

Curriculum Vitae

Rhiju Das

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Born: 1978, Houston, Texas

Professional

Stanford University

2023 Professor, Biochemistry Department
2022 Investigator, Howard Hughes Medical Institute
2020 Stanford Medicine Endowed Faculty Scholar (anonymous donor)
2016 Associate Professor, Biochemistry Department and, by courtesy, Physics Department
2009 Faculty, Biophysics and Biomedical Informatics programs
2009 Assistant Professor, Biochemistry Department and, by courtesy, Physics Department

University of Washington/Howard Hughes Medical Institute

2008 Jane Coffin Childs postdoctoral fellow (with D. Baker)

Education

2005 Ph.D., physics; Stanford University (with D. Herschlag, S. Doniach)
2000 M.Res., biocomplexity; University College London (with Z. Yang, J. Mallet)
1999 M.Phil., physics; Trinity College, Cambridge University (with R. Saunders)
1998 A.B. *s.c.l.*, physics; Harvard University (research with S. Mishra, G. Feldman)

Awards and Honors

Stanford University

2021 Selected as Howard Hughes Medical Institute Investigator
2020 Stanford Medicine Endowed Faculty Scholar (anonymous)
2017, 2020 Stanford School of Medicine Discovery Innovation Award
2015 American Chemical Society OpenEye Outstanding Junior Faculty Award
2012 W. M. Keck Foundation Medical Research Grant Award

University of Washington/Howard Hughes Medical Institute

2008 Burroughs-Wellcome Career Award at the Scientific Interface
2006 Jane Coffin Childs Foundation, Damon Runyon Cancer Foundation Fellowships

Stanford University

2000 Stanford Graduate Fellow; National Science Foundation Graduate Fellow

Harvard University

1998 British Marshall Scholar

Oklahoma School of Science and Mathematics

1995 Gold medal, International Physics Olympiad; top US score; second place worldwide

Invited Lectures (selected out of >100)

2023	Machine Learning in Structural Biology, NeurIPS (keynote)
2023	Gordon Research Conference, RNA Nanotechnology
2022	CASP15 conference
2022	Nucleic Acids Chemistry & Biomedicine Symposium in honor of Marv Caruthers
2022	Next Generation Biophysics, MRC LMB, Cambridge, UK
2022	RiboClub (keynote)
2021	National Cancer Institute RNA retreat (keynote)
2021	Iowa State University, Biochemistry (student invited)
2020	Biophysical Society Symposium: “Biophysicists Address COVID-19 Challenges”
2020	Rustbelt RNA 2020 (plenary)
2020	Stanford University School of Medicine COVID-19 town hall
2019	Harvard T.H. Chan School of Public Health
2019	Gordon Research Conference, Computer-Aided Drug Design
2018	North Eastern Structure Symposium
2018	Tsinghua International Symposium of Computational Structural Biology and Biophysics
2018	J. James Woods Lecture in Science and Mathematics, Butler University
2018	NIH/UCSF Crowdsourcing & Interactive Digital Media (opening keynote)
2017	Gordon Research Conference, RNA Nanotechnology
2016	NIH Center for Excellence in Genomic Sciences (keynote)
2016	EMBO RNA structure meets function, Stockholm
2015	Oregon State University, Biochemistry (student invited)
2015	U. Rochester, Cellular & Molecular Biology (student-invited)
2014	DNA 20, Kyoto, Japan (keynote)
2014	Gordon Research Conference, Computational Chemistry
2014	Genentech Innovation Summit (keynote)
2013	Design Research Conference, Chicago (keynote)
2011	Foundations of Nanotechnology (keynote)

