
Rhiju Das
Curriculum Vitae

B400, Beckman Center
279 Campus Drive West
Stanford University School of Medicine
Stanford, CA 94305
Phone: (650) 723-5976
rhiju@stanford.edu

<http://daslab.stanford.edu/>

Positions and Employment

- 2009 - present Assistant Professor, Biochemistry Department and, by courtesy, Physics Department, Stanford University.
- 2009 - present Affiliated faculty, Stanford Biophysics and Biomedical Informatics Ph.D. programs.
- 2005 - 2008 Postdoctoral research with Dr. David Baker, Howard Hughes Medical Institute and University of Washington
- 2001 - 2005 Graduate research with Drs. D. Herschlag and S. Doniach, Stanford University. Thesis: "Visualizing Forces and Folds of Self-Assembling RNA Molecules".
- 2000 - 2001 Teaching fellow, full year of Advanced Freshman Physics, Stanford University
- 1999 - 2000 Graduate research with Drs. Z. Yang and J. Mallet, University College London. Thesis: "Theoretical basis of likelihood methods in molecular phylogenetic inference".
- 1998 - 1999 Graduate research with Dr. R. Saunders, Cambridge University, at Ryle Telescope, Mullard Radio Astronomy Observatory. Thesis: "Analysis of Sunyaev-Zel'dovich decrements".
- 1998 - 1999 Supervisor, Trinity College, Cambridge University, for 2nd year physics undergraduates.
- 1995 - 1998 Research with Dr. S. Mishra, Harvard University; searches for new exotic particles and neutrino oscillations, decays, and magnetic moments at Neutrino Oscillation Magnetic Detector (CERN).

Education

- 2000 - 2005 Ph.D., Physics, Stanford University
- 1999 - 2000 M.Res., Biocomplexity, Centre for Mathematics and Physics in the Life Sciences and Experimental Biology, University College London
- 1998 - 1999 M.Phil., Physics, Trinity College, Cambridge University
- 1995 - 1998 A.B. *summa cum laude*, Physics, Harvard University
- 1993 - 1995 Oklahoma School of Science and Mathematics

Honors and Awards

- 2008 - present Burroughs-Wellcome Career Award at the Scientific Interface
- 2006 - 2008 Jane Coffin Childs Foundation Fellowship
- 2006 Damon Runyon Fellowship (declined due to J.C.C. acceptance)
- 2005 - 2006 NIH Interdisciplinary Training Fellowship in Genome Sciences (U. Washington)
- 2000 - 2005 Stanford Graduate Fellow
- 2000 - 2003 National Science Foundation Graduate Fellow (Stanford)
- 1998 - 2000 British Marshall Scholar (Cambridge; University College London)
- 1996 - 1998 John Harvard Scholar; Goldwater Scholar; Phi Beta Kappa (Harvard)
- 1995 Scholar: National Merit, Robert C. Byrd Honors, Harvard National.
- 1995 Gold medal, International Physics Olympiad; second place overall; top American score
- 1994, 1995 Top 20 placement in US Physics Olympiad and National Chemistry Olympiad; top 100 placement in US Mathematical Olympiad

Professional Memberships and Other Experience

- 2010 - present Founder, Bio-X Games Center, Stanford University
- 2008 - present Principal Investigator, RosettaCommons
- 2005 - present Member, American Chemical Society
- 2003 - present Speaker (invited): Stanford Synchrotron Radiation Laboratory Users Meeting; Cornell High Energy Synchrotron Source Users Meeting; American Crystallographic Association; Case

Western Reserve University, Center for Proteomics; CCP4 Study Weekend, Leeds; Stanford, Biochemistry; Harvard, Chemistry; UC Berkeley, Computational Biology; NIH/UCSF Workshop, Protein Models in Biomedical Research; FNANO (keynote); ISMB.

