

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

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

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 Critical Assessment of Structure Prediction (CASP15)
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

1. Milton, K. A., & **Das, R.** (1996). “Finite-element lattice Hamiltonian matrix elements: Anharmonic oscillators.” *Letters in Mathematical Physics*, 36(2), 177–187.
2. Albà, M. M., **Das, R.**, Orengo, C. A., & Kellam, P. (2001). “Genomewide function conservation and phylogeny in the Herpesviridae.” *Genome Research*, 11(1), 43–54.
3. Grainger, W. F., **Das, R.**, Grainge, K., Jones, M. E., Kneissl, R., Pooley, G. G., & 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(4),

1207–1214.

4. 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., & 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), 1–6.
5. Cotter, G., Buttery, H. J., **Das, R.**, Jones, M. E., Grainge, K., Pooley, G. G., & 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(2), 323–326.
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., & Others. (2003). “A measurement of H_0 from Ryle Telescope, ASCA and ROSAT observations of Abell 773.” *Monthly Notices of the Royal Astronomical Society*, 341(3), 937–940.
7. **Das, R.**, Mills, T. T., Kwok, L. W., Maskel, G. S., Millett, I. S., Doniach, S., Finkelstein, K. D., Herschlag, D., & Pollack, L. (2003). “Counterion distribution around DNA probed by solution X-ray scattering.” *Physical Review Letters*, 90(18), 188103.
8. Bartley, L. E., Zhuang, X., **Das, R.**, Chu, S., & 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(5), 1011–1026.
9. **Das, R.**, Kwok, L. W., Millett, I. S., Bai, Y., Mills, T. T., Jacob, J., Maskel, G. S., Seifert, S., Mochrie, S. G. J., Thiyagarajan, P., Doniach, S., Pollack, L., & Herschlag, D. (2003). “The fastest global events in RNA folding: Electrostatic relaxation and tertiary collapse of the Tetrahymena ribozyme.” *Journal of Molecular Biology*, 332(2), 311–319.
10. Takamoto, K.*, Das, R.*, He, Q., Doniach, S., Brenowitz, M., Herschlag, D., & Chance, M. R. (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(5), 1195–1206
11. Naumov, D., Chukanov, A., Naumova, E., Popov, B., Astier, P., Autiero, D., Baldisseri, A., Baldo-Ceolin, M., Banner, M., Bassompierre, G., Benslama, K., Besson, N., Bird, I., Blumenfeld, B., Bobisut, F., Bouchez, J., Boyd, S., ... [NOMAD collaboration], & Zuccon, P. (2004). “A study of strange particles produced in neutrino neutral current interactions in the NOMAD experiment.” *Nuclear Physics B*, 700(1), 51–68.
12. Andresen, K., **Das, R.**, Park, H. Y., Smith, H., Kwok, L. W., Lamb, J. S., Kirkland, E. J., Herschlag, D., Finkelstein, K. D., & Pollack, L. (2004). “Spatial distribution of competing ions around DNA in solution.” *Physical Review Letters*, 93(24), 248103.
13. Bai, Y., **Das, R.**, Millett, I. S., Herschlag, D., & Doniach, S. (2005). “Probing counterion modulated repulsion and attraction between nucleic acid duplexes in solution.” *Proceedings of the National Academy of Sciences of the United States of America*, 102(4), 1035–1040.
14. **Das, R.***, Laederach, A.*, Pearlman, S.M., Herschlag, D., & Altman, R.B. (2005). “SAFA: Semi-automated footprinting analysis software for high-throughput quantification of nucleic acid footprinting experiments.” *RNA*, 11(3), 344–354.
15. **Das, R.**, Travers, K. J., Bai, Y., & Herschlag, D. (2005). “Determining the Mg^{2+} stoichiometry for folding an RNA metal ion core.” *Journal of the American Chemical Society*, 127(23), 8272–8273.
16. Russell, R., **Das, R.**, Suh, H., Travers, K. J., Laederach, A., Engelhardt, M. A., & Herschlag, D. (2006). “The paradoxical behavior of a highly structured misfolded intermediate in RNA folding.” *Journal of Molecular Biology*, 363(2), 531–544.

