



## Rhiju Das

Associate Professor of Biochemistry

 Curriculum Vitae available Online

### Bio

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#### BIO

Dr. Das is an Associate Professor of Biochemistry at Stanford University School of Medicine. After training in particle physics and cosmology at Harvard, Cambridge, University College London, and Stanford, Dr. Das did postdoctoral research in computational protein folding at the University of Washington with David Baker. On returning to Stanford, Dr. Das set up his lab to focus on computer modeling and design of RNA molecules, which underlie important molecular machines in biology and medicine. As a core part of this research, Dr. Das leads Eterna, an open science platform that crowdsources intractable RNA design problems to 250,000 players of an online videogame and provides scoring feedback based on actual wet-lab experiments. Dr. Das has been recognized by the Burroughs-Wellcome Career Award at the Interface of Science, the Stanford Medicine Endowed Faculty Scholar award, and selection as an investigator of the Howard Hughes Medical Institute. In response to the COVID-19 pandemic, Dr. Das and Eterna have launched the OpenVaccine challenge to develop refrigerator-stable mRNA vaccines needed for world-wide immunization.

#### ACADEMIC APPOINTMENTS

- Associate Professor, Biochemistry
- Member, Bio-X
- Member, Wu Tsai Neurosciences Institute

#### HONORS AND AWARDS

- Gold Medal, Top US score, 2nd place worldwide, International Physics Olympiad (1995)
- British Marshall Scholar, Marshall Aid Commemoration Commission (1998-2000)
- Jane Coffin Childs Foundation Fellowship, Jane Coffin Childs Foundation (2006-2008)
- Career Award at the Scientific Interface, Burroughs-Wellcome Foundation (2008-2015)
- Keck Medical Research Grant award, W. M. Keck Foundation (2012)
- OpenEye Outstanding Junior Faculty Award, American Chemical Society (2015)
- Discovery Innovation Award, Stanford University School of Medicine (2016)
- Stanford Medicine Endowed Faculty Scholar, Anonymous donor, Stanford School of Medicine (2020)
- Selected as HHMI Investigator, Howard Hughes Medical Institute (2021)

#### BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- COVID-19 Research Oversight Committee, Stanford University (2020 - 2020)
- Structural Biology Review Committee, SLAC Linac Coherent Light Source (2020 - 2020)
- Co-author, RNA Synthetic Biology Roadmap, Engineering Biology Research Consortium (2019 - present)

- Editorial Advisory Board, Biochemistry (2017 - present)

## PROFESSIONAL EDUCATION

- Ph.D., Stanford University , Physics (2005)
- M.Res., University College London , Biocomplexity (2000)
- M.Phil., Cambridge University , Physics (Radio Astronomy) (1999)
- A.B., s.c.l., Harvard University , Physics (1998)

## LINKS

- Das Lab: <http://daslab.stanford.edu>
- Eterna Videogame/Massive Open Laboratory: <http://eterna.stanford.edu>
- RNA Mapping Database: <http://rmdb.stanford.edu>

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our lab strives to predict and design how biopolymer sequences define and regulate biopolymer structure/function, focusing on medically important RNA and RNA/protein complexes.

We develop algorithms to predict the structures and energetics of RNAs and RNA/protein interfaces at high resolution, with an increasing focus on ribosomes and viruses. We test these ideas through community-wide blind trials and by solving molecule structures and structure ensembles with chemical mapping, NMR, crystallographic, and cryoelectron microscopy data. Notable achievements include top models in the majority of RNA-Puzzles blind structure prediction challenges and first experimental structures of several historically and biomedically important RNA molecules, such as the Tetrahymena ribozyme.

Complementary to this computational research, we are developing information-rich biochemical methods to model the myriad structures of non-coding RNAs that remain unknown. Current efforts focus on probing the extent and biological impact of RNA structure and conformational change in fundamental processes like splicing and mRNA transport in brain cells and viruses.

In addition to modeling RNAs, we aim to design new ones for basic science, diagnostics, therapeutics, and vaccines. Our videogame project Eterna seeks missing rules and novel molecules for medicine by giving citizen scientists access to high-throughput wet-lab experiments. Notable achievements include the first algorithm for automated 3D RNA design, development of the current community benchmark for RNA design, discovery of optimal 'zero-energy' switches made of RNA, and invention of RNA calculators for point-of-care diagnostics responsive to complex gene signatures for active tuberculosis. This project has also given rise to several firsts in citizen science, including the first papers written by videogame players as lead authors and as sole authors.