Publications & Preprints

- Cordero, P., Lucks, J., and **Das, R.** (2011) "The Stanford RNA Mapping Database for sharing and visualizing RNA structure mapping experiments", submitted.
- Kladwang, W., VanLang, C.C., Cordero, P., and **Das, R.** (2011) "Two-dimensional chemical mapping for non-coding RNAs", in revision.
- Sripakdeevong, P., Kladwang, W., and **Das, R.** (2011) "Enumerating biopolymer structures: Atomic-accuracy RNA loop modeling by a stepwise ansatz", in revision.
- Frederiksen, J.K., Li, N-S., **Das, R.**†, Herschlag, D.†, and Piccirilli, J.A.† (2011) "Metal ion rescue revisited: Biochemical detection of site-bound metal ions important for RNA folding", in revision.
- Molski, M.A., Goodman, J.L., Baker, D., **Das, R.**, and Schepartz, A. (2011) "Rational remodeling of a β -peptide bundle protein", in revision.
44. Kladwang, W., VanLang, C.C., Cordero P., and **Das, R.** (2011) "Understanding the errors of SHAPE-directed RNA structure modeling", *Biochemistry*, accepted.
43. **Das, R.** (2011) "Four small puzzles that Rosetta doesn't solve". *PLoS One*, 6(5): e20044.
42. Beauchamp, K.A., Ensign, D.L., **Das, R.**†, and Pande, V.S.† (2011), "Quantitative comparison of villin headpiece subdomain simulations and triplet-triplet energy transfer experiments", *Proc. Natl. Acad. Sci., USA* 108: 12734-9.
41. Yoon, S.†, Kim, J., Hum J., Kim, H., Kladwang, W., and **Das, R.** † (2011) "HiTRACE: High-throughput robust analysis for capillary electrophoresis", *Bioinformatics*, 27(13):1798-805.
40. Rocca-Serra, P., Bellaousov, S., Birmingham, A., Chen, C., Cordero, P., **Das, R.**, Davis-Neulander, L., Duncan, C., Halvorsen, M., Knight, R., Leontis, N., Mathews, D.H., Ritz, J., Stombaugh, J., Weeks, K., Zirbel, C., Laederach, A. (2011) "Sharing and archiving nucleic acid structure mapping data", *RNA*, 17(7):1204-12
39. Beauchamp, K., Sripakdeevong, P., **Das, R.** (2011) "Why Can't We Predict RNA Structure At Atomic Resolution?" in *RNA 3D Structure Analysis and Prediction*, eds. Leontis, N. and Westhof, E., Springer Press, in press. [Preprint available: <http://arxiv.org/abs/1103.3042>]
38. Kladwang, W., Cordero P., and **Das, R.** (2011) "A mutate-and-map strategy accurately infers the base pairs of a 35-nucleotide model RNA". *RNA*, 17: 522-534.
37. Leaver-Fay, A., Tyka, M., Lewis, S.M., Lange, O.F., Thompson, J. Jacak, R., Kaufmann, K.W., Renfrew, P.D., Smith, C.A., Sheffler, W., Davis, I.W., Cooper, S., Treuille, A., Mandell, D.J., Richter, F., Ban, Y-E., Fleishman, S.J., Corn, J.E., Kim, D.E., Lyskov, S., Berrondo, M., Mentzer, S., Popovic, Z., Havranek, J.J., Karanicolas, J., **Das, R.**, Meiler, J., Kortemme, T., Gray, J.J., Kuhlman, B., Baker, D., Bradley, P. (2011) "ROSETTA3: An Object-Oriented Software Suite for the Simulation and Design of Macromolecules". *Methods in Enzymology*, 487: 545-574.
36. Fleishman, S.J., Corn, J.E., Strauch, E.M., Whitehead, T.A., André, I., Thompson, J., Havranek, J.J., **Das, R.**, Bradley, P. and Baker D. (2010), "Rosetta in CAPRI rounds 13-19", *Proteins*, **78**: 15.
35. Kladwang, W. and **Das, R.** (2010) "A mutate-and-map strategy for inferring base pairs in structured nucleic acids: proof of concept on a DNA/RNA helix", *Biochemistry* **49**: 7414-6.