17. **Das, R.**, & Doniach, S. (2006). “Structural studies of proteins and nucleic acids in solution using small angle X-ray scattering (SAXS).” In R. Pecora & R. Borsali (Eds.), *Soft Matter: Scattering, Imaging and Manipulation* (pp. 1084–1408). Kluwer Press. (Invited book chapter)
18. **Das, R.***, Qian, B.*, Raman, S., Vernon, R., Thompson, J., Bradley, P., Khare, S., Tyka, M. D., Bhat, D., Chivian, D., Kim, D. E., Sheffler, W. H., Malmström, L., Wollacott, A. M., Wang, C., Andre, I., & Baker, D. (2007). “Structure prediction for CASP7 targets using extensive all-atom refinement with Rosetta@home.” *Proteins*, *69 Suppl 8*, 118–128.
19. Blum, B., Baker, D., Jordan, M. I., Bradley, P., **Das, R.**, & Kim, D. E. (2007). “Feature selection methods for improving protein structure prediction with Rosetta.” In J. C. Platt, D. Koller, Y. Singer, & S. T. Roweis (Eds.), *Advances in Neural Information Processing Systems 20*. MIT Press. Pages 137 – 144.
20. Lipfert, J., **Das, R.**, Chu, V. B., Kudaravalli, M., Boyd, N., Herschlag, D., & Doniach, S. (2007). “Structural transitions and thermodynamics of a glycine-dependent riboswitch from *Vibrio cholerae*.” *Journal of Molecular Biology*, *365*(5), 1393–1406.
21. **Das, R.**, & Baker, D. (2007). “Automated de novo prediction of native-like RNA tertiary structures.” *Proceedings of the National Academy of Sciences of the United States of America*, *104*(37), 14664–14669.
22. Qian, B.*, Raman, 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*(7167), 259–264. [Highlight: Dodson, E. J. (2007). “Computational biology: protein predictions.” *Nature*, *450*(7167), 176–177.]
23. Laederach, A., **Das, R.**, Vicens, Q., Pearlman, S. M., Brenowitz, M., Herschlag, D., & Altman, R. B. (2008). “Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments.” *Nature Protocols*, *3*(9), 1395–1401. [Cover]
24. **Das, R.**, Kudaravalli, M., Jonikas, M., Laederach, A., Fong, R., Schwans, J. P., Baker, D., Piccirilli, J. A., Altman, R. B., & Herschlag, D. (2008). “Structural inference of native and partially folded RNA by high-throughput contact mapping.” *Proceedings of the National Academy of Sciences of the United States of America*, *105*(11), 4144–4149.
25. Mathew-Fenn, R. S.*, **Das, R.***, & Harbury, P. A. B. (2008). “Remeasuring the double helix.” *Science*, *322*(5900), 446–449. [Highlight: Lilley, D. M. J. (2008). “DNA revisited.” *Nature Chemical Biology*, *4*(12), 725–726.]
26. Mathew-Fenn, R. S., **Das, R.**, Silverman, J. A., Walker, P. A., & Harbury, P. A. B. (2008). “A molecular ruler for measuring quantitative distance distributions.” *PLoS One*, *3*(10), e3229.
27. **Das, R.**, & Baker, D. (2008). “Macromolecular modeling with rosetta.” *Annual Review of Biochemistry*, *77*, 363–382. (Invited review)
28. 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 Suppl 9*, 89–99.
29. **Das, R.**, & Baker, D. (2009). “Prospects for de novo phasing with de novo protein models.” *Acta Crystallographica. Section D, Biological Crystallography*, *65*(Pt 2), 169–175.
30. Jonikas, M. A., Radmer, R. J., Laederach, A., **Das, R.**, Pearlman, S., Herschlag, D., & Altman, R. B. (2009). “Coarse-grained modeling of large RNA molecules with knowledge-based potentials and structural filters.” *RNA*, *15*(2), 189–199.
31. Schwede, T., Sali, A., Honig, B., Levitt, M., Berman, H. M., Jones, D., Brenner, S. E., Burley, S. K., **Das, R.**, Dokholyan, N. V., Dunbrack, R. L., Jr, Fidelis, K., Fiser, A., Godzik, A., Huang, Y. J., Humblet, C., Jacobson, M. P., ... Wilson, I. A. (2009). “Outcome of a workshop on applications of protein models in

