Stanford

# Rhiju Das

Associate Professor of Biochemistry

Curriculum Vitae available Online

## Bio

### BIO

Dr. Das is a computational biochemist at Stanford University School of Medicine. His lab seeks a predictive understanding of how RNA molecules code for complex biological machines. The lab's computer algorithms have consistently achieved leading predictions in world-wide structure prediction trials. Complementary to these computer methods, Dr. Das is developing high-throughput ‘multidimensional chemical mapping’ experiments to uncover three-dimensional structures and conformational changes of non-coding RNAs in their biological milieu, leading to discoveries relevant to human development and viral infection. Towards novel molecules of biomedical interest, Dr. Das leads the Eterna massive open laboratory, which couples a 100,000-player videogame to the lab’s massively parallel experimental tools and deep learning, the first such platform in citizen science. Dr. Das’s research has been recognized with the Burroughs-Wellcome Career Award at the Interface of Science, a W.M. Keck Medical Research Program award, and the OpenEye/American Chemical Society Outstanding Junior Faculty Award. Dr. Das mentors students from the biochemistry, biophysics, biomedical informatics, chemistry, and learning sciences Ph.D. programs.

### ACADEMIC APPOINTMENTS

- Associate Professor, Biochemistry
- Member, Bio-X

### HONORS AND AWARDS

- 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-present)
- Keck Medical Research Grant award, W. M. Keck Foundation (2012)
- OpenEye Outstanding Junior Faculty Award, American Chemical Society (2015)

### 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 Game/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 are exploring algorithms to predict the structures and energetics of RNAs and RNA/protein interfaces at high resolution, focusing initially on small building blocks. We test these ideas through community-wide blind trials and by solving molecule structures and structure ensembles with sparse chemical mapping, NMR, crystallographic, and cryoelectron microscopy data.

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 of RNA structure and conformational change inside cells and viruses, in close collaboration with expert biologists at Stanford.

In addition to modeling RNAs, we aim to design new ones for basic science, diagnostics, and therapeutics. Our videogame project EteRNA seeks missing rules and novel molecules for medicine by giving citizen scientists access to high-throughput wet-lab experiments.

# Teaching

## COURSES

**2019-20**

- Development of Thesis Research: BIOC 350 (Aut)

**2018-19**

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

**2017-18**

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

**2016-17**

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

## STANFORD ADVISEES

**Doctoral Dissertation Reader (AC)**

Namrata Anand, Gun Woo Byeon, Raphael Eguchi, Naomi Genuth, Anthony Ho, Elisabeth Meyer, Yong Tang, Alex Yoshikawa

**Postdoctoral Faculty Sponsor**

Andrew Watkins

**Doctoral Dissertation Advisor (AC)**

Matt Adrianowycz, Kate Coppess, Ramya Rangan, Ved Topkar, Hannah Wayment-Steele, Ivan Zheludev

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

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

## Publications

### PUBLICATIONS

- **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
- **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
- **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., Herschlag, D., Greenleaf, W. J., Das, R.
  2019
- **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., 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, 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., Coppess, K. R., Portela, F., Das, R.
  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
- **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., 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, 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
- **The Rosetta All-Atom Energy Function for Macromolecular Modeling and Design.** *Journal of chemical theory and computation*
  Alford, R. F., Leaver-Fay, A., Jeliazkov, 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

- **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

- **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): 9876–81

- **Controllable molecular motors engineered from myosin and RNA.** *Nature nanotechnology*
  Omabegho, T., Gurel, P. S., Cheng, C. Y., Kim, L. Y., Ruijgrok, P. V., Das, R., Alushin, G. M., Bryant, Z.
  2017

- **Functional 5' UTR mRNA structures in eukaryotic translation regulation and how to find them.** *Nature reviews. Molecular cell biology*
  Leppek, K., Das, R., Barna, M.
  2017

- **Primerize-2D: automated primer design for RNA multidimensional chemical mapping.** *Bioinformatics (Oxford, England)*
  Tian, S., Das, R.
  2017; 33 (9): 1405–6

- **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

- **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 $^{1}$H NMR chemical shifts.** *Nature methods*
  Sripakdeevong, P., Cevec, M., Chang, A. T., Erat, M. C., Ziegeler, M., Zhao, Q., Fox, G. E., Gao, X., Kennedy, S. D., Kierzek, R., Nikonowicz, E. P., Schwalbe, H., Sigel, et al
  2014; 11 (4): 413-416

- **Bayesian energy landscape tilting: towards concordant models of molecular ensembles.** *Biophysical journal*
  Beauchamp, K. A., Pande, V. S., Das, R.
  2014; 106 (6): 1381-1390