Selected Professional Activities and Service

2022, 2024	Assessor, 15 th and 16 th Critical Assessment of Structure Prediction (CASP)
2020	Stanford University COVID-19 research oversight committee
2019	Co-author, RNA Synthetic Biology Roadmap, Engineering Biology Research Consortium
2017-20	Editorial advisory board, <i>Biochemistry</i>
2015-24	Co-organizer, EternaCon, Stanford CA
2015	Advisor, NOVA RNA Lab
2013	National Institutes of Health NIGMS RNA advisory meeting
2011-15	Co-organizer, Stanford Frontiers in Quantitative Biology seminar series
2011	Co-organizer, RosettaCon, Leavenworth WA
2009	Co-founder and principal investigator, Eterna videogame
2008	Principal investigator, RosettaCommons consortium
2007-8	Advisor, Foldit videogame

Publications

158. Kretsch, R.C., Xu, L., Zheludev, I.N., Zhou, X., Huang, R., Nye, G., Li, S., Zhang, K., Chiu, W.,[†] **Das, R.**[†] (2024) “Tertiary folds of the SL5 RNA from the 5’ proximal region of SARS-CoV-2 and related coronaviruses.” *Proceedings of the National Academy of Sciences of the United States of America*, 121 (10), e2320493121.

157. Tangpradabkul, T., Palo, M., Townley, J., Hsu, K.B., Eterna participants, Smaga, S., Das, R., Schepartz, A. (2024) “Minimization of the E. coli ribosome, aided and optimized by community science.” *Nucleic Acids Research*, 52 (3), 1027-1042.
156. **Das, R.**,*† Kretsch, R.* , Simpkin, A., Mulvaney, T., Pham, P., Rangan, R., Bu, F., Keegan, R., Topf, M., Rigden, D., Miao, Z.†, Westhof, E.† (2023) “Assessment of three-dimensional RNA structure prediction in CASP15.” *Proteins: Structure, Function, and Bioinformatics*, 91 (12), 1747 – 1770.
155. Mulvaney, T., Kretsch, R., Elliott, L., Beton, J., Kryshtafovych, A., Rigden, D.J., **Das, R.**, Topf, M. (2023) “CASP15 cryoEM protein and RNA targets: refinement and analysis using experimental maps” *Proteins: Structure, Function, and Bioinformatics*, 91 (12), 1935-1951.
154. Kretsch, R., Andersen, E., Bujnicki, J., Chiu, W., **Das, R.**, Luo, B., Masquida, B., McRae, E., Schroeder, G., Su, Z., Wedekind, J., Xu, L., Zhang, K., Zheludev, I., Moul, J., Kryshtafovych, A. (2023) “RNA target highlights in CASP15: Evaluation of predicted models by structure providers.” *Proteins: Structure, Function, and Bioinformatics*, 91 (12), 1600-1615. (reverse cover image)
153. Kryshtafovych, A., Antczak, M., Szachniuk, M., Zok, T., Kretsch, R., Rangan, R., Pham, P., **Das, R.**, Robin, X., Studer, G., Durairaj, J., Eberhardt, J., Sweeney, A., Topf, M., Schwede, T., Fidelis, K., Moul, J. (2023) “New prediction categories in CASP15.” *Proteins: Structure, Function, and Bioinformatics*, 91 (12), 1550-1557.