## Teaching

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### COURSES

#### 2020-21

- Biological Macromolecules: BIOC 241, BIOE 241, BIOPHYS 241, SBIO 241 (Aut)
- Development of Thesis Research: BIOC 350 (Aut)

#### 2019-20

- Development of Thesis Research: BIOC 350 (Aut)

#### 2018-19

- Biological Macromolecules: BIOC 241 (Spr)
- Development of Thesis Research: BIOC 350 (Aut)

## STANFORD ADVISEES

### Doctoral Dissertation Reader (AC)

Raphael Eguchi, Elisabeth Meyer

### Doctoral Dissertation Advisor (AC)

Rachael Kretsch, Ramya Rangan, Ved Topkar

### Doctoral Dissertation Co-Advisor (AC)

Christian Choe

## GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (Phd Program)
- Biomedical Informatics (Phd Program)
- Biomedical Informatics (Masters Program)
- Biophysics (Phd Program)

## Publications

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### PUBLICATIONS

- **Three-dimensional structure-guided evolution of a ribosome with tethered subunits.** *Nature chemical biology*  
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
- **Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular switches.** *Proceedings of the National Academy of Sciences of the United States of America*  
Andreasson, J. O., Gotrik, M. R., Wu, M. J., Wayment-Steele, H. K., Kladwang, W., Portela, F., Wellington-Oguri, R., Eterna Participants, Das, R., Greenleaf, W. J.  
2022; 119 (18): e2112979119
- **Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics.** *Nature communications*  
Leppek, K., Byeon, G. W., Kladwang, W., Wayment-Steele, H. K., Kerr, C. H., Xu, A. F., Kim, D. S., Topkar, V. V., Choe, C., Rothschild, D., Tiu, G. C., Wellington-Oguri, R., Fujii, et al  
2022; 13 (1): 1536
- **RiboDraw: semiautomated two-dimensional drawing of RNA tertiary structure diagrams.** *NAR genomics and bioinformatics*  
Das, R., Watkins, A. M.  
2021; 3 (4): lqab091
- **Ensuring scientific reproducibility in bio-macromolecular modeling via extensive, automated benchmarks.** *Nature communications*  
Koehler Leman, J., Lyskov, S., Lewis, S. M., Adolf-Bryfogle, J., Alford, R. F., Barlow, K., Ben-Aharon, Z., Farrell, D., Fell, J., Hansen, W. A., Harmalkar, A., Jeliaskov, J., Kuenze, et al  
2021; 12 (1): 6947
- **Theoretical basis for stabilizing messenger RNA through secondary structure design.** *Nucleic acids research*  
Wayment-Steele, H. K., Kim, D. S., Choe, C. A., Nicol, J. J., Wellington-Oguri, R., Watkins, A. M., Parra Sperberg, R. A., Huang, P., Participants, E., Das, R.  
2021
- **How to Kinetically Dissect an RNA Machine.** *Biochemistry*  
Das, R., Russell, R.  
2021

