

Rhiju Das

List of Publications by Year in descending order

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Version: 2024-02-01

137
papers

15,932
citations

26630

56
h-index

20961

115
g-index

177
all docs

177
docs citations

177
times ranked

15966
citing authors

#	ARTICLE	IF	CITATIONS
1	Rosetta3. <i>Methods in Enzymology</i> , 2011, 487, 545-574.	1.0	1,620
2	The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3031-3048.	5.3	1,032
3	Macromolecular Modeling with Rosetta. <i>Annual Review of Biochemistry</i> , 2008, 77, 363-382.	11.1	841
4	Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them. <i>Nature Reviews Molecular Cell Biology</i> , 2018, 19, 158-174.	37.0	577
5	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513
6	Structure prediction for CASP8 with all-atom refinement using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 89-99.	2.6	425
7	Automated <i>de novo</i> prediction of native-like RNA tertiary structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 14664-14669.	7.1	397
8	Spontaneous driving forces give rise to protein-RNA condensates with coexisting phases and complex material properties. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 7889-7898.	7.1	365
9	Understanding Nucleic Acid-Ion Interactions. <i>Annual Review of Biochemistry</i> , 2014, 83, 813-841.	11.1	358
10	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). <i>PLoS ONE</i> , 2013, 8, e63906.	2.5	348
11	Are Protein Force Fields Getting Better? A Systematic Benchmark on 524 Diverse NMR Measurements. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 1409-1414.	5.3	347
12	Atomic accuracy in predicting and designing noncanonical RNA structure. <i>Nature Methods</i> , 2010, 7, 291-294.	19.0	328
13	Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters. <i>Rna</i> , 2009, 15, 189-199.	3.5	300
14	SAFA: Semi-automated footprinting analysis software for high-throughput quantification of nucleic acid footprinting experiments. <i>Rna</i> , 2005, 11, 344-354.	3.5	299
15	High-resolution structure prediction and the crystallographic phase problem. <i>Nature</i> , 2007, 450, 259-264.	27.8	296
16	RNA design rules from a massive open laboratory. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2122-2127.	7.1	264
17	RNA regulons in Hox 5' UTRs confer ribosome specificity to gene regulation. <i>Nature</i> , 2015, 517, 33-38.	27.8	258
18	RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	3.5	241

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19	RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: a first look. <i>Rna</i> , 2020, 26, 937-959.	3.5	211
20	Remeasuring the Double Helix. <i>Science</i> , 2008, 322, 446-449.	12.6	200
21	Geometric deep learning of RNA structure. <i>Science</i> , 2021, 373, 1047-1051.	12.6	190
22	Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 118-128.	2.6	178
23	Double-stranded RNA under force and torque: Similarities to and striking differences from double-stranded DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 15408-15413.	7.1	162
24	<i>RNA-Puzzles</i> Round II: assessment of RNA structure prediction programs applied to three large RNA structures. <i>Rna</i> , 2015, 21, 1066-1084.	3.5	161
25	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. <i>Rna</i> , 2017, 23, 655-672.	3.5	158
26	Simultaneous prediction of protein folding and docking at high resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 18978-18983.	7.1	145
27	Correcting pervasive errors in RNA crystallography through enumerative structure prediction. <i>Nature Methods</i> , 2013, 10, 74-76.	19.0	138
28	FARFAR2: Improved De Novo Rosetta Prediction of Complex Global RNA Folds. <i>Structure</i> , 2020, 28, 963-976.e6.	3.3	134
29	The Fastest Global Events in RNA Folding: Electrostatic Relaxation and Tertiary Collapse of the Tetrahymena Ribozyme. <i>Journal of Molecular Biology</i> , 2003, 332, 311-319.	4.2	130
30	Quantitative Dimethyl Sulfate Mapping for Automated RNA Secondary Structure Inference. <i>Biochemistry</i> , 2012, 51, 7037-7039.	2.5	119
31	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020, 17, 699-707.	19.0	119
32	Principles of RNA Compaction: Insights from the Equilibrium Folding Pathway of the P4-P6 RNA Domain in Monovalent Cations. <i>Journal of Molecular Biology</i> , 2004, 343, 1195-1206.	4.2	118
33	Structural Transitions and Thermodynamics of a Glycine-Dependent Riboswitch from <i>Vibrio cholerae</i> . <i>Journal of Molecular Biology</i> , 2007, 365, 1393-1406.	4.2	116
34	A unified mechanism for intron and exon definition and back-splicing. <i>Nature</i> , 2019, 573, 375-380.	27.8	114
35	A two-dimensional mutate-and-map strategy for non-coding RNA structure. <i>Nature Chemistry</i> , 2011, 3, 954-962.	13.6	113
36	Spatial Distribution of Competing Ions around DNA in Solution. <i>Physical Review Letters</i> , 2004, 93, 248103.	7.8	106