152. Ma, H., Pham, P., Luo, B., Rangan, R., Kappel, K., Su, Z., **Das, R.** (2023) “Auto-DRRAFTER: automated RNA modeling based on cryo-EM density.” *Methods Mol Biol.*, 2568, 193 – 211. (invited book chapter)
151. Krüger, A, Watkins A.M., Wellington-Oguri R., Romano, J., Kofman, C., DeFoe, A., Kim, Y., Anderson-Lee, J., Fisker, E., Townley J., Eterna Participants, d'Aquino, A.E., Das, R.†, and Jewett, M.C.† (2023) “Community science designed ribosomes with beneficial phenotypes.” *Nature Communications*, 14, 961.
150. Watkins, A.M. and **Das, R.** (2023) “RNA 3D Modeling with FARFAR2, Online.” *Methods Mol Biol*, 2586, 233 – 249. (invited book chapter)
149. Kofman, C., Watkins, A., Kim, D., Willi, J., Wooldredge, A., Karim, A., **Das, R.**, Jewett, M. (2022) “Computationally-guided design and selection of high performing ribosomal active site mutants.” *Nucleic Acids Research*, 50 (22), 13143-13154
148. Wayment-Steele, H.K.,* Kladwang, W.,* Watkins, A.M.,* Kim, D.S.,* Tunguz, B.,* Reade, W., Demkin, M., Romano, J., Wellington-Oguri, R., Nicol, J.J., Gao, J., Onodera, K., Fujikawa, K., Mao, H., Vandewiele, G., Tinti, M., Steenwinckel, B., Ito, T., Noumi, T., He, S., Ishi, K., Lee, Y., Öztürk, F., Chiu, K.Y., Öztürk, E., Amer, K., Fares, M., Eterna Participants & **Das, R.** (2022). “Deep learning models for predicting RNA degradation via dual crowdsourcing.” *Nature Machine Intelligence*, 4, 1174-1184.
147. Ma, H., Pham, P., Luo, B., Rangan, R., Kappel, K., Su, Z.,† & **Das, R.**† (2022) “Auto-DRRAFTER: automated RNA modeling based on cryo-EM density.” *Methods Mol Biol.*, 2568, 193-211. (invited book chapter)
146. Wayment-Steele, H. K., Kladwang, W., Eterna Participants, & **Das, R.** (2022). “RNA secondary structure packages ranked and improved by high-throughput experiments.” *Nature Methods*, 19, 1234-1242.
145. Li, S., Palo, M.Z., Pintilie, G., Zhang, X., Su, Z., Kappel, K., Chiu, W.,† Zhang, K.,† & **Das, R.**† (2022) “Topological crossing in the misfolded Tetrahymena ribozyme resolved by cryo-EM.” *Proceedings of the National Academy of Sciences* 119 (37), e2209146119.
144. Hagey, R.J., Elazar, M., Pham, E.A., Tian, S., Ben-Avi, L., Bernardin-Souibgui, C., Yee, M.F., Moreira, F.R., Rabinovitch, M.V., Meganck, R.M., Fram, B., Beck, A., Gibson, S.A., Lam, G., Devera, J., Kladwang, W., Nguyen, K., Xiong, A., Schaffert, S., Avisar, T., Liu, P., Rustagi, A., Fichtenbaum, C.J., Pang, P.S., Khatri, P., Tseng, C., Taubenberger, J.K., Blish, C.A., Hurst, B.L., Sheahan, T.P., Das, R., & Glenn, J.S. (2022) “Programmable antivirals targeting critical conserved viral RNA secondary structures from influenza A virus and SARS-CoV-2.” *Nature Medicine*, 28, 1944-1955.

