Stanford



Rhiju Das

Professor of Biochemistry

Curriculum Vitae available Online

Bio

BIO

Dr. Das is a 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.

ACADEMIC APPOINTMENTS

- 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 (2020-2023)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Assessor, RNA Category, 15th and 16th Critical Assessments of Structure Prediction (CASP15 and CASP16) (2022 - present)
- 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 - 2020)

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

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

COURSES

2026-27

- Biochemistry Department Minicourse: BIOC 202 (Aut)
- Biological Macromolecules: BIOC 241, BIOE 241, BIOPHYS 241, SBIO 241 (Aut)

2025-26

- Biochemistry Department Minicourse: BIOC 202 (Aut)

- Currents in Biochemistry: BIOC 257 (Aut)

2024-25

- Biochemistry Department Minicourse: BIOC 202 (Aut)
- Biological Macromolecules: BIOC 241, BIOE 241, BIOPHYS 241, SBIO 241 (Aut)
- Currents in Biochemistry: BIOC 257 (Aut)

2023-24

- Biological Macromolecules: BIOC 241, BIOE 241, BIOPHYS 241, SBIO 241 (Aut)

STANFORD ADVISEES

Doctoral Dissertation Reader (AC)

Steven Dunne, Varun Shanker

Postdoctoral Faculty Sponsor

Chaitanya Joshi, Deni Szokoli, Jigyasa Verma

Doctoral Dissertation Advisor (AC)

Hamish Blair

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biochemistry (PhD Program)
- Biomedical Data Science (PhD Program)
- Biomedical Data Science (Masters Program)
- Biophysics (PhD Program)

Publications

PUBLICATIONS

- **De novo design of RNA pseudoknots with deep learning.** *Science (New York, N.Y.)*
  Townley, J., Kladwang, W., Baker, D., Blair, H. M., Choe, C. A., El Nesr, G., Favor, A., Fisker, E., Haack, D. B., He, S., Hingey, J., Huang, P. S., Huang, et al
  2026; 393 (6814): 931-937

- **Structures of nucleotide-bound human telomerase at several steps of its telomeric DNA repeat addition cycle.** *Nature communications*
  Balch, S., Franco-Echevarria, E., Ghanim, G. E., Kretsch, R. C., Das, R., Nguyen, T. H.
  2026

- **Template-based RNA structure prediction advanced through a blind code competition.** *bioRxiv : the preprint server for biology*
  Lee, Y., He, S., Oda, T., Rao, G. J., Kim, Y., Kim, R., Kim, H., Heng, C. K., Kowerko, D., Li, H., Nguyen, H., Sampathkumar, A., Gómez, et al
  2025

- **RNA switch model for localization and translation of the myelin basic protein mRNA.** *bioRxiv : the preprint server for biology*
  Topkar, V. V., Wu, V., Ho, L. T., Ambiel, N., Valenzuela, A., Yoshimura, K., Zuchero, J. B., Fu, M. M., Das, R.
  2025

- **Compact RNA sensors for increasingly complex functions of multiple inputs.** *Nature chemistry*
  Choe, C. A., Andreasson, J. O., Melaine, F., Kladwang, W., Wu, M. J., Portela, F., Wellington-Oguri, R., Nicol, J. J., Wayment-Steele, H. K., Gotrik, M., Khatri, P., Greenleaf, W. J., Das, et al
  2025

- **Blind Prediction of Complex Water and Ion Ensembles Around RNA in CASP16.** *Proteins*

Kretsch, R. C., Posani, E., Baulin, E. F., Bujnicki, J. M., Bussi, G., Cheatham, T. E., Chen, S. J., Elofsson, A., Farsani, M. A., Fisher, O. N., Gromiha, M. M., Gupta, A., Hamada, et al
2025

- **Assessment of Protein Complex Predictions in CASP16: Are We Making Progress?** *Proteins*
  Zhang, J., Yuan, R., Kryshtafovych, A., Pei, J., Kretsch, R. C., Schaeffer, R. D., Zhou, J., Das, R., Grishin, N. V., Cong, Q.
  2025

- **Assessment of Nucleic Acid Structure Prediction in CASP16.** *Proteins*
  Kretsch, R. C., Hummer, A. M., He, S., Yuan, R., Zhang, J., Karagianes, T., Cong, Q., Kryshtafovych, A., Das, R.
  2025

- **Functional Relevance of CASP16 Nucleic Acid Predictions as Evaluated by Structure Providers.** *Proteins*
  Kretsch, R. C., Albrecht, R., Andersen, E. S., Chen, H. A., Chiu, W., Das, R., Gezelle, J. G., Hartmann, M. D., Höbartner, C., Hu, Y., Jadhav, S., Johnson, P. E., Jones, et al
  2025

- **Cryo-EM structure of human telomerase dimer reveals H/ACA RNP-mediated dimerization.** *Science (New York, N.Y.)*
  Balch, S., Sekne, Z., Franco-Echevarría, E., Ludzia, P., Kretsch, R. C., Sun, W., Yu, H., Ghanim, G. E., Thorkelsson, S., Ding, Y., Das, R., Nguyen, T. H.
  2025; 389 (6756): eadr5817

- **Comprehensive analysis of Saccharomyces cerevisiae intron structures in vivo.** *Nature structural & molecular biology*
  Rangan, R., Huang, R., Hunter, O., Pham, P., Ares, M. J., Das, R.
  2025

- **OpenASO: RNA Rescue - designing splice-modulating antisense oligonucleotides through community science.** *RNA (New York, N.Y.)*
  Tse, V., Guiterrez, M., Townley, J., Romano, J., Pearl, J., Chacaltana, G., Players, E., Das, R., Sanford, J., Stone, M.
  2025