- **Geometric deep learning of RNA structure.** *Science (New York, N.Y.)*  
Townshend, R. J., Eismann, S., Watkins, A. M., Rangan, R., Karelina, M., Das, R., Dror, R. O.  
2021; 373 (6558): 1047-1051
- **Cryo-EM and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome.** *Nature structural & molecular biology*  
Zhang, K., Zheludev, I. N., Hagey, R. J., Haslecker, R., Hou, Y. J., Kretsch, R., Pintilie, G. D., Rangan, R., Kladwang, W., Li, S., Wu, M. T., Pham, E. A., Bernardin-Souibgui, et al  
2021
- **Interpretation of RNA cryo-EM maps of various resolutions**  
Kretsch, R., Das, R., Chiu, W.  
INT UNION CRYSTALLOGRAPHY.2021: A217
- **RNA structure: a renaissance begins?** *Nature methods*  
Das, R.  
2021; 18 (5): 439
- **Structure of human telomerase holoenzyme with bound telomeric DNA.** *Nature*  
Ghanim, G. E., Fountain, A. J., van Roon, A. M., Rangan, R., Das, R., Collins, K., Nguyen, T. H.  
2021
- **Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions.** *Nature genetics*  
Byeon, G. W., Cenik, E. S., Jiang, L., Tang, H., Das, R., Barna, M.  
2021
- **PyRosetta Jupyter Notebooks Teach Biomolecular Structure Prediction and Design.** *Biophysicist (Rockville, Md.)*  
Le, K. H., Adolf-Bryfogle, J., Klima, J. C., Lyskov, S., Labonte, J., Bertolani, S., Burman, S. S., Leaver-Fay, A., Weitzner, B., Maguire, J., Rangan, R., Adrianowycz, M. A., Alford, et al  
2021; 2 (1): 108-122
- **De novo 3D models of SARS-CoV-2 RNA elements from consensus experimental secondary structures.** *Nucleic acids research*  
Rangan, R., Watkins, A. M., Chacon, J., Kretsch, R., Kladwang, W., Zheludev, I. N., Townley, J., Rynge, M., Thain, G., Das, R.  
2021
- **Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR-mediated mutagenesis.** *Nature communications*  
Liu, X., Sun, T., Shcherbina, A., Li, Q., Jarmoskaite, I., Kappel, K., Ramaswami, G., Das, R., Kundaje, A., Li, J. B.  
2021; 12 (1): 2165
- **Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 Å resolution.** *Nature*  
Su, Z., Zhang, K., Kappel, K., Li, S., Palo, M. Z., Pintilie, G. D., Rangan, R., Luo, B., Wei, Y., Das, R., Chiu, W.  
2021
- **Theoretical basis for stabilizing messenger RNA through secondary structure design.** *bioRxiv : the preprint server for biology*  
Wayment-Steele, H. K., Kim, D. S., Choe, C. A., Nicol, J. J., Wellington-Oguri, R., Watkins, A. M., Sperberg, R. A., Huang, P. S., Participants, E., Das, R.  
2020
- **Macromolecular modeling and design in Rosetta: recent methods and frameworks.** *Nature methods*  
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, et al  
2020
- **Anomalous Reverse Transcription through Chemical Modifications in Polyadenosine Stretches.** *Biochemistry*  
Kladwang, W., Topkar, V. V., Liu, B., Rangan, R., Hodges, T. L., Keane, S. C., Al-Hashimi, H., Das, R.  
2020
- **RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: a first look.** *RNA (New York, N.Y.)*  
Rangan, R., Zheludev, I. N., Das, R.  
2020
- **RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers.** *RNA (New York, N.Y.)*

- Miao, Z., Adamiak, R. W., Antczak, M., Boniecki, M. J., Bujnicki, J. M., Chen, S., Cheng, C. Y., Cheng, Y., Chou, F., Das, R., Dokholyan, N. V., Ding, F., Geniesse, et al  
2020
- **Transcription polymerase-catalyzed emergence of novel RNA replicons.** *Science (New York, N.Y.)*  
Jain, N. n., Blauch, L. R., Szymanski, M. R., Das, R. n., Tang, S. K., Yin, Y. W., Fire, A. Z.  
2020
  - **Folding heterogeneity in the essential human telomerase RNA three-way junction.** *RNA (New York, N.Y.)*  
Palka, C. n., Forino, N. n., Hentschel, J. n., Das, R. n., Stone, M. D.  
2020
  - **FARFAR2: Improved De Novo Rosetta Prediction of Complex Global RNA Folds.** *Structure (London, England : 1993)*  
Watkins, A. M., Rangan, R. n., Das, R. n.  
2020
  - **Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures.** *Nature methods*  
Kappel, K. n., Zhang, K. n., Su, Z. n., Watkins, A. M., Kladwang, W. n., Li, S. n., Pintilie, G. n., Topkar, V. V., Rangan, R. n., Zheludev, I. N., Yesselman, J. D., Chiu, W. n., Das, et al  
2020; 17 (7): 699–707
  - **RNA 3D structure prediction guided by independent folding of homologous sequences.** *BMC bioinformatics*  
Magnus, M., Kappel, K., Das, R., Bujnicki, J. M.  
2019; 20 (1): 512
  - **A unified mechanism for intron and exon definition and back-splicing.** *Nature*  
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, et al  
2019
  - **A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites.** *Nature communications*  
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; 10 (1): 3629
  - **Automated Design of Diverse Stand-Alone Riboswitches** *ACS SYNTHETIC BIOLOGY*  
Wu, M. J., Andreasson, J. L., Kladwang, W., Greenleaf, W., Das, R.  
2019; 8 (8): 1838–46
  - **Scientific Discovery Games for Biomedical Research.** *Annual review of biomedical data science*  
Das, R., Keep, B., Washington, P., Riedel-Kruse, I. H.  
2019; 2 (1): 253-279
  - **Structure and ligand binding of the glutamine-II riboswitch.** *Nucleic acids research*  
Huang, L., Wang, J., Watkins, A. M., Das, R., Lilley, D. M.  
2019
  - **A Quantitative and Predictive Model for RNA Binding by Human Pumilio Proteins** *MOLECULAR CELL*  
Jarmoskaite, I., Denny, S. K., Vaidyanathan, P. P., Becker, W. R., Andreasson, J. L., Layton, C. J., Kappel, K., Shivashankar, V., Sreenivasan, R., Das, R., Greenleaf, W. J., Herschlag, D.  
2019; 74 (5): 966-+
  - **Blind tests of RNA-protein binding affinity prediction** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Kappel, K., Jarmoskaite, I., Vaidyanathan, P. P., Greenleaf, W. J., Herschlag, D., Das, R.  
2019; 116 (17): 8336–41
  - **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*  
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., Gitler, A. D.  
2019; 116 (16): 7889–98
  - **Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution.** *Nature communications*