143. Kim, D.S., Watkins, A., Bidstrup, E., Lee, J., Topkar, V., Kofman, C., Schwarz, K.J., Liu, Y., Pintilie, G., Roney, E., **Das, R.**, & Jewett, M.C. (2022) “Three-dimensional structure-guided evolution of a ribosome with tethered subunits.” *Nature Chemical Biology*, 18 (9), 990-998.
142. Andreasson, J.O.L., Gotrik, M.R., Wu, M.J., Wayment-Steele, H.K., Kladwang, W., Portela, F., Wellington-Oguri, R., **Das, R.**†, & Greenleaf, W.J.† (2022) “Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular sensors.” *Proceedings of the National Academy of Sciences of the United States of America*, 119 (18) e211297919.
141. Leppek, K.*, Byeon, G.W.*, Kladwang, W. *, Wayment-Steele, H.K. *, Kerr, C.*, Xu, A.F., Kim, D.S., Topkar, V.V., Choe, C., Rothschild, D., Tiu, G.C., Wellington-Oguri, R., Fujii, K., Sharma, E., Watkins, A.M., Nicol, J.J., Romano, J., Tunguz, B., Diaz F., Cai, H., Guo, P., Wu, J., Meng, F., Shi, S., Eterna Participants, Dormitzer, P.R., Solórzano, A., Barna, M.†, & **Das, R.**† (2022) “Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics.” *Nature Communications* 13, 1536.
140. **Das, R.**† & Watkins, A.M. (2021) “RiboDraw: semiautomated two-dimensional drawing of RNA tertiary structure diagrams.” *NAR Genomics and Bioinformatics*. 3(4).
139. Wayment-Steele, H. K., Kim, D.S., Choe, C. A., Nicol, J. J., Wellington-Oguri, R., Parra Sperberg, R.A., Huang, P.S., Eterna Participants, & **Das, R.** (2021). “Theoretical basis for stabilizing messenger RNA through secondary structure design.” *Nucleic Acids Research*, 49(18), 10604 – 10617.
138. **Das, R.**† & Russell, R.† (2021) “How to kinetically dissect an RNA machine.” *Biochemistry* 60 (46), 3485–3490. (invited perspective)
137. Zhang, K., *Zheludev, I. N.,* Hagey, R. J., Wu, M. T.-P., Haslecker, R., Hou, Y. J., Kretsch, R., Pintilie, G. D., Rangan, R., Kladwang, W., Li, S., Pham, E. A., Bernardin-Souibgui, C., Baric, R. S., Sheahan, T. P., D Souza, V., Glenn, J. S.†, Chiu, W.†, & Das, R.† (2021). “Cryo-electron microscopy and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome.” *Nature Structure and Molecular Biology*, 28, 747–754.
136. Su, Z.†*, Zhang, K.,* Kappel, K.,* Li, S., Palo, M., Pintilie, G., Rangan, R., Luo, B., Wei, Y., **Das, R.**†, & Chiu, W.† (2021). “Cryo-EM Structures of the full-length *Tetrahymena* ribozyme at 3.1 Å resolution”, *Nature*, 596, 603–607.
135. Townshend, R.,* Watkins, A.M.,* Eismann, S.,* Rangan, R., **Das, R.**†, & Dror R.† (2021) “Geometric deep learning of RNA structure.” *Science*, 373(6558), 1047–1051. [Highlight: Weeks, K.M. (2021) “Piercing the fog of the RNA structure-ome.” *Science*, 373(6558),964-965.]
134. **Das R.** (2021) “RNA structure: a renaissance begins?” *Nature Methods*, 18,439. (invited perspective)
133. Ghanim, G.E., Fountain, A.J., van Roon, A.M., **Das, R.**, Collins, K., & Nguyen, T.H.D. (2021), “Structure of human telomerase holoenzyme with bound telomeric DNA.” *Nature*, 593(7859), 449–453.
132. Rangan, R., Watkins, A.M, Chacon, J, Kretsch, R., Kladwang, W., Zheludev, I.N., Townley, J., Rynge, M., Thain, G., & **Das, R.** (2021) “De novo 3D models of SARS-CoV-2 RNA elements and small- molecule-binding RNAs to aid drug discovery.” *Nucleic Acids Research*, 49(6), 3092–3108.
131. Liu, X., Sun, T., Shcherbina, A., Li, Q., Kappel, K., Jarmoskaite, I., Ramaswami, G., **Das, R.**, Kundaje, A., & Li, J. (2021) "Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR- mediated mutagenesis." *Nature Communications*, Apr 12;12(1),2165.
130. Byeon, G. W., Cenik, E. S., Jiang, L., Tang, H., **Das, R.**, & Barna, M. (2021). “Functional and structural basis of extreme conservation in vertebrate 5’ untranslated regions.” *Nature Genetics*, 53, 729–741.
129. Le, K., Adolf-Bryfogle, J., Klima, J., Lyskov, S., Labonte, J., Bertolani, S., Roy Burman, S., Leaver-Fay, A., Weitzner, B., Maguire, J., Rangan, R., Adrianowycz, M., Alford, R., Adal, A., Nance, M., Das, R., Dunbrack, R., Schief, W., Kuhlman, B., Siegel, J., & Gray, J. (2021) “PyRosetta jupyter notebooks teach biomolecular structure prediction and design.” *The Biophysicist*, 2 (1), 108 – 122.
128. Palka, C., Forino, N., Hentschel, J., **Das, R.**, & Stone, M. D. (2020). “Folding heterogeneity in the essential human telomerase RNA three-way junction.” *RNA*, 26(12), 1787–1800.