- biomedical research.” *Structure*, 17(2), 151–159.
32. Kim, J., Yu, S., Shim, B., Kim, H., Min, H., Chung, E.-Y., **Das, R.**, & Yoon, S. (2009). “A robust peak detection method for RNA structure inference by high-throughput contact mapping.” *Bioinformatics*, 25(9), 1137–1144.
 33. Mathew-Fenn, R. S., **Das, R.**, Fenn, T. D., Schneiders, M., & Harbury, P. A. B. (2009). “Response to Comment on ‘Remeasuring the Double Helix.’” *Science*, 325(5940), 538–538.
 34. **Das, R.***, André, I.*, Shen, Y., Wu, Y., Lemak, A., Bansal, S., Arrowsmith, C. H., Szyperski, T., & Baker, D. (2009). “Simultaneous prediction of protein folding and docking at high resolution.” *Proceedings of the National Academy of Sciences of the United States of America*, 106(45), 18978–18983.
 35. **Das, R.**†, Karanicolas, J., & Baker, D.† (2010). “Atomic accuracy in predicting and designing noncanonical RNA structure.” *Nature Methods*, 7(4), 291–294. [Highlight: Westhof, E. (2010). “Toward atomic accuracy in RNA design.” *Nature Methods*, 7(4), 272–273. doi: 10.1038/nmeth0410-272.]
 36. Kladwang, W., & **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(35), 7414–7416.
 37. 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). “Rosetta in CAPRI rounds 13-19.” *Proteins*, 78(15), 3212–3218.
 38. Kladwang, W., Cordero, P., & **Das, R.** (2011). “A mutate-and-map strategy accurately infers the base pairs of a 35-nucleotide model RNA.” *RNA*, 17(3), 522–534.
 39. **Das, R.** (2011). “Four small puzzles that Rosetta doesn’t solve.” *PLoS One*, 6(5), e20044
 40. Rocca-Serra, P., Bellaousov, S., Birmingham, A., Chen, C., Cordero, P., **Das, R.**, Davis-Neulander, L., Duncan, C. D. S., Halvorsen, M., Knight, R., Leontis, N. B., Mathews, D. H., Ritz, J., Stombaugh, J., Weeks, K. M., Zirbel, C. L., & Laederach, A. (2011). “Sharing and archiving nucleic acid structure mapping data.” *RNA*, 17(7), 1204–1212.
 41. Yoon, S.†, Kim, J., Hum, J., Kim, H., Park, S., Kladwang, W., & **Das, R.**† (2011). “HiTRACE: High-throughput robust analysis for capillary electrophoresis.” *Bioinformatics*, 27(13), 1798–1805.
 42. Beauchamp, K. A., Ensign, D. L., **Das, R.**†, & Pande, V. S.† (2011). “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*, 108(31), 12734–12739.
 43. Kladwang, W., VanLang, C. C., Cordero, P., & **Das, R.** (2011b). “Understanding the errors of SHAPE-directed RNA structure modeling.” *Biochemistry*, 50(37), 8049–8056.
 44. Kladwang, W., VanLang, C. C., Cordero, P., & **Das, R.** (2011a). “A two-dimensional mutate-and-map strategy for non-coding RNA structure.” *Nature Chemistry*, 3(12), 954–962. [Highlight: Petzold, K., & Al-Hashimi, H. M. (2011). “RNA structure: Adding a second dimension.” *Nature Chemistry*, 3(12), 913–915. Highlight: (2011). “Mutate-and-map’ RNA structure characterization.” *Nature Methods*, 8, 997.]
 45. Sripakdeevong, P., Kladwang, W., & **Das, R.** (2011). “An enumerative stepwise ansatz enables atomic-accuracy RNA loop modeling.” *Proceedings of the National Academy of Sciences of the United States of America*, 108(51), 20573–20578.
 46. 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, A., Mandell, D. J., Richter, F., Ban, Y.-E. A., 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. (Invited book chapter)
 47. Kladwang, W., Chou, F.-C., & **Das, R.** (2012). “Automated RNA structure prediction uncovers a kink-turn linker in double glycine riboswitches.” *Journal of the American Chemical Society*, 134(3), 1404–1407.