34. **Das, R.**, Karanicolas, J., and Baker, D. (2010), "Atomic accuracy in predicting and designing non-canonical RNA structure", *Nature Methods* **7**: 272-3. [highlighted in Westhof, E., "News and views: Toward atomic accuracy in RNA design", *Nature Methods* **7**: 272-3.]
33. **Das, R.***, André, I.*, Shen, Y., Wu, Y., Lemak, A., Bansal, S., Arrowsmith, C.H., Szyperski, T., and Baker, D. (2009), "Simultaneous prediction of protein folding and docking at high resolution", *PNAS* **105**: 18979-83. (Track II)
32. Raman, S., Vernon, R., Thompson, J., Tyka, M., Sadreyev, R., Pei, J., Kim, D., Kellogg, E., DiMaio, F., Lange, O., Kinch, L., Sheffler, W., Kim, B.H., **Das, R.**, Grishin, N.V., Baker, D. (2009) "Structure prediction for CASP8 with all-atom refinement using Rosetta." *Proteins* **77**: S89-99.
31. Kim, J., Yu, S., Shim, B., Kim, H., Min, H., Chung, E-Y., **Das, R.**, and Yoon S. (2009) "A robust peak detection method for RNA structure inference by high-throughput contact mapping", *Bioinformatics* **25**: 1137-1144.
30. Schwede, T., Sali, A., Honig, B., Levitt, M., Berman, H.M., Jones, D., Brenner, S.E., Burley, S.K., **Das, R.**, et al. (2009), "Outcome of a workshop on applications of protein models in biomedical research", *Structure* **17**: 151-9
29. Jonikas, M.A., Radmer, R.J., Laederach, A., **Das, R.**, Pearlman, S., Herschlag, D., and Altman, R.B. (2009), "Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters", *RNA* **15**: 189-99.
28. **Das, R.**, and Baker, D. (2009) "Prospects for *de novo* phasing with protein *de novo* models". *Acta Cryst. D* **65**: 169-175
27. Mathew-Fenn, R.S., **Das, R.**, Fenn, T.D., Schneiders, M., Harbury, P.B. (2009), "Response to comment on 'Remeasuring the double helix' ", *Science* **325**: 538.
26. Mathew-Fenn, R.S.*, **Das, R.***, and Harbury, P.B. (2008) "Remeasuring the double helix" *Science*, **322**: 446-449. [Highlighted in Lilley, D.M.J., "DNA revisited", *Nature Chemical Biology* **4**: 725-6.]
25. Mathew-Fenn, R.S., **Das, R.**, Silverman, J.A., Fenn, T.D., Walker, P. and Harbury, P.B. (2008) "An X-ray molecular ruler for the measurement of distance distributions in solution", *PLoS One* **3**(10): e3229.
24. Laederach, A., **Das, R.**, Vicens, Q., Pearlman, S., Brenowitz, M., Herschlag, D., and Altman, R.B. (2008) "Semi-automated and rapid quantification of nucleic acid footprinting and structure mapping experiments", *Nature Protocols* **3**: 1395-401. [cover figure]
23. **Das, R.** and Baker, D. (2008) "Macromolecular modeling with Rosetta", *Annual Review of Biochemistry* **77**: 363-382.
22. **Das, R.**, Kudaravalli, M., Jonikas, M., Laederach, A., Fong, R., Schwans, J.P., Baker, D., Piccirilli, J.A., Altman, R.B., and Herschlag, D. (2008) "Structural inference of native and partially folded RNA by high throughput contact mapping", *Proceedings of the National Academy of Sciences U.S.A* **105**: 4144-4149. (Track II)
21. Qian, B.*, Raman, V.S.*, **Das, R.***, Bradley, P., McCoy, A.J., Read, R.J., Baker, D. (2007) "High resolution structure prediction and the crystallographic phase problem", *Nature* **450**, 259-264. [Highlighted in Dodson, E., "News and Views, computational biology: protein predictions", *Nature* **450**: 176-177.]
20. **Das, R.***, Qian, B.*, Raman, V.S., Vernon, R., Thompson, J., Bradley, P., Khare, S., Tyka, M., Bhat, D., Chivian, D.C., Kim, D.E., Sheffler, W., Malmström, L., Wollacott, A., Wang, C., Andre, I., and Baker, D. (2007) "Structure prediction for CASP7 targets using extensive all-atom

refinement with Rosetta@home”, *Proteins* **69**: S118-128.