127. Watkins, A. M., Rangan, R., & **Das, R.** (2020). “FARFAR2: Improved de novo Rosetta prediction of complex global RNA folds.” *Structure*, 28(8), 963–976.e6.
126. Rangan, R., Zheludev, I. N., Hagey, R. J., Pham, E. A., Wayment-Steele, H. K., Glenn, J. S.†, & **Das, R.†** (2020). “RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: A first look.” *RNA*, 26(8), 937–959.
125. Miao, Z., Adamiak, R. W., Antczak, M., Boniecki, M. J., Bujnicki, J., Chen, S.-J., Cheng, C. Y., Cheng, Y., Chou, F.-C., Das, R., Dokholyan, N. V., Ding, F., Geniesse, C., Jiang, Y., Joshi, A., Krokhotin, A., Magnus, M., ... Westhof, E. (2020). “RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers.” *RNA*, 26(8), 982–995.
124. Kappel, K.,* Zhang, K.,* Su, Z.,* Watkins, A. M., Kladwang, W., Li, S., Pintilie, G., Topkar, V. V., Rangan, R., Zheludev, I. N., Yesselman, J., Chiu, W.†, & **Das, R.†** (2020). “Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures.” *Nature Methods*, 17(7), 699–707. [Highlight: Richardson, J. S. (2020). “A new way to see RNAs.” *Nature Methods*, 17(7), 663–664.]
123. Leman, J. K., Weitzner, B. D., Lewis, S. M., Adolf-Bryfogle, J., Alam, N., Alford, R. F., Aprahamian, M., Baker, D., Barlow, K. A., Barth, P., Basanta, B., Bender, B. J., Blacklock, K., Bonet, J., Boyken, S. E., Bradley, P., Bystroff, C., Conway, P., Cooper, S., Correia, B.E., Coventry, B., **Das, R.**, ... Bonneau, R. (2020). “Macromolecular modeling and design in Rosetta: Recent methods and frameworks.” *Nature Methods*, 17(7), 665–680.
122. Kladwang, W., Topkar, V. V., Liu, B., Rangan, R., Hodges, T. L., Keane, S. C., Al-Hashimi, H., & **Das, R.** (2020). “Anomalous reverse transcription through chemical modifications in polyadenosine stretches.” *Biochemistry*, 59(23), 2154–2170.
121. Jain, N., Blauch, L. R., Szymanski, M. R., **Das, R.**, Tang, S. K. Y., Yin, Y. W., & Fire, A. Z. (2020). “Transcription polymerase-catalyzed emergence of novel RNA replicons.” *Science*, 368(6487).
120. Watkins, A. M., Rangan, R., & **Das, R.** (2019). “Using Rosetta for RNA homology modeling.” *Methods in Enzymology*, 623, 177–207. (Invited book chapter.)
119. Wayment-Steele, H., Wu, M., Gotrik, M., & **Das, R.** (2019). “Evaluating riboswitch optimality.” *Methods in Enzymology*, 623, 417–450. (Invited book chapter.)
118. **Das, R.†**, Keep, B., Washington, P., & Riedel-Kruse, I. H.† (2019). “Scientific discovery games for biomedical research.” *Annual Review of Biomedical Data Science*, 2(1), 253–279. (Invited review.)
117. Zhang, K.,* Li, S.,* Kappel, K.,* Pintilie, G., Su, Z., Mou, T.-C., Schmid, M. F., **Das, R.†**, & Chiu, W.† (2019). “Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution.” *Nature Communications*, 10(1), 5511.
116. Magnus, M.†, Kappel, K., **Das, R.†**, & Bujnicki, J. M. (2019). “RNA 3D structure prediction guided by independent folding of homologous sequences.” *BMC Bioinformatics*, 20(1), 512.
115. Li, X., Liu, S., Zhang, L., Issaian, A., Hill, R. C., Espinosa, S., Shi, S., Cui, Y., Kappel, K., **Das, R.**, Hansen, K. C., Zhou, Z. H., & Zhao, R. (2019). “A unified mechanism for intron and exon definition and back-splicing.” *Nature*, 573(7774), 375–380.
114. Yesselman, J. D., Eiler, D., Carlson, E. D., Gotrik, M. R., d’Aquino, A. E., Ooms, A. N., Kladwang, W., Carlson, P. D., Shi, X., Costantino, D. A., Herschlag, D., Lucks, J. B., Jewett, M. C., Kieft, J. S., & Das, R. (2019). “Computational design of three-dimensional RNA structure and function.” *Nature Nanotechnology*, 14(9), 866–873.
113. Huang, L., Wang, J., Watkins, A. M., **Das, R.**, & Lilley, D. M. J. (2019). “Structure and ligand binding of the glutamine-II riboswitch.” *Nucleic Acids Research*, 47(14), 7666–7675.
112. Yesselman, J., Denny, S. K., Bisaria, N., Herschlag, D. †, Greenleaf, W. J.†, & **Das, R.†** (2019). “Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation.” *Proceedings of the National Academy of Sciences of the United States of America*, 116(34), 16847–16855.
111. Wu, M. J., Andreasson, J. O. L., Kladwang, W., Greenleaf, W., & **Das, R.** (2019). “Automated design of diverse stand-alone riboswitches.” *ACS Synthetic Biology*, 8(8), 1838–1846.