- Zhang, K. n., Li, S. n., Kappel, K. n., Pintilie, G. n., Su, Z. n., Mou, T. C., Schmid, M. F., Das, R. n., Chiu, W. n.  
2019; 10 (1): 5511
- **Scientific Discovery Games for Biomedical Research** *ANNUAL REVIEW OF BIOMEDICAL DATA SCIENCE, VOL 2, 2019*  
Das, R., Keep, B., Washington, P., Riedel-Kruse, I. H., Altman, R. B., Levitt, M.  
2019; 2: 253–79
  - **Computational design of three-dimensional RNA structure and function.** *Nature nanotechnology*  
Yesselman, J. D., Eiler, D. n., Carlson, E. D., Gotrik, M. R., d'Aquino, A. E., Ooms, A. N., Kladwang, W. n., Carlson, P. D., Shi, X. n., Costantino, D. A., Herschlag, D. n., Lucks, J. B., Jewett, et al  
2019
  - **EternaBrain: Automated RNA design through move sets and strategies from an Internet-scale RNA videogame.** *PLoS computational biology*  
Koodli, R. V., Keep, B. n., Coppess, K. R., Portela, F. n., Das, R. n.  
2019; 15 (6): e1007059
  - **Using Rosetta for RNA homology modeling.** *Methods in enzymology*  
Watkins, A. M., Rangan, R., Das, R.  
2019; 623: 177–207
  - **Evaluating riboswitch optimality.** *Methods in enzymology*  
Wayment-Steele, H., Wu, M., Gotrik, M., Das, R.  
2019; 623: 417–50
  - **Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation.** *Proceedings of the National Academy of Sciences of the United States of America*  
Yesselman, J. D., Denny, S. K., Bisaria, N. n., Herschlag, D. n., Greenleaf, W. J., Das, R. n.  
2019
  - **Ribosome-induced RNA conformational changes in a viral 3'-UTR sense and regulate translation levels** *NATURE COMMUNICATIONS*  
Hartwick, E. W., Costantino, D. A., MacFadden, A., Nix, J. C., Tian, S., Das, R., Kieft, J. S.  
2018; 9
  - **De novo computational RNA modeling into cryo-EM maps of large ribonucleoprotein complexes.** *Nature methods*  
Kappel, K., Liu, S., Larsen, K. P., Skiniotis, G., Puglisi, E. V., Puglisi, J. D., Zhou, Z. H., Zhao, R., Das, R.  
2018
  - **Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking.** *Structure (London, England : 1993)*  
Kappel, K., Das, R.  
2018
  - **High-Throughput Investigation of Diverse Junction Elements in RNA Tertiary Folding.** *Cell*  
Denny, S. K., Bisaria, N., Yesselman, J. D., Das, R., Herschlag, D., Greenleaf, W. J.  
2018
  - **Recording and Analyzing Nucleic Acid Distance Distributions with X-Ray Scattering Interferometry (XSI).** *Current protocols in nucleic acid chemistry*  
Zettl, T., Das, R., Harbury, P. A., Herschlag, D., Lipfert, J., Mathew, R. S., Shi, X.  
2018; 73 (1): e54
  - **Blind prediction of noncanonical RNA structure at atomic accuracy.** *Science advances*  
Watkins, A. M., Geniesse, C., Kladwang, W., Zakrevsky, P., Jaeger, L., Das, R.  
2018; 4 (5): eaar5316
  - **Hidden Structural Modules in a Cooperative RNA Folding Transition** *CELL REPORTS*  
Gracia, B., Al-Hashimi, H. M., Bisaria, N., Das, R., Herschlag, D., Russell, R.  
2018; 22 (12): 3240–50
  - **Allosteric mechanism of the V-vulnificus adenine riboswitch resolved by four-dimensional chemical mapping** *ELIFE*  
Tian, S., Kladwang, W., Das, R.  
2018; 7