- **RNA design rules from a massive open laboratory** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Lee, J., Kladwang, W., Lee, M., Cantu, D., Azizyan, M., Kim, H., Limpaecher, A., Yoon, S., Treuille, A., Das, R.
  2014; 111 (6): 2122-2127

- **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** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*

Kryshtafovych, A., Moult, J., Bales, P., Bazan, J. F., Biasini, M., Burgin, A., Chen, C., Cochran, F. V., Craig, T. K., Das, R., Fass, D., Garcia-Doval, C., Herzberg, et al
2014; 82: 26-42

- **The Mutate-and-Map Protocol for Inferring Base Pairs in Structured RNA.** *Methods in molecular biology (Clifton, N.J.)*
  Cordero, P., Kladwang, W., VanLang, C. C., Das, R.
  2014; 1086: 53-77

- **Massively Parallel RNA Chemical Mapping with a Reduced Bias MAP-Seq Protocol.** *Methods in molecular biology (Clifton, N.J.)*
  Seetin, M. G., Kladwang, W., Bida, J. P., Das, R.
  2014; 1086: 95-117

- **Atomic-Accuracy Prediction of Protein Loop Structures through an RNA-Inspired Ansatz** *PLOS ONE*
  Das, R.
  2013; 8 (10)

- **Adding Diverse Noncanonical Backbones to Rosetta: Enabling Peptidomimetic Design** *PLOS ONE*
  Drew, K., Renfrew, P. D., Craven, T. W., Butterfoss, G. L., Chou, F., Lyskov, S., Bullock, B. N., Watkins, A., Labonte, J. W., Pacella, M., Kilambi, K. P., Leaver-Fay, A., Kuhlman, et al
  2013; 8 (7)

- **HiTRACE-Web: an online tool for robust analysis of high-throughput capillary electrophoresis** *NUCLEIC ACIDS RESEARCH*
  Kim, H., Cordero, P., Das, R., Yoon, S.
  2013; 41 (W1): W492-W498

- **Serverification of Molecular Modeling Applications: The Rosetta Online Server That Includes Everyone (ROSIE)** *PLOS ONE*
  Lyskov, S., Chou, F., Conchuir, S. O., Der, B. S., Drew, K., Kuroda, D., Xu, J., Weitzner, B. D., Renfrew, P. D., Sripakdeevong, P., Borgo, B., Havranek, J. J., Kuhlman, et al
  2013; 8 (5)

- **Remodeling a beta-peptide bundle** *CHEMICAL SCIENCE*
  Molski, M. A., Goodman, J. L., Chou, F., Baker, D., Das, R., Schepartz, A.
  2013; 4 (1): 319-324

- **Correcting pervasive errors in RNA crystallography through enumerative structure prediction** *NATURE METHODS*
  Chou, F., Sripakdeevong, P., Dibrov, S. M., Hermann, T., Das, R.
  2013; 10 (1): 74-U105

- **Advances, Interactions, and Future Developments in the CNS, Phenix, and Rosetta Structural Biology Software Systems** *ANNUAL REVIEW OF BIOPHYSICS, VOL 42*
  Adams, P. D., Baker, D., Brunger, A. T., Das, R., DiMaio, F., Read, R. J., Richardson, D. C., Richardson, J. S., Terwilliger, T. C.
  2013; 42: 265-287

- **An RNA Mapping DataBase for curating RNA structure mapping experiments** *BIOINFORMATICS*
  Cordero, P., Lucks, J. B., Das, R.
  2012; 28 (22): 3006-3008

- **Quantitative Dimethyl Sulfate Mapping for Automated RNA Secondary Structure Inference** *BIOCHEMISTRY*
  Cordero, P., Kladwang, W., VanLang, C. C., Das, R.
  2012; 51 (36): 7037-7039

- **Squaring theory with practice in RNA design** *CURRENT OPINION IN STRUCTURAL BIOLOGY*
  Bida, J. P., Das, R.
  2012; 22 (4): 457-466

- **Ultraviolet Shadowing of RNA Can Cause Significant Chemical Damage in Seconds** *SCIENTIFIC REPORTS*
  Kladwang, W., Hum, J., Das, R.
  2012; 2

- **Metal-ion rescue revisited: Biochemical detection of site-bound metal ions important for RNA folding** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  Frederiksen, J. K., Li, N., Das, R., Herschlag, D., Piccirilli, J. A.