48. Cruz, J. A., Blanchet, M.-F., Boniecki, M., Bujnicki, J. M., Chen, S.-J., Cao, S., **Das, R.**, Ding, F., Dokholyan, N. V., Flores, S. C., Huang, L., Lavender, C. A., Lisi, V., Major, F., Mikolajczak, K., Patel, D. J., Philips, A., ... Westhof, E. (2012). "RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction." *RNA*, *18*(4), 610–625.
49. Beauchamp, K. A., Lin, Y.-S., **Das, R.**, & Pande, V. S. (2012). "Are protein force fields getting better? A systematic benchmark on 524 diverse NMR measurements." *Journal of Chemical Theory and Computation*, *8*(4), 1409–1414.
50. Frederiksen, J. K., Li, N.-S., **Das, R.**[†], Herschlag, D.[†], & Piccirilli, J. A.[†] (2012). "Metal-ion rescue revisited: biochemical detection of site-bound metal ions important for RNA folding." *RNA*, *18*(6), 1123–1141.
51. Kladwang, W., Hum, J., & **Das, R.** (2012). "Ultraviolet shadowing of RNA can cause significant chemical damage in seconds." *Scientific Reports*, *2*, 517.
52. Cordero, P., Kladwang, W., VanLang, C. C., & **Das, R.** (2012). "Quantitative dimethyl sulfate mapping for automated RNA secondary structure inference." *Biochemistry*, *51*(36), 7037–7039.
53. Cordero, P., Lucks, J. B., & **Das, R.** (2012). "An RNA mapping database for curating RNA structure mapping experiments." *Bioinformatics*, *28*(22), 3006–3008.
54. Sripakdeevong, P., Beauchamp, K., & **Das, R.** (2012). "Why can't we predict RNA structure at atomic resolution?" In N. Leontis & E. Westhof (Eds.), *RNA 3D Structure Analysis and Prediction* (pp. 43–65). Springer Berlin Heidelberg. (Invited book chapter)
55. Bida, J. P., & **Das, R.** (2012). "Squaring theory with practice in RNA design." *Current Opinion in Structural Biology*, *22*(4), 457–466. (Invited review)
56. Molski, M. A., Goodman, J. L., Chou, F.-C., Baker, D.[†], **Das, R.**[†], & Schepartz, A.[†] (2013). "Remodeling a β -peptide bundle." *Chemical Science*, *4*(1), 319–324
57. Chou, F.-C., Sripakdeevong, P., Dibrov, S. M., Hermann, T., & **Das, R.** (2013). "Correcting pervasive errors in RNA crystallography through enumerative structure prediction." *Nature Methods*, *10*(1), 74–76.
58. Lyskov, S., Chou, F.-C., Conchúir, S. Ó., Der, B. S., Drew, K., Kuroda, D., Xu, J., Weitzner, B. D., Renfrew, P. D., Sripakdeevong, P., Borgo, B., Havranek, J. J., Kuhlman, B., Kortemme, T., Bonneau, R., Gray, J. J., & **Das, R.** (2013). "Serverification of molecular modeling applications: The Rosetta Online Server that Includes Everyone (ROSIE)." *PLoS One*, *8*(5), e63906.
59. Kim, H., Cordero, P., **Das, R.**[†], & Yoon, S.[†] (2013). "HiTRACE-Web: An online tool for robust analysis of high-throughput capillary electrophoresis." *Nucleic Acids Research*, *41*(Web Server issue), W492–W498.
60. Drew, K., Renfrew, P. D., Craven, T. W., Butterfoss, G. L., Chou, F.-C., Lyskov, S., Bullock, B. N., Watkins, A., Labonte, J. W., Pacella, M., Kilambi, K. P., Leaver-Fay, A., Kuhlman, B., Gray, J. J., Bradley, P., Kirshenbaum, K., Arora, P. S., **Das, R.**, & Bonneau, R. (2013). "Adding diverse noncanonical backbones to rosetta: enabling peptidomimetic design." *PLoS One*, *8*(7), e67051.
61. **Das, R.** (2013). "Atomic-accuracy prediction of protein loop structures through an RNA-inspired Ansatz." *PLoS One*, *8*(10), e74830.
62. 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). "Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems." *Annual Review of Biophysics*, *42*, 265–287. (Invited review)
63. Kryzhtafovych, A., Moulton, 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, O., Lorimer, D., Luecke, H., Ma, X., Nelson, D. C., ... Schwede, T. (2014). "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*, *82* Suppl 2, 26–42.