- **Updates to the RNA mapping database (RMDB), version 2** *NUCLEIC ACIDS RESEARCH*  
Yesselman, J. D., Tian, S., Liu, X., Shi, L., Li, J., Das, R.  
2018; 46 (D1): D375–D379
- **An Activity Switch in Human Telomerase Based on RNA Conformation and Shaped by TCAB1.** *Cell*  
Chen, L. n., Roake, C. M., Freund, A. n., Batista, P. J., Tian, S. n., Yin, Y. A., Gajera, C. R., Lin, S. n., Lee, B. n., Pech, M. F., Venteicher, A. S., Das, R. n., Chang, et al  
2018
- **Web-accessible molecular modeling with Rosetta: The Rosetta Online Server that Includes Everyone (ROSIE)** *PROTEIN SCIENCE*  
Moretti, R., Lyskov, S., Das, R., Meiler, J., Gray, J. J.  
2018; 27 (1): 259–68
- **RNA structure inference through chemical mapping after accidental or intentional mutations.** *Proceedings of the National Academy of Sciences of the United States of America*  
Cheng, C. Y., Kladwang, W., Yesselman, J. D., Das, R.  
2017; 114 (37): 9876-9881
- **The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design.** *Journal of chemical theory and computation*  
Alford, R. F., Leaver-Fay, A., Jeliaskov, J. R., O'Meara, M. J., DiMaio, F. P., Park, H., Shapovalov, M. V., Renfrew, P. D., Mulligan, V. K., Kappel, K., Labonte, J. W., Pacella, M. S., Bonneau, et al  
2017
- **Primerize-2D: automated primer design for RNA multidimensional chemical mapping.** *Bioinformatics (Oxford, England)*  
Tian, S., Das, R.  
2017; 33 (9): 1405-1406
- **Single-molecule FRET-Rosetta reveals RNA structural rearrangements during human telomerase catalysis** *RNA*  
Parks, J. W., Kappel, K., Das, R., Stone, M. D.  
2017; 23 (2): 175-188
- **RNA-Puzzles Round III: 3D RNA structure prediction of five riboswitches and one ribozyme.** *RNA (New York, N.Y.)*  
Miao, Z., Adamiak, R. W., Antczak, M., Batey, R. T., Becka, A. J., Biesiada, M., Boniecki, M. J., Bujnicki, J., Chen, S., Cheng, C. Y., Chou, F., Ferré-D'Amaré, A. R., Das, et al  
2017
- **Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them.** *Nature reviews. Molecular cell biology*  
Leppek, K. n., Das, R. n., Barna, M. n.  
2017
- **Controllable molecular motors engineered from myosin and RNA.** *Nature nanotechnology*  
Omabegho, T. n., Gurel, P. S., Cheng, C. Y., Kim, L. Y., Ruijgrok, P. V., Das, R. n., Alushin, G. M., Bryant, Z. n.  
2017
- **Blind tests of RNA nearest-neighbor energy prediction** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Chou, F., Kladwang, W., Kappel, K., Das, R.  
2016; 113 (30): 8430-8435
- **RNA structure through multidimensional chemical mapping** *QUARTERLY REVIEWS OF BIOPHYSICS*  
Tian, S., Das, R.  
2016; 49
- **Principles for Predicting RNA Secondary Structure Design Difficulty.** *Journal of molecular biology*  
Anderson-Lee, J., Fisker, E., Kosaraju, V., Wu, M., Kong, J., Lee, J., Lee, M., Zada, M., Treuille, A., Das, R.  
2016; 428 (5): 748-757
- **RNA Structure Refinement Using the ERRASER-Phenix Pipeline.** *Methods in molecular biology (Clifton, N.J.)*  
Chou, F., Echols, N., Terwilliger, T. C., Das, R.  
2016; 1320: 269-282