- **Naturally ornate RNA-only complexes revealed by cryo-EM.** *Nature*
  Kretsch, R. C., Wu, Y., Shabalina, S. A., Lee, H., Nye, G., Koonin, E. V., Gao, A., Chiu, W., Das, R.
  2025

- **Complex water networks visualized by cryogenic electron microscopy of RNA.** *Nature*
  Kretsch, R. C., Li, S., Pintilie, G., Palo, M. Z., Case, D. A., Das, R., Zhang, K., Chiu, W.
  2025

- **RNA-Puzzles Round V: blind predictions of 23 RNA structures.** *Nature methods*
  Bu, F., Adam, Y., Adamiak, R. W., Antczak, M., de Aquino, B. R., Badepally, N. G., Batey, R. T., Baulin, E. F., Boinski, P., Boniecki, M. J., Bujnicki, J. M., Carpenter, K. A., Chacon, et al
  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*
  Kretsch, R. C., Xu, L., Zheludev, I. N., Zhou, X., Huang, R., Nye, G., Li, S., Zhang, K., Chiu, W., Das, R.
  2024; 121 (10): e2320493121

- **Ribonanza: deep learning of RNA structure through dual crowdsourcing.** *bioRxiv : the preprint server for biology*
  He, S., Huang, R., Townley, J., Kretsch, R. C., Karagianes, T. G., Cox, D. B., Blair, H., Penzar, D., Vyaltsev, V., Aristova, E., Zinkevich, A., Bakulin, A., Sohn, et al
  2024

- **Minimization of the E. coli ribosome, aided and optimized by community science.** *Nucleic acids research*
  Tangpradabkul, T., Palo, M., Townley, J., Hsu, K. B., Participants, E., Smaga, S., Das, R., Schepartz, A.
  2024

- **CASP15 cryo-EM protein and RNA targets: Refinement and analysis using experimental maps.** *Proteins*
  Mulvaney, T., Kretsch, R. C., Elliott, L., Beton, J. G., Kryshtafovych, A., Rigden, D. J., Das, R., Topf, M.
  2023; 91 (12): 1935-1951

- **Assessment of three-dimensional RNA structure prediction in CASP15.** *Proteins*
  Das, R., Kretsch, R. C., Simpkin, A. J., Mulvaney, T., Pham, P., Rangan, R., Bu, F., Keegan, R. M., Topf, M., Rigden, D. J., Miao, Z., Westhof, E.
  2023
- **RNA target highlights in CASP15: Evaluation of predicted models by structure providers.** *Proteins*
  Kretsch, R. C., Andersen, E. S., Bujnicki, J. M., Chiu, W., Das, R., Luo, B., Masquida, B., McRae, E. K., Schroeder, G. M., Su, Z., Wedekind, J. E., Xu, L., Zhang, et al
  2023
- **New prediction categories in CASP15.** *Proteins*
  Kryshtafovych, A., Antczak, M., Szachniuk, M., Zok, T., Kretsch, R. C., Rangan, R., Pham, P., Das, R., Robin, X., Studer, G., Durairaj, J., Eberhardt, J., Sweeney, et al
  2023
- **Community science designed ribosomes with beneficial phenotypes.** *Nature communications*
  Kruger, 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., et al
  2023; 14 (1): 961
- **Auto-DRRAFTER: Automated RNA Modeling Based on Cryo-EM Density.** *Methods in molecular biology (Clifton, N.J.)*
  Ma, H., Pham, P., Luo, B., Rangan, R., Kappel, K., Su, Z., Das, R.
  2023; 2568: 193-211
- **RNA 3D Modeling with FARFAR2, Online.** *Methods in molecular biology (Clifton, N.J.)*
  Watkins, A. M., Das, R.
  2023; 2586: 233-249
- **Computationally-guided design and selection of high performing ribosomal active site mutants.** *Nucleic acids research*
  Kofman, C., Watkins, A. M., Kim, D. S., Willi, J. A., Wooldredge, A. C., Karim, A. S., Das, R., Jewett, M. C.
  2022
- **Learning RNA structure prediction from crowd-designed RNAs** *NATURE METHODS*
  Wayment-Steele, H. K., Das, R.
  2022: 1181-1182
- **RNA secondary structure packages evaluated and improved by high-throughput experiments.** *Nature methods*
  Wayment-Steele, H. K., Kladwang, W., Strom, A. I., Lee, J., Treuille, A., Becka, A., Eterna Participants, Das, R.
  2022
- **Topological crossing in the misfolded Tetrahymena ribozyme resolved by cryo-EM.** *Proceedings of the National Academy of Sciences of the United States of America*
  Li, S., Palo, M. Z., Pintilie, G., Zhang, X., Su, Z., Kappel, K., Chiu, W., Zhang, K., Das, R.
  2022; 119 (37): e2209146119
- **Programmable antivirals targeting critical conserved viral RNA secondary structures from influenza A virus and SARS-CoV-2.** *Nature medicine*
  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, et al
  2022
- **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

- **Deep learning models for predicting RNA degradation via dual crowdsourcing.** *Nature machine intelligence*
  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, et al
  2022; 4 (12): 1174-1184
- **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., Jeliazkov, 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
- **Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures** *Nature Methods*
  Kappel, K., Zhang, K., Su, Z., Watkins, A., Kiadwant, W., Li, S., Pintilie, G., Topkar, V., Rangam, R., Zheludev, I. N., Yesselman, J. D., Chiu, W., Das, et al
  2020; 17: 699-707
- **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. O. 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. O. 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

- **Sampling Native-like Structures of RNA-Protein Complexes through Rosetta Folding and Docking** *STRUCTURE*
  Kappel, K., Das, R.
  2019; 27 (1): 140-+

- **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.
  edited by 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*
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