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37	Structure of human telomerase holoenzyme with bound telomeric DNA. <i>Nature</i> , 2021, 593, 449-453.	27.8	106
38	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
39	Determining the Mg ²⁺ Stoichiometry for Folding an RNA Metal Ion Core. <i>Journal of the American Chemical Society</i> , 2005, 127, 8272-8273.	13.7	98
40	Probing counterion modulated repulsion and attraction between nucleic acid duplexes in solution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 1035-1040.	7.1	97
41	Exploration of the Transition State for Tertiary Structure Formation between an RNA Helix and a Large Structured RNA. <i>Journal of Molecular Biology</i> , 2003, 328, 1011-1026.	4.2	96
42	An RNA Mapping DataBase for curating RNA structure mapping experiments. <i>Bioinformatics</i> , 2012, 28, 3006-3008.	4.1	93
43	Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics. <i>Nature Communications</i> , 2022, 13, 1536.	12.8	93
44	The Paradoxical Behavior of a Highly Structured Misfolded Intermediate in RNA Folding. <i>Journal of Molecular Biology</i> , 2006, 363, 531-544.	4.2	92
45	Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome. <i>Nature Structural and Molecular Biology</i> , 2021, 28, 747-754.	8.2	91
46	Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution. <i>Nature Communications</i> , 2019, 10, 5511.	12.8	90
47	Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems. <i>Annual Review of Biophysics</i> , 2013, 42, 265-287.	10.0	88
48	Understanding the Errors of SHAPE-Directed RNA Structure Modeling. <i>Biochemistry</i> , 2011, 50, 8049-8056.	2.5	86
49	HiTRACE: high-throughput robust analysis for capillary electrophoresis. <i>Bioinformatics</i> , 2011, 27, 1798-1805.	4.1	86
50	Modeling Complex RNA Tertiary Folds with Rosetta. <i>Methods in Enzymology</i> , 2015, 553, 35-64.	1.0	84
51	Structural inference of native and partially folded RNA by high-throughput contact mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4144-4149.	7.1	79
52	Structure determination of noncanonical RNA motifs guided by 1H NMR chemical shifts. <i>Nature Methods</i> , 2014, 11, 413-416.	19.0	72
53	High-Throughput Investigation of Diverse Junction Elements in RNA Tertiary Folding. <i>Cell</i> , 2018, 174, 377-390.e20.	28.9	72
54	Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments. <i>Nature Protocols</i> , 2008, 3, 1395-1401.	12.0	70

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55	Principles for Predicting RNA Secondary Structure Design Difficulty. <i>Journal of Molecular Biology</i> , 2016, 428, 748-757.	4.2	67
56	Theoretical basis for stabilizing messenger RNA through secondary structure design. <i>Nucleic Acids Research</i> , 2021, 49, 10604-10617.	14.5	67
57	Quantitative comparison of villin headpiece subdomain simulations and triplet-triplet energy transfer experiments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 12734-12739.	7.1	64
58	Ultraviolet Shadowing of RNA Can Cause Significant Chemical Damage in Seconds. <i>Scientific Reports</i> , 2012, 2, 517.	3.3	64
59	An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1. <i>Cell</i> , 2018, 174, 218-230.e13.	28.9	64
60	An enumerative stepwise ansatz enables atomic-accuracy RNA loop modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20573-20578.	7.1	63
61	Standardization of RNA Chemical Mapping Experiments. <i>Biochemistry</i> , 2014, 53, 3063-3065.	2.5	63
62	Four Small Puzzles That Rosetta Doesn't Solve. <i>PLoS ONE</i> , 2011, 6, e20044.	2.5	61
63	<i>De novo</i> 3D models of SARS-CoV-2 RNA elements from consensus experimental secondary structures. <i>Nucleic Acids Research</i> , 2021, 49, 3092-3108.	14.5	61
64	Massively Parallel RNA Chemical Mapping with a Reduced Bias MAP-Seq Protocol. <i>Methods in Molecular Biology</i> , 2014, 1086, 95-117.	0.9	60
65	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. <i>PLoS ONE</i> , 2013, 8, e67051.	2.5	59
66	Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1Å... resolution. <i>Nature</i> , 2021, 596, 603-607.	27.8	59
67	Bayesian Energy Landscape Tilting: Towards Concordant Models of Molecular Ensembles. <i>Biophysical Journal</i> , 2014, 106, 1381-1390.	0.5	58
68	A Molecular Ruler for Measuring Quantitative Distance Distributions. <i>PLoS ONE</i> , 2008, 3, e3229.	2.5	57
69	Consistent global structures of complex RNA states through multidimensional chemical mapping. <i>ELife</i> , 2015, 4, e07600.	6.0	57
70	High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states. <i>Rna</i> , 2014, 20, 1815-1826.	3.5	55
71	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. <i>Molecular Cell</i> , 2019, 74, 966-981.e18.	9.7	55
72	RNA structure inference through chemical mapping after accidental or intentional mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9876-9881.	7.1	54