110. Koirala, D., Shao, Y., Koldobskaya, Y., Fuller, J. R., Watkins, A. M., Shelke, S. A., Pilipenko, E. V., **Das, R.**, Rice, P. A., & Piccirilli, J. A. (2019). “A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites.” *Nature Communications*, *10*(1), 3629.
109. Jarmoskaite, I., Denny, S. K., Vaidyanathan, P. P., Becker, W. R., Andreasson, J. O. L., Layton, C. J., Kappel, K., Shivashankar, V., Sreenivasan, R., **Das, R.**, Greenleaf, W. J., & Herschlag, D. (2019). “A quantitative and predictive model for RNA binding by human Pumilio proteins.” *Molecular Cell*, *74*(5), 966–981.e18.
108. Koodli, R. V., Keep, B., Coppess, K. R., Portela, F., Eterna participants, & **Das, R.** (2019). “EternaBrain: Automated RNA design through move sets and strategies from an Internet-scale RNA videogame.” *PLoS Computational Biology*, *15*(6), e1007059. (Issue image)
107. Kappel, K., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D., & **Das, R.** (2019). “Blind tests of RNA-protein binding affinity prediction.” *Proceedings of the National Academy of Sciences of the United States of America*, *116*(17), 8336–8341.
106. Boeynaems, S., Holehouse, A. S., Weinhardt, V., Kovacs, D., Van Lindt, J., Larabell, C., Van Den Bosch, L., **Das, R.**, Tompa, P. S., Pappu, R. V., & Gitler, A. D. (2019). “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*, *116*(16), 7889–7898.
105. Kappel, K., & **Das, R.** (2019). “Sampling native-like structures of RNA-protein complexes through Rosetta folding and docking.” *Structure*, *27*(1), 140–151.e5.
104. Leppek, K., **Das, R.**[†], & Barna, M.[†] (2018). “Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them.” *Nature Reviews Molecular Cell Biology*, *19*(3), 158–174. (Invited review)
103. Zettl, T., **Das, R.**, Harbury, P. A. B.[‡], Herschlag, D.[‡], Lipfert, J.[‡], Mathew, R. S., & Shi, X. (2018). “Recording and analyzing nucleic acid distance distributions with X-ray scattering interferometry (XSI).” *Current Protocols in Nucleic Acid Chemistry*, edited by Serge L. Beaucage., *73*(1), e54. (Invited book chapter)
102. Hartwick, E. W., Costantino, D. A., MacFadden, A., Nix, J. C., Tian, S., **Das, R.**, & Kieft, J. S. (2018). “Ribosome-induced RNA conformational changes in a viral 3'-UTR sense and regulate translation levels.” *Nature Communications*, *9*(1), 5074.
101. Kappel, K., Liu, S., Larsen, K. P., Skinnotis, G., Puglisi, E. V., Puglisi, J. D., Zhou, Z. H., Zhao, R., & **Das, R.** (2018). “De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes.” *Nature Methods*, *15*(11), 947–954.