- **Modeling Small Noncanonical RNA Motifs with the Rosetta FARFAR Server.** *Methods in molecular biology (Clifton, N.J.)*  
Yesselman, J. D., Das, R.  
2016; 1490: 187-198
- **Rich RNA Structure Landscapes Revealed by Mutate-and-Map Analysis** *PLOS COMPUTATIONAL BIOLOGY*  
Cordero, P., Das, R.  
2015; 11 (11)
- **Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles.** *Bioinformatics*  
Lee, S., Kim, H., Tian, S., Lee, T., Yoon, S., Das, R.  
2015; 31 (17): 2808-2815
- **RNA-Redesign: a web server for fixed-backbone 3D design of RNA.** *Nucleic acids research*  
Yesselman, J. D., Das, R.  
2015; 43 (W1): W498-501
- **Primerize: automated primer assembly for transcribing non-coding RNA domains.** *Nucleic acids research*  
Tian, S., Yesselman, J. D., Cordero, P., Das, R.  
2015; 43 (W1): W522-6
- **Consistent global structures of complex RNA states through multidimensional chemical mapping** *ELIFE*  
Cheng, C. Y., Chou, F., Kladwang, W., Tian, S., Cordero, P., Das, R.  
2015; 4
- **RNA-Puzzles Round II: assessment of RNA structure prediction programs applied to three large RNA structures** *RNA*  
Miao, Z., Adamiak, R. W., Blanchet, M., Boniecki, M., Bujnicki, J. M., Chen, S., Cheng, C., Chojnowski, G., Chou, F., Cordero, P., Cruz, J. A., Ferre-D'Amare, A. R., Das, et al  
2015; 21 (6): 1066-1084
- **Modeling complex RNA tertiary folds with rosetta.** *Methods in enzymology*  
Cheng, C. Y., Chou, F., Das, R.  
2015; 553: 35-64
- **Consistent global structures of complex RNA states through multidimensional chemical mapping.** *eLife*  
Cheng, C. Y., Chou, F., Kladwang, W., Tian, S., Cordero, P., Das, R.  
2015; 4
- **RNA regulons in Hox 5' UTRs confer ribosome specificity to gene regulation.** *Nature*  
Xue, S., Tian, S., Fujii, K., Kladwang, W., Das, R., Barna, M.  
2015; 517 (7532): 33-38
- **High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states** *RNA-A PUBLICATION OF THE RNA SOCIETY*  
Tian, S., Cordero, P., Kladwang, W., Das, R.  
2014; 20 (11): 1815-1826
- **Scientific rigor through videogames.** *Trends in biochemical sciences*  
Treuille, A., Das, R.  
2014; 39 (11): 507-509
- **Double-stranded RNA under force and torque: similarities to and striking differences from double-stranded DNA.** *Proceedings of the National Academy of Sciences of the United States of America*  
Lipfert, J., Skinner, G. M., Keegstra, J. M., Hensgens, T., Jager, T., Dulin, D., Köber, M., Yu, Z., Donkers, S. P., Chou, F., Das, R., Dekker, N. H.  
2014; 111 (43): 15408-15413
- **Blind predictions of DNA and RNA tweezers experiments with force and torque.** *PLoS computational biology*  
Chou, F., Lipfert, J., Das, R.  
2014; 10 (8)
- **Understanding nucleic Acid-ion interactions.** *Annual review of biochemistry*  
Lipfert, J., Doniach, S., Das, R., Herschlag, D.



2014; 83: 813-841

- **Standardization of RNA chemical mapping experiments.** *Biochemistry*  
Kladwang, W., Mann, T. H., Becka, A., Tian, S., Kim, H., Yoon, S., Das, R.  
2014; 53 (19): 3063-3065
- **Structure determination of noncanonical RNA motifs guided by <sup>1</sup>H NMR chemical shifts.** *Nature methods*  
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