64. Lee, J., Kladwang, W., Lee, M., Cantu, D., Azizyan, M., Kim, H., Limpaecher, A., Yoon, S., Treuille, A., **Das, R.**, & EteRNA Participants. (2014). “RNA design rules from a massive open laboratory.” *Proceedings of the National Academy of Sciences of the United States of America*, 111(6), 2122–2127. [Highlight: Bohannon, J. (2014). “Online video game plugs players into remote-controlled biochemistry lab.” *Science*, 343(6170), 475.]
65. Beauchamp, K. A., Pande, V. S.†, & **Das, R.**† (2014). “Bayesian energy landscape tilting: towards concordant models of molecular ensembles.” *Biophysical Journal*, 106(6), 1381–1390.
66. 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, R. K. O., Turner, D. H., & **Das, R.** (2014). “Structure determination of noncanonical RNA motifs guided by ¹H NMR chemical shifts.” *Nature Methods*, 11(4), 413–416.
67. Kladwang, W., Mann, T. H., Becka, A., Tian, S., Kim, H., Yoon, S., & **Das, R.** (2014). “Standardization of RNA chemical mapping experiments.” *Biochemistry*, 53(19), 3063–3065.
68. Chou, F.-C., Lipfert, J., & **Das, R.** (2014). “Blind predictions of DNA and RNA tweezers experiments with force and torque.” *PLoS Computational Biology*, 10(8), e1003756.
69. Lipfert, J., Skinner, G. M., Keegstra, J. M., Hensgens, T., Jager, T., Dulin, D., Köber, M., Yu, Z., Donkers, S. P., Chou, F.-C., **Das, R.**, & Dekker, N. H. (2014). “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*, 111(43), 15408–15413.
70. Tian, S., Cordero, P., Kladwang, W., & **Das, R.** (2014). “High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states.” *RNA*, 20(11), 1815–1826.
71. Treuille, A., & **Das, R.** (2014). “Scientific rigor through videogames.” *Trends in Biochemical Sciences*, 39(11), 507–509. (Invited perspective)
72. Lipfert, J., Doniach, S., **Das, R.**, & Herschlag, D. (2014). “Understanding nucleic acid-ion interactions.” *Annual Review of Biochemistry*, 83, 813–841. (Invited review.)
73. Seetin, M. G., Kladwang, W., Bida, J. P., & **Das, R.** (2014). “Massively parallel RNA chemical mapping with a reduced bias MAP-seq protocol.” In C. Waldsich (Ed.), *RNA Folding: Methods and Protocols* (pp. 95–117). Humana Press. (Invited book chapter.)
74. Cordero, P., Kladwang, W., VanLang, C. C., & **Das, R.** (2014). “The mutate-and-map protocol for inferring base pairs in structured RNA.” In C. Waldsich (Ed.), *RNA Folding: Methods and Protocols* (pp. 53–77). Humana Press. (Invited book chapter)
75. Xue, S., Tian, S., Fujii, K., Kladwang, W., **Das, R.**, & Barna, M. (2015). “RNA regulons in Hox 5' UTRs confer ribosome specificity to gene regulation.” *Nature*, 517(7532), 33–38.
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