100. Denny, S. K., Bisaria, N., Yesselman, J. D., **Das, R.**, Herschlag, D., & Greenleaf, W. J. (2018). “High-throughput investigation of diverse junction elements in RNA tertiary folding.” *Cell*, *174*(2), 377–390.e20. [Highlight: Perkel, J. M. (2018). “The hackers teaching old DNA sequencers new tricks.” *Nature*, *559*(7715), 643–645. doi: 10.1038/d41586-018-05769-8.]
99. Chen, L., Roake, C. M., Freund, A., Batista, P. J., Tian, S., Yin, Y. A., Gajera, C. R., Lin, S., Lee, B., Pech, M. F., Venteicher, A. S., Das, R., Chang, H. Y., & Artandi, S. E. (2018). “An activity switch in human telomerase based on RNA conformation and shaped by TCAB1.” *Cell*, *174*(1), 218–230.e13.
98. Watkins, A. M., Geniesse, C., Kladwang, W., Zakrevsky, P., Jaeger, L., & **Das, R.** (2018). “Blind prediction of noncanonical RNA structure at atomic accuracy.” *Science Advances*, *4*(5), eaar5316.
97. Gracia, B., Al-Hashimi, H. M., Bisaria, N., **Das, R.**, Herschlag, D., & Russell, R. (2018). “Hidden structural modules in a cooperative RNA folding transition.” *Cell Reports*, *22*(12), 3240–3250.
96. Tian, S., Kladwang, W., & **Das, R.** (2018). “Allosteric mechanism of the *V. vulnificus* adenine riboswitch resolved by four-dimensional chemical mapping.” *eLife*, *7*. <https://doi.org/10.7554/eLife.29602>
95. Yesselman, J. D., Tian, S., Liu, X., Shi, L., Li, J. B., & **Das, R.** (2018). “Updates to the RNA mapping database (RMDB), version 2.” *Nucleic Acids Research*, *46*(D1), D375–D379.
94. Moretti, R., Lyskov, S., **Das, R.**, Meiler, J., & Gray, J. J. (2018). “Web-accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE).” *Protein Science*, *27*(1), 259–268.

93. Omabegho, T., Gurel, P. S., Cheng, C. Y., Kim, L. Y., Ruijgrok, P. V., **Das, R.**, Alushin, G. M., & Bryant, Z. (2018). “Controllable molecular motors engineered from myosin and RNA.” *Nature Nanotechnology*, 13(1), 34–40. [Highlight: Borman, S. (2017). “Engineered myosin motor uses RNA arm to march on protein fibers.” *Chemical & Engineering News*, 95(45), 8.]
92. Cheng, C. Y., Kladwang, W., Yesselman, J. D., & **Das, R.** (2017). “RNA structure inference through chemical mapping after accidental or intentional mutations.” *Proceedings of the National Academy of Sciences of the United States of America*, 114(37), 9876–9881. [Highlight: Weidman, A. G. (2017). “Mutate-and-map’ plus next-generation sequencing reveals RNA secondary structure.” *ACS Chemical Biology*, 12(10), 2479–2481.]
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Patents

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