13, 939-951.	1.6	60
101	Toward Turbo Decoding of RNA Secondary Structure. , 2007, , .		4
102	Efficient parameter estimation for RNA secondary structure prediction. Bioinformatics, 2007, 23, i19-i28.	1.8	169
103	RNA Secondary Structure Prediction. Current Protocols in Nucleic Acid Chemistry, 2007, 28, Unit 11.2.	0.5	91
104	Probabilistic Methods for Improving Efficiency of RNA Secondary Structure Prediction across Multiple Sequences. Conference Record of the Asilomar Conference on Signals, Systems and Computers, 2007, , .	0.0	1
105	NMR Reveals the Absence of Hydrogen Bonding in Adjacent UU and AG Mismatches in an Isolated Internal Loop from Ribosomal RNA[,]. Biochemistry, 2007, 46, 12665-12678.	1.2	21
106	Efficient siRNA selection using hybridization thermodynamics. Nucleic Acids Research, 2007, 36, 640-647.	6.5	126
107	Efficient pairwise RNA structure prediction using probabilistic alignment constraints in Dynalign. BMC Bioinformatics, 2007, 8, 130.	1.2	94
108	Nudged Elastic Band Calculation of Minimal Energy Paths for the Conformational Change of a GG Non-canonical Pair. Journal of Molecular Biology, 2006, 357, 1683-1693.	2.0	47

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109	Revolutions in RNA Secondary Structure Prediction. Journal of Molecular Biology, 2006, 359, 526-532.	2.0	167
110	Nearest neighbor parameters for Watson-Crick complementary heteroduplexes formed between 2'-O-methyl RNA and RNA oligonucleotides. Nucleic Acids Research, 2006, 34, 3609-3614.	6.5	36
111	RNA Secondary Structure Analysis Using RNAstructure. Current Protocols in Bioinformatics, 2006, 13, Unit 12.6.	25.8	73
112	Predicting RNA secondary structure by free energy minimization. Theoretical Chemistry Accounts, 2006, 116, 160-168.	0.5	20
113	Prediction of RNA secondary structure by free energy minimization. Current Opinion in Structural Biology, 2006, 16, 270-278.	2.6	339
114	Detection of non-coding RNAs on the basis of predicted secondary structure formation free energy change. BMC Bioinformatics, 2006, 7, 173.	1.2	150
115	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
116	RNA secondary structure prediction. , 2005, , .		4
117	Predicting a set of minimal free energy RNA secondary structures common to two sequences. Bioinformatics, 2005, 21, 2246-2253.	1.8	109
118	Using an RNA secondary structure partition function to determine confidence in base pairs predicted by free energy minimization. Rna, 2004, 10, 1178-1190.	1.6	315
119	Secondary structure models of the 3' untranslated regions of diverse R2 RNAs. Rna, 2004, 10, 978-987.	1.6	23
120	Incorporating chemical modification constraints into a dynamic programming algorithm for prediction of RNA secondary structure. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7287-7292.	3.3	1,332
121	Experimentally Derived Nearest-Neighbor Parameters for the Stability of RNA Three- and Four-Way Multibranch Loopsâ€. Biochemistry, 2002, 41, 869-880.	1.2	73
122	Dynalign: an algorithm for finding the secondary structure common to two RNA sequences. Journal of Molecular Biology, 2002, 317, 191-203.	2.0	340
123	Thermodynamics of Three-Way Multibranch Loops in RNAâ€. Biochemistry, 2001, 40, 6971-6981.	1.2	88
124	Thermodynamics of RNA Secondary Structure Formation. , 1999, , 21-47.		7
125	Predicting oligonucleotide affinity to nucleic acid targets. Rna, 1999, 5, 1458-1469.	1.6	228
126	Expanded sequence dependence of thermodynamic parameters improves prediction of RNA secondary structure. Journal of Molecular Biology, 1999, 288, 911-940.	2.0	3,486

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127	An Updated Recursive Algorithm for RNA Secondary Structure Prediction with Improved Thermodynamic Parameters. ACS Symposium Series, 1997, , 246-257.	0.5	21
128	Quantitative prediction of variant effects on alternative splicing in MAPT using endogenous pre-messenger RNA structure probing. ELife, 0, 11, .	2.8	6