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73	Challenging the state of the art in protein structure prediction: Highlights of experimental target structures for the 10th Critical Assessment of Techniques for Protein Structure Prediction Experiment CASP10. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 26-42.	2.6	53
74	Rich RNA Structure Landscapes Revealed by Mutate-and-Map Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004473.	3.2	49
75	Computational design of three-dimensional RNA structure and function. <i>Nature Nanotechnology</i> , 2019, 14, 866-873.	31.5	49
76	Automated RNA Structure Prediction Uncovers a Kink-Turn Linker in Double Glycine Riboswitches. <i>Journal of the American Chemical Society</i> , 2012, 134, 1404-1407.	13.7	47
77	Web-accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE). <i>Protein Science</i> , 2018, 27, 259-268.	7.6	47
78	RNA structure through multidimensional chemical mapping. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e7.	5.7	46
79	A mutate-and-map strategy accurately infers the base pairs of a 35-nucleotide model RNA. <i>Rna</i> , 2011, 17, 522-534.	3.5	45
80	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. <i>Nature Methods</i> , 2018, 15, 947-954.	19.0	45
81	The Mutate-and-Map Protocol for Inferring Base Pairs in Structured RNA. <i>Methods in Molecular Biology</i> , 2014, 1086, 53-77.	0.9	43
82	Primerize: automated primer assembly for transcribing non-coding RNA domains. <i>Nucleic Acids Research</i> , 2015, 43, W522-W526.	14.5	41
83	Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 16847-16855.	7.1	38
84	Blind prediction of noncanonical RNA structure at atomic accuracy. <i>Science Advances</i> , 2018, 4, eaar5316.	10.3	37
85	Metal-ion rescue revisited: Biochemical detection of site-bound metal ions important for RNA folding. <i>Rna</i> , 2012, 18, 1123-1141.	3.5	36
86	Blind Predictions of DNA and RNA Tweezers Experiments with Force and Torque. <i>PLoS Computational Biology</i> , 2014, 10, e1003756.	3.2	36
87	A Mutate-and-Map Strategy for Inferring Base Pairs in Structured Nucleic Acids: Proof of Concept on a DNA/RNA Helix. <i>Biochemistry</i> , 2010, 49, 7414-7416.	2.5	34
88	HiTRACE-Web: an online tool for robust analysis of high-throughput capillary electrophoresis. <i>Nucleic Acids Research</i> , 2013, 41, W492-W498.	14.5	34
89	Automated Design of Diverse Stand-Alone Riboswitches. <i>ACS Synthetic Biology</i> , 2019, 8, 1838-1846.	3.8	34
90	Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking. <i>Structure</i> , 2019, 27, 140-151.e5.	3.3	34

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91	Prospects for de novo phasing with de novo protein models. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 169-175.	2.5	32
92	Blind tests of RNA nearest-neighbor energy prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8430-8435.	7.1	29
93	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	3.5	28
94	A measurement of H α from Ryle Telescope, ASCA and ROSAT observations of Abell 773. <i>Monthly Notices of the Royal Astronomical Society</i> , 2003, 341, 937-940.	4.4	26
95	RNA Structure Refinement Using the ERRASER-Phenix Pipeline. <i>Methods in Molecular Biology</i> , 2016, 1320, 269-282.	0.9	24
96	Single-molecule FRET-Rosetta reveals RNA structural rearrangements during human telomerase catalysis. <i>Rna</i> , 2017, 23, 175-188.	3.5	23
97	Primerize-2D: automated primer design for RNA multidimensional chemical mapping. <i>Bioinformatics</i> , 2017, 33, 1405-1406.	4.1	22
98	Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles. <i>Bioinformatics</i> , 2015, 31, 2808-2815.	4.1	21
99	RNA 3D structure prediction guided by independent folding of homologous sequences. <i>BMC Bioinformatics</i> , 2019, 20, 512.	2.6	21
100	Blind tests of RNA-protein binding affinity prediction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 8336-8341.	7.1	21
101	Rosetta in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3212-3218.	2.6	20
102	Hidden Structural Modules in a Cooperative RNA Folding Transition. <i>Cell Reports</i> , 2018, 22, 3240-3250.	6.4	20
103	Controllable molecular motors engineered from myosin and RNA. <i>Nature Nanotechnology</i> , 2018, 13, 34-40.	31.5	19
104	Ribosome-induced RNA conformational changes in a viral 3'-UTR sense and regulate translation levels. <i>Nature Communications</i> , 2018, 9, 5074.	12.8	19
105	Updates to the RNA mapping database (RMDb), version 2. <i>Nucleic Acids Research</i> , 2018, 46, D375-D379.	14.5	19
106	Transcription polymerase-catalyzed emergence of novel RNA replicons. <i>Science</i> , 2020, 368, .	12.6	19
107	Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular switches. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2112979119.	7.1	19
108	Remodeling a β -peptide bundle. <i>Chemical Science</i> , 2013, 4, 319-324.	7.4	18