2012; 18 (6): 1123-1141

- **RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  Cruz, J. A., Blanchet, M., Boniecki, M., Bujnicki, J. M., Chen, S., Cao, S., Das, R., Ding, F., Dokholyan, N. V., Flores, S. C., Huang, L., Lavender, C. A., Lisi, et al
  2012; 18 (4): 610-625

- **Automated RNA Structure Prediction Uncovers a Kink-Turn Linker in Double Glycine Riboswitches** *JOURNAL OF THE AMERICAN CHEMICAL SOCIETY*
  Kladwang, W., Chou, F., Das, R.
  2012; 134 (3): 1404-1407

- **Are Protein Force Fields Getting Better? A Systematic Benchmark on 524 Diverse NMR Measurements.** *Journal of chemical theory and computation*
  Beauchamp, K. A., Lin, Y. S., Das, R., Pande, V. S.
  2012; 8 (4): 1409–14

- **An enumerative stepwise ansatz enables atomic-accuracy RNA loop modeling** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Sripakdeevong, P., Kladwang, W., Das, R.
  2011; 108 (51): 20573-20578

- **A two-dimensional mutate-and-map strategy for non-coding RNA structure** *NATURE CHEMISTRY*
  Kladwang, W., VanLang, C. C., Cordero, P., Das, R.
  2011; 3 (12): 954-962

- **Understanding the Errors of SHAPE-Directed RNA Structure Modeling** *BIOCHEMISTRY*
  Kladwang, W., VanLang, C. C., Cordero, P., Das, R.
  2011; 50 (37): 8049-8056

- **Quantitative comparison of villin headpiece subdomain simulations and triplet-triplet energy transfer experiments** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Beauchamp, K. A., Ensign, D. L., Das, R., Pande, V. S.
  2011; 108 (31): 12734-12739

- **HiTRACE: high-throughput robust analysis for capillary electrophoresis** *BIOINFORMATICS*
  Yoon, S., Kim, J., Hum, J., Kim, H., Park, S., Kladwang, W., Das, R.
  2011; 27 (13): 1798-1805

- **Sharing and archiving nucleic acid structure mapping data** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  Rocca-Serra, P., Bellaousov, S., Birmingham, A., Chen, C., Cordero, P., Das, R., Davis-Neulander, L., Duncan, C. D., Halvorsen, M., Knight, R., Leontis, N. B., Mathews, D. H., Ritz, et al
  2011; 17 (7): 1204-1212

- **Four Small Puzzles That Rosetta Doesn't Solve** *PLOS ONE*
  Das, R.
  2011; 6 (5)

- **A mutate-and-map strategy accurately infers the base pairs of a 35-nucleotide model RNA** *RNA-A PUBLICATION OF THE RNA SOCIETY*
  Kladwang, W., Cordero, P., Das, R.
  2011; 17 (3): 522-534

- **ROSETTA3: AN OBJECT-ORIENTED SOFTWARE SUITE FOR THE SIMULATION AND DESIGN OF MACROMOLECULES** *METHODS IN ENZYMOLOGY, VOL 487: COMPUTER METHODS, PT C*
  Leaver-Fay, A., Tyka, M., Lewis, S. M., Lange, O. F., Thompson, J., Jacak, R., Kaufman, K., Renfrew, P. D., Smith, C. A., Sheffler, W., Davis, I. W., Cooper, S., Treuille, et al
  2011: 545-574

- **Rosetta in CAPRI rounds 13-19** *PROTEINS-STRUCTURE FUNCTION AND BIOINFORMATICS*
  Fleishman, S. J., Corn, J. E., Strauch, E. M., Whitehead, T. A., Andre, I., Thompson, J., Havranek, J. J., Das, R., Bradley, P., Baker, D.
  2010; 78 (15): 3212-3218

- **A Mutate-and-Map Strategy for Inferring Base Pairs in Structured Nucleic Acids: Proof of Concept on a DNA/RNA Helix** *BIOCHEMISTRY*

Kladwang, W., Das, R.
2010; 49 (35): 7414-7416

- **Atomic accuracy in predicting and designing noncanonical RNA structure** *NATURE METHODS*
  Das, R., Karanicolas, J., Baker, D.
  2010; 7 (4): 291-294

- **Simultaneous prediction of protein folding and docking at high resolution** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*
  Das, R., Andre, I., Shen, Y., Wu, Y., Lemak, A., Bansal, S., Arrowsmith, C. H., Szyperski, T., Baker, D.
  2009; 106 (45): 18978-18983

- **A robust peak detection method for RNA structure inference by high-throughput contact mapping** *BIOINFORMATICS*
  Kim, J., Yu, S., Shim, B., Kim, H., Min, H., Chung, E., Das, R., Yoon, S.
  2009; 25 (9): 1137-1144

- **Prospects for de novo phasing with de novo protein models** *ACTA CRYSTALLOGRAPHICA SECTION D-BIOLOGICAL CRYSTALLOGRAPHY*
  Das, R., Baker, D.
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