

Rhiju Das

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1195587/publications.pdf>

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	Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics. <i>Nature Communications</i> , 2022, 13, 1536.	12.8	93
2	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
3	Three-dimensional structure-guided evolution of a ribosome with tethered subunits. <i>Nature Chemical Biology</i> , 2022, 18, 990-998.	8.0	7
4	<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
5	Structure of human telomerase holoenzyme with bound telomeric DNA. <i>Nature</i> , 2021, 593, 449-453.	27.8	106
6	Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis. <i>Nature Communications</i> , 2021, 12, 2165.	12.8	9
7	PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design. <i>The Biophysicist</i> , 2021, 2, 108-122.	0.3	8
8	Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions. <i>Nature Genetics</i> , 2021, 53, 729-741.	21.4	17
9	RNA structure: a renaissance begins?. <i>Nature Methods</i> , 2021, 18, 439-439.	19.0	10
10	Geometric deep learning of RNA structure. <i>Science</i> , 2021, 373, 1047-1051.	12.6	190
11	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
12	Cryo-EM structures of full-length <i>Tetrahymena</i> ribozyme at 3.1 Å resolution. <i>Nature</i> , 2021, 596, 603-607.	27.8	59
13	How to Kinetically Dissect an RNA Machine. <i>Biochemistry</i> , 2021, 60, 3485-3490.	2.5	3
14	Theoretical basis for stabilizing messenger RNA through secondary structure design. <i>Nucleic Acids Research</i> , 2021, 49, 10604-10617.	14.5	67
15	RiboDraw: semiautomated two-dimensional drawing of RNA tertiary structure diagrams. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab091.	3.2	6
16	Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks. <i>Nature Communications</i> , 2021, 12, 6947.	12.8	16
17	Folding heterogeneity in the essential human telomerase RNA three-way junction. <i>Rna</i> , 2020, 26, 1787-1800.	3.5	14
18	Macromolecular modeling and design in Rosetta: recent methods and frameworks. <i>Nature Methods</i> , 2020, 17, 665-680.	19.0	513

#	ARTICLE	IF	CITATIONS
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	Anomalous Reverse Transcription through Chemical Modifications in Polyadenosine Stretches. <i>Biochemistry</i> , 2020, 59, 2154-2170.	2.5	8
21	FARFAR2: Improved De Novo Rosetta Prediction of Complex Global RNA Folds. <i>Structure</i> , 2020, 28, 963-976.e6.	3.3	134
22	Transcription polymerase-catalyzed emergence of novel RNA replicons. <i>Science</i> , 2020, 368, .	12.6	19
23	Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures. <i>Nature Methods</i> , 2020, 17, 699-707.	19.0	119
24	RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers. <i>Rna</i> , 2020, 26, 982-995.	3.5	100
25	A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites. <i>Nature Communications</i> , 2019, 10, 3629.	12.8	15
26	Computational design of three-dimensional RNA structure and function. <i>Nature Nanotechnology</i> , 2019, 14, 866-873.	31.5	49
27	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
28	Automated Design of Diverse Stand-Alone Riboswitches. <i>ACS Synthetic Biology</i> , 2019, 8, 1838-1846.	3.8	34
29	Scientific Discovery Games for Biomedical Research. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 253-279.	6.5	13
30	EternaBrain: Automated RNA design through move sets and strategies from an Internet-scale RNA videogame. <i>PLoS Computational Biology</i> , 2019, 15, e1007059.	3.2	16
31	RNA 3D structure prediction guided by independent folding of homologous sequences. <i>BMC Bioinformatics</i> , 2019, 20, 512.	2.6	21
32	A unified mechanism for intron and exon definition and back-splicing. <i>Nature</i> , 2019, 573, 375-380.	27.8	114
33	Structure and ligand binding of the glutamine-II riboswitch. <i>Nucleic Acids Research</i> , 2019, 47, 7666-7675.	14.5	17
34	Using Rosetta for RNA homology modeling. <i>Methods in Enzymology</i> , 2019, 623, 177-207.	1.0	17
35	Evaluating riboswitch optimality. <i>Methods in Enzymology</i> , 2019, 623, 417-450.	1.0	9
36	A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins. <i>Molecular Cell</i> , 2019, 74, 966-981.e18.	9.7	55