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109	Atomic-Accuracy Prediction of Protein Loop Structures through an RNA-Inspired Ansatz. PLoS ONE, 2013, 8, e74830.	2.5	17
110	Structure and ligand binding of the glutamine-II riboswitch. Nucleic Acids Research, 2019, 47, 7666-7675.	14.5	17
111	Using Rosetta for RNA homology modeling. Methods in Enzymology, 2019, 623, 177-207.	1.0	17
112	Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions. Nature Genetics, 2021, 53, 729-741.	21.4	17
113	A robust peak detection method for RNA structure inference by high-throughput contact mapping. Bioinformatics, 2009, 25, 1137-1144.	4.1	16
114	Allosteric mechanism of the <i>V. vulnificus</i> adenine riboswitch resolved by four-dimensional chemical mapping. ELife, 2018, 7, .	6.0	16
115	EternaBrain: Automated RNA design through move sets and strategies from an Internet-scale RNA videogame. PLoS Computational Biology, 2019, 15, e1007059.	3.2	16
116	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. Nature Communications, 2021, 12, 6947.	12.8	16
117	Scientific rigor through videogames. Trends in Biochemical Sciences, 2014, 39, 507-509.	7.5	15
118	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. Nature Communications, 2019, 10, 3629.	12.8	15
119	Folding heterogeneity in the essential human telomerase RNA three-way junction. Rna, 2020, 26, 1787-1800.	3.5	14
120	Response to Comment on "Remeasuring the Double Helix". Science, 2009, 325, 538-538.	12.6	13
121	Scientific Discovery Games for Biomedical Research. Annual Review of Biomedical Data Science, 2019, 2, 253-279.	6.5	13
122	Modeling Small Noncanonical RNA Motifs with the Rosetta FARFAR Server. Methods in Molecular Biology, 2016, 1490, 187-198.	0.9	11
123	RNA structure: a renaissance begins?. Nature Methods, 2021, 18, 439-439.	19.0	10
124	Detection of a cosmic microwave background decrement towards a cluster of mJy radio sources. Monthly Notices of the Royal Astronomical Society, 2002, 331, 1-6.	4.4	9
125	A maximum-likelihood approach to removing radio sources from observations of the Sunyaev-Zel'dovich effect, with application to Abell 611. Monthly Notices of the Royal Astronomical Society, 2002, 337, 1207-1214.	4.4	9
126	Evaluating riboswitch optimality. Methods in Enzymology, 2019, 623, 417-450.	1.0	9

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127	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. Nature Communications, 2021, 12, 2165.	12.8	9
128	Why Can't We Predict RNA Structure At Atomic Resolution?. Nucleic Acids and Molecular Biology, 2012, , 43-65.	0.2	8
129	RNA-Redesign: a web server for fixed-backbone 3D design of RNA: Figure 1.. Nucleic Acids Research, 2015, 43, W498-W501.	14.5	8
130	Recording and Analyzing Nucleic Acid Distance Distributions with X-Ray Scattering Interferometry (XSI). Current Protocols in Nucleic Acid Chemistry, 2018, 73, e54.	0.5	8
131	Anomalous Reverse Transcription through Chemical Modifications in Polyadenosine Stretches. Biochemistry, 2020, 59, 2154-2170.	2.5	8
132	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. The Biophysicist, 2021, 2, 108-122.	0.3	8
133	Three-dimensional structure-guided evolution of a ribosome with tethered subunits. Nature Chemical Biology, 2022, 18, 990-998.	8.0	7
134	RiboDraw: semiautomated two-dimensional drawing of RNA tertiary structure diagrams. NAR Genomics and Bioinformatics, 2021, 3, lqab091.	3.2	6
135	Observations of the Sunyaev-Zel'dovich effect in the z=0.78 cluster MS 1137.5+6625. Monthly Notices of the Royal Astronomical Society, 2002, 334, 323-326.	4.4	4
136	How to Kinetically Dissect an RNA Machine. Biochemistry, 2021, 60, 3485-3490.	2.5	3
137	"Hidden" states are pervasive in RNA folding: detection and dissection through mutate-and-map experiments. FASEB Journal, 2013, 27, 96.2.	0.5	0