

Curriculum Vitae
Rhiju Das

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Born: 1978, Houston, Texas

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)

Professional

University of Washington/Howard Hughes Medical Institute

- 2008** Jane Coffin Childs postdoctoral fellow (with D. Baker)

Stanford University

- 2009** Assistant Professor, Biochemistry Department and, by courtesy, Physics Department
- 2009** Faculty, Biophysics and Biomedical Informatics programs
- 2016** Associate Professor, Biochemistry Department and, by courtesy, Physics Department

Awards and Honors

Oklahoma School of Science and Mathematics

- 1995** Gold medal, International Physics Olympiad; top US score, second place world-wide

Harvard University

- 1998** British Marshall Scholar

Stanford University

- 2000** Stanford Graduate Fellow; National Science Foundation Graduate Fellow

University of Washington/Howard Hughes Medical Institute

- 2006** Jane Coffin Childs Foundation, Damon Runyon Cancer Foundation Fellowships
- 2008** Burroughs-Wellcome Career Award at the Scientific Interface

Stanford University

- 2012** W. M. Keck Foundation Medical Research Grant Award
- 2015** American Chemical Society OpenEye Outstanding Junior Faculty Award
- 2017** Stanford School of Medicine Discovery Innovation Award

Selected Invited Lectures

- 2011** Foundations of Nanotechnology (keynote)
- 2013** Design Research Conference, Chicago (keynote)
- 2014** Genentech Innovation Summit (keynote)
- 2014** Gordon Research Conference, Computational Chemistry
- 2014** DNA 20, Kyoto, Japan (keynote)
- 2015** U. Rochester, Cellular & Molecular Biology (student-invited)
- 2015** Oregon State University, Biochemistry (student invited)
- 2016** EMBO RNA structure meets function, Stockholm
- 2016** NIH Center for Excellence in Genomic Sciences (keynote)
- 2017** Gordon Research Conference, RNA Nanotechnology
- 2018** NIH/UCSF Crowdsourcing & Interactive Digital Media (opening keynote)

2018 J. James Woods Lecture in Science and Mathematics, Butler University
 2018 Tsinghua International Symposium of Computational Structural Biology and Biophysics
 2018 North Eastern Structure Symposium
 2019 Gordon Research Conference, Computer-Aided Drug Design
 2019 Harvard T.H. Chan School of Public Health

Selected Professional Activities

2007-8 Advisor, Foldit videogame
 2008- Principal investigator, RosettaCommons consortium
 2009- Co-founder and principal investigator, Eterna videogame
 2011 Co-organizer, RosettaCon, Leavenworth WA
 2011-15 Co-organizer, Stanford Frontiers in Quantitative Biology seminar series
 2013 National Institutes of Health NIGMS RNA advisory meeting
 2015 Advisor, NOVA RNA Lab
 2015-19 Co-organizer, EternaCon, Stanford CA
 2017-19 Editorial advisory board, *Biochemistry*

Publications

1. Milton, K. and **Das, R.** (1996) "Finite element lattice Hamiltonian matrix elements. Anharmonic oscillators", *Letters in Mathematical Physics* **36**: 177-187.
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.
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.
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.
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.
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 H_0 from Ryle Telescope, ASCA and ROSAT observations of Abell 773", *Monthly Notices of the Royal Astronomical Society* **341**: 937-940.
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.
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.
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.
10. Naumov, D. Chukanov, A., Naumova, E., Popv, B., Astier, et al. [NOMAD collaboration] (2004) "A study of strange particles produced in neutrino neutral current interactions in the NOMAD experiment", *Nuclear Physics B* **700**: 51-68.

11. 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.
12. 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.
13. **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.
14. 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”, *Proc. Natl. Acad. Sci. U.S.A.* **102**: 959-960.
15. **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.
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.
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.
18. **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 (invited book chapter).
19. 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 (NeurIPS)* **21**: eds. Platt, J., Koller, D., Singer, Y., and McCallum, A., MIT Press.
20. **Das, R.** and Baker, D. (2007) “Automated *de novo* prediction of native-like RNA tertiary structures”, *Proc. Natl. Acad. Sci. U.S.A.* **104**: 14644–14669.
21. **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.
22. 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.
Highlight: Dodson, E., “News and Views, computational biology: protein predictions”, *Nature* **450**: 176-177.
23. **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”, *Proc. Natl. Acad. Sci. U.S.A.* **105**: 4144-4149.
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**).
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.
26. **Das, R.** and Baker, D. (2008) “Macromolecular modeling with Rosetta”, *Annual Review of Biochemistry* **77**: 363-382 (invited review).
27. Mathew-Fenn, R.S.*, **Das, R.***, and Harbury, P.B. (2008) “Remeasuring the double helix”, *Science* **322**: 446-449. **Highlight:** Lilley, D.M.J., “DNA revisited”, *Nature Chemical Biology* **4**: 725-6.
28. 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.