#	ARTICLE	IF	CITATIONS
37	Blind tests of RNA-protein binding affinity prediction. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8336-8341.	7.1	21
38	Spontaneous driving forces give rise to protein-RNA condensates with coexisting phases and complex material properties. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 7889-7898.	7.1	365
39	Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution. Nature Communications, 2019, 10, 5511.	12.8	90
40	Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking. Structure, 2019, 27, 140-151.e5.	3.3	34
41	Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them. Nature Reviews Molecular Cell Biology, 2018, 19, 158-174.	37.0	577
42	Hidden Structural Modules in a Cooperative RNA Folding Transition. Cell Reports, 2018, 22, 3240-3250.	6.4	20
43	Web-accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE). Protein Science, 2018, 27, 259-268.	7.6	47
44	Controllable molecular motors engineered from myosin and RNA. Nature Nanotechnology, 2018, 13, 34-40.	31.5	19
45	Ribosome-induced RNA conformational changes in a viral 3'-UTR sense and regulate translation levels. Nature Communications, 2018, 9, 5074.	12.8	19
46	De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes. Nature Methods, 2018, 15, 947-954.	19.0	45
47	Updates to the RNA mapping database (RMDB), version 2. Nucleic Acids Research, 2018, 46, D375-D379.	14.5	19
48	An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1. Cell, 2018, 174, 218-230.e13.	28.9	64
49	Blind prediction of noncanonical RNA structure at atomic accuracy. Science Advances, 2018, 4, eaar5316.	10.3	37
50	Allosteric mechanism of the <i>V. vulnificus</i> adenine riboswitch resolved by four-dimensional chemical mapping. ELife, 2018, 7, .	6.0	16
51	High-Throughput Investigation of Diverse Junction Elements in RNA Tertiary Folding. Cell, 2018, 174, 377-390.e20.	28.9	72
52	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
53	Primerize-2D: automated primer design for RNA multidimensional chemical mapping. Bioinformatics, 2017, 33, 1405-1406.	4.1	22
54	RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme. Rna, 2017, 23, 655-672.	3.5	158

#	ARTICLE	IF	CITATIONS
55	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
56	Single-molecule FRET-Rosetta reveals RNA structural rearrangements during human telomerase catalysis. <i>Rna</i> , 2017, 23, 175-188.	3.5	23
57	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
58	RNA structure through multidimensional chemical mapping. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e7.	5.7	46
59	Modeling Small Noncanonical RNA Motifs with the Rosetta FARFAR Server. <i>Methods in Molecular Biology</i> , 2016, 1490, 187-198.	0.9	11
60	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
61	Principles for Predicting RNA Secondary Structure Design Difficulty. <i>Journal of Molecular Biology</i> , 2016, 428, 748-757.	4.2	67
62	RNA Structure Refinement Using the ERRASER-Phenix Pipeline. <i>Methods in Molecular Biology</i> , 2016, 1320, 269-282.	0.9	24
63	Rich RNA Structure Landscapes Revealed by Mutate-and-Map Analysis. <i>PLoS Computational Biology</i> , 2015, 11, e1004473.	3.2	49
64	Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles. <i>Bioinformatics</i> , 2015, 31, 2808-2815.	4.1	21
65	RNA-Redesign: a web server for fixed-backbone 3D design of RNA: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W498-W501.	14.5	8
66	Primerize: automated primer assembly for transcribing non-coding RNA domains. <i>Nucleic Acids Research</i> , 2015, 43, W522-W526.	14.5	41
67	Modeling Complex RNA Tertiary Folds with Rosetta. <i>Methods in Enzymology</i> , 2015, 553, 35-64.	1.0	84
68	<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
69	RNA regulons in Hox 5â€™ UTRs confer ribosome specificity to gene regulation. <i>Nature</i> , 2015, 517, 33-38.	27.8	258
70	Consistent global structures of complex RNA states through multidimensional chemical mapping. <i>ELife</i> , 2015, 4, e07600.	6.0	57
71	Structure determination of noncanonical RNA motifs guided by ¹ H NMR chemical shifts. <i>Nature Methods</i> , 2014, 11, 413-416.	19.0	72
72	Blind Predictions of DNA and RNA Tweezers Experiments with Force and Torque. <i>PLoS Computational Biology</i> , 2014, 10, e1003756.	3.2	36

#	ARTICLE	IF	CITATIONS
73	High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states. <i>Rna</i> , 2014, 20, 1815-1826.	3.5	55
74	Bayesian Energy Landscape Tilting: Towards Concordant Models of Molecular Ensembles. <i>Biophysical Journal</i> , 2014, 106, 1381-1390.	0.5	58
75	Understanding Nucleic Acid-Ion Interactions. <i>Annual Review of Biochemistry</i> , 2014, 83, 813-841.	11.1	358
76	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
77	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
78	Scientific rigor through videogames. <i>Trends in Biochemical Sciences</i> , 2014, 39, 507-509.	7.5	15
79	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
80	Standardization of RNA Chemical Mapping Experiments. <i>Biochemistry</i> , 2014, 53, 3063-3065.	2.5	63
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	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
83	Remodeling a β -peptide bundle. <i>Chemical Science</i> , 2013, 4, 319-324.	7.4	18
84	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
85	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
86	Correcting pervasive errors in RNA crystallography through enumerative structure prediction. <i>Nature Methods</i> , 2013, 10, 74-76.	19.0	138
87	Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design. <i>PLoS ONE</i> , 2013, 8, e67051.	2.5	59
88	Atomic-Accuracy Prediction of Protein Loop Structures through an RNA-Inspired Ansatz. <i>PLoS ONE</i> , 2013, 8, e74830.	2.5	17
89	Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE). <i>PLoS ONE</i> , 2013, 8, e63906.	2.5	348
90	â€˜Hiddenâ€™ states are pervasive in RNA folding: detection and dissection through mutate-and-map experiments. <i>FASEB Journal</i> , 2013, 27, 96.2.	0.5	0