19. **Das, R.** and Baker, D. (2007) “Automated *de novo* prediction of native-like RNA tertiary structures”, *Proceedings of the National Academy of Sciences U.S.A.* **104**: 14644–14669. (Track II)
18. Blum, B., Jordan, M.I., Kim, D., **Das, R.**, Bradley, P., and Baker, D. (2007) “Feature selection methods for improving protein structure prediction with Rosetta”, in *Advances in Neural Information Processing Systems (NIPS)* **21**: eds. Platt, J., Koller, D., Singer, Y., and McCallum, A., MIT Press.
17. Lipfert, J., **Das, R.**, Chu, V.B., Kudaravalli, M., Boyd, N., Herschlag, D. and Doniach, S. (2006) “Structural transitions and thermodynamics of a glycine-dependent riboswitch from *Vibrio cholerae*”, *Journal of Molecular Biology* **365**: 1393–1406.
16. Russell, R., **Das, R.**, Suh, H., Travers, K., Laederach, A., Engelhardt, M., and Herschlag D. (2006) “The paradoxical behavior of a highly structured misfolded intermediate in RNA folding”, *Journal of Molecular Biology* **363**: 531-544.
15. **Das, R.** and Doniach, S. (2006) “Structural studies of proteins and nucleic acids in solution using small angle x-ray scattering (SAXS),” in *Soft Matter: Scattering, Imaging and Manipulation*, eds. Pecora, R. and Borsali, R., Kluwer Press.
14. **Das, R.**, Travers, K.J., Bai, Y., and Herschlag, D. (2005) “Determining the Mg²⁺ stoichiometry for folding an RNA’s metal ion core”, *Journal of the American Chemical Society* **127**: 8272-8273.
13. Bai, Y., **Das, R.**, Millett, I.S., Herschlag, D., and Doniach, S. (2005) “Probing counterion modulated repulsion and attraction between nucleic acid duplexes in solution.” *Proceedings of the National Academy of Sciences U.S.A.* **102**: 959-960. (Track II)
12. **Das, R.***, Laederach, A.*, Pearlman, S.M., Herschlag, D., and Altman, R.B. (2005) “SAFA: Semi-Automated Footprinting Analysis software for high-throughput quantification of nucleic acid footprinting experiments.” *RNA* **11**: 344-354.
11. Andresen, K., **Das, R.**, Park, H.Y., Smith, H., Kwok, L.W., Lamb, J.S., Kirkland, E.J., Herschlag, D., Finkelstein, K.D., and Pollack, L. (2004) “Spatial distribution of competing ions around DNA in solution.” *Physical Review Letters* **93**: 248013.
10. Takamoto, K.*, **Das, R.***, He, Q., Doniach, S., Brenowitz, M., Herschlag, D., and Chance, M. (2004) “Principles of RNA compaction: insights from the equilibrium folding pathway of the P4-P6 RNA domain in monovalent cations.” *Journal of Molecular Biology* **343**: 1195-206.
9. **Das, R.**, Kwok, L.W., Millet, I.S., Bai, Y., Mills, T.T., Jacob, J., Maskel, G.S., Seifert, S., Simon, M.G.J., Thiyagarajan, P., Doniach, S., Pollack, L., and Herschlag, D. (2003) “The fastest global events in RNA folding: electrostatic relaxation and tertiary collapse of the Tetrahymena ribozyme.” *Journal of Molecular Biology* **332**: 311-319.
8. **Das, R.**, Mills, T.T., Kwok, L.W., Maskel, G.S., Millett, I.S., Doniach, S., Finkelstein, K.D., Herschlag, D. and Pollack, L. (2003) “The counterion distribution around DNA probed by solution x-ray scattering.” *Physical Review Letters* **90**: 188103.
7. Bartley, L., Zhuang, X., **Das, R.**, Chu, S., and Herschlag, D. (2003) “Exploration of the transition state for tertiary structure formation between an RNA helix and a large structured RNA.” *Journal of Molecular Biology* **328**: 1011-1026.
6. Saunders, R., Kneissl, R., Grainge, K., Grainger, W.F., Jones, M.E., Maggi, A., **Das, R.**, Edge, A.C., Lasenby, A.N., Pooley, G.G., Shigeru, J.M., Tsuruta, T., Yamashita, K., Tawara, Y., Furuzawa, A., Harada, A., and Hatsukade I. (2003) “A measurement of H₀ from Ryle Telescope, ASCA and ROSAT observations of Abell 773.” *Monthly Notices of the Royal Astronomical Society* **341**:

937-940.

5. Grainger, W.F., **Das, R.**, Grainge, K., Jones, M. E., Kneissl, R., Pooley, G.G., and Saunders, R.D.E. (2002) "A maximum-likelihood approach to removing radio sources from observations of the Sunyaev-Zel'dovich effect, with application to Abell 611." *Monthly Notices of the Royal Astronomical Society* **337**: 1207-1214.
4. Cotter, G., Buttery, H.J., **Das, R.**, Jones, M.E., Grainge, K., Pooley, G.G, and Saunders, R. (2002) "Observations of the Sunyaev-Zel'dovich effect in the $z = 0.78$ cluster MS 1137.5+6625." *Monthly Notices of the Royal Astronomical Society* **334**: 323-326.
3. Cotter G., Buttery, H.J., Rawlings, S., Croft, S., Hill, G.J., Gay, P., **Das, R.**, Drory, N., Grainge, K.; Grainger, W.F., Jones, M.E., Pooley, G.G., and Saunders, R. (2002) "Detection of a cosmic microwave background decrement towards a cluster of mJy radio sources." *Monthly Notices of the Royal Astronomical Society* **331**: 1-6.
2. Alba, M.M., **Das, R.**, Orengo, C.A., and Kellam, P. (2001) "Genomewide function conservation and phylogeny in the Herpesviridae." *Genome Research* **11**: 43-54.
1. Milton, K. and **Das, R.** (1996) "Finite element lattice Hamiltonian matrix elements. Anharmonic oscillators." *Letters in Mathematical Physics* **36**: 177-187.

* Contributed equally

† Co-corresponding author