#	ARTICLE	IF	CITATIONS
91	Ultraviolet Shadowing of RNA Can Cause Significant Chemical Damage in Seconds. <i>Scientific Reports</i> , 2012, 2, 517.	3.3	64
92	An RNA Mapping DataBase for curating RNA structure mapping experiments. <i>Bioinformatics</i> , 2012, 28, 3006-3008.	4.1	93
93	<i>RNA-Puzzles</i>: A CASP-like evaluation of RNA three-dimensional structure prediction. <i>Rna</i> , 2012, 18, 610-625.	3.5	241
94	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
95	Quantitative Dimethyl Sulfate Mapping for Automated RNA Secondary Structure Inference. <i>Biochemistry</i> , 2012, 51, 7037-7039.	2.5	119
96	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
97	Why Canâ€™t We Predict RNA Structure At Atomic Resolution?. <i>Nucleic Acids and Molecular Biology</i> , 2012, , 43-65.	0.2	8
98	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
99	Understanding the Errors of SHAPE-Directed RNA Structure Modeling. <i>Biochemistry</i> , 2011, 50, 8049-8056.	2.5	86
100	HiTRACE: high-throughput robust analysis for capillary electrophoresis. <i>Bioinformatics</i> , 2011, 27, 1798-1805.	4.1	86
101	A two-dimensional mutate-and-map strategy for non-coding RNA structure. <i>Nature Chemistry</i> , 2011, 3, 954-962.	13.6	113
102	Rosetta3. <i>Methods in Enzymology</i> , 2011, 487, 545-574.	1.0	1,620
103	Four Small Puzzles That Rosetta Doesn't Solve. <i>PLoS ONE</i> , 2011, 6, e20044.	2.5	61
104	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
105	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
106	Sharing and archiving nucleic acid structure mapping data. <i>Rna</i> , 2011, 17, 1204-1212.	3.5	28
107	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
108	Rosetta in CAPRI rounds 13â€™19. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 3212-3218.	2.6	20

#	ARTICLE	IF	CITATIONS
109	Atomic accuracy in predicting and designing noncanonical RNA structure. <i>Nature Methods</i> , 2010, 7, 291-294.	19.0	328
110	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
111	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
112	A robust peak detection method for RNA structure inference by high-throughput contact mapping. <i>Bioinformatics</i> , 2009, 25, 1137-1144.	4.1	16
113	Response to Comment on "Remeasuring the Double Helix". <i>Science</i> , 2009, 325, 538-538.	12.6	13
114	Structure prediction for CASP8 with all-atom refinement using Rosetta. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 89-99.	2.6	425
115	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
116	Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters. <i>Rna</i> , 2009, 15, 189-199.	3.5	300
117	Macromolecular Modeling with Rosetta. <i>Annual Review of Biochemistry</i> , 2008, 77, 363-382.	11.1	841
118	Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments. <i>Nature Protocols</i> , 2008, 3, 1395-1401.	12.0	70
119	Remeasuring the Double Helix. <i>Science</i> , 2008, 322, 446-449.	12.6	200
120	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
121	A Molecular Ruler for Measuring Quantitative Distance Distributions. <i>PLoS ONE</i> , 2008, 3, e3229.	2.5	57
122	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
123	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
124	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
125	High-resolution structure prediction and the crystallographic phase problem. <i>Nature</i> , 2007, 450, 259-264.	27.8	296
126	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

#	ARTICLE	IF	CITATIONS
127	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
128	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
129	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
130	Spatial Distribution of Competing Ions around DNA in Solution. <i>Physical Review Letters</i> , 2004, 93, 248103.	7.8	106
131	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
132	A measurement of H ₀ 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
133	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
134	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
135	Detection of a cosmic microwave background decrement towards a cluster of mJy radio sources. <i>Monthly Notices of the Royal Astronomical Society</i> , 2002, 331, 1-6.	4.4	9
136	Observations of the Sunyaev-Zel'dovich effect in the z=0.78 cluster MS 1137.5+6625. <i>Monthly Notices of the Royal Astronomical Society</i> , 2002, 334, 323-326.	4.4	4
137	A maximum-likelihood approach to removing radio sources from observations of the Sunyaev-Zel'dovich effect, with application to Abell 611. <i>Monthly Notices of the Royal Astronomical Society</i> , 2002, 337, 1207-1214.	4.4	9