29. **Das, R.** and Baker, D. (2009) “Prospects for *de novo* phasing with protein *de novo* models”. *Acta Cryst. D.* **65**: 169-175.
30. 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**: 189-199.
31. 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.
32. 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.
33. 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.
34. **Das, R.***, André, I.*, Shen, Y., Wu, Y., Lemak, A., Bansal, S., Arrowsmith, C.H., Szyperki, T., and Baker, D. (2009), “Simultaneous prediction of protein folding and docking at high resolution”, *Proc. Natl. Acad. Sci. U.S.A.* **105**: 18979-83.
35. **Das, R.†**, Karanicolas, J., and Baker, D.† (2010), “Atomic accuracy in predicting and designing non-canonical RNA structure”, *Nature Methods*, **7**: 272-3. **Highlight:** Westhof, E., “News and views: Toward atomic accuracy in RNA design”, *Nature Methods* **7**: 272-3.
36. 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.
37. 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.
38. 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 (invited review).
39. 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.
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.
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.
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. U.S.A.* **108**: 12734-9.
43. **Das, R.** (2011) “Four small puzzles that Rosetta doesn't solve”. *PLoS One* **6**(5): e20044.
44. Kladwang, W., VanLang, C.C., Cordero P., and **Das, R.** (2011) “Understanding the errors of SHAPE-directed RNA structure modeling”, *Biochemistry* **50**: 8049–8056.
45. Kladwang, W., VanLang, C.C., Cordero, P., and **Das, R.** (2011) “A two-dimensional mutate-and-map strategy for non-coding RNA structure”, *Nature Chemistry*, **3**: 954-962. **Highlight:** Petzold, K. and al-Hashimi, H. “News and views: RNA structure: Adding a second dimension”, *Nature Chemistry* **3**: 913-15. **Highlight:** “News in brief: 'Mutate-and-map' RNA structure characterization”, *Nature Methods* **8**: 997.
46. Sripakdeevong, P., Kladwang, W., and **Das, R.** (2011) “An enumerative stepwise ansatz enables atomic-accuracy RNA loop modeling”, *Proc. Natl. Acad. Sci. U.S.A.* **108**: 20573-20578.

47. Beauchamp, K., Sripakdeevong, P., **Das, R.** (2012) “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, Nucleic Acids and Molecular Biology **27**: 43-65 (invited book chapter).
48. Kladwang, W., Chou, F.-C., and **Das, R.** (2012) “Automated RNA structure prediction uncovers a kink-turn linker in double glycine riboswitches”, *J. Am. Chem. Soc.* **134** (3):1404–1407.
49. Frederiksen, J.K., Li, N.-S., **Das, R.**[†], Herschlag, D.[†], and Piccirilli, J.A.[†] (2012) “Metal ion rescue revisited: biochemical detection of site-bound metal ions important for RNA folding”, *RNA* **18**:1123-41.
50. Bida, J.P. and **Das, R.** (2012) “Squaring theory with practice in RNA design”, *Curr. Opinion in Structural Biology* **22**: 457-466 (invited review).
51. Cruz, J.A., Blanchet, M., Boniecki, M., Bujnicki, J., 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., Puton, T., Santalucia, J., Sijenyi, F., Hermann, T., Rother, K., Rother, M., Serganov, A., Skorupski, M., Soltysinski, T., Sripakdeevong, P., Tuszynska, I., Weeks, K.M., Waldsich, C., Wildauer, M., Leontis, N.B., and Westhof, E. (2012) “RNA-Puzzles: A CASP-like evaluation of RNA three-dimensional structure prediction”, *RNA* **18**: 610-25.
52. Beauchamp, K., Lin, Y.-S., **Das, R.**, and Pande, V.S. (2012) “Are protein force fields getting better? A systematic benchmark on 524 diverse NMR measurements”, *J. Comp. Theor. Chem.* **8** (4): 1409–1414
53. Kladwang, W., Hum, J., and **Das, R.** (2012), “Ultraviolet shadowing of RNA can cause substantial chemical damage in seconds”, *Scientific Reports* **2**: 517.
54. Cordero, P., Kladwang, W., VanLang, C.C., and **Das, R.** (2012) “Quantitative dimethyl sulfate (DMS) mapping for automated RNA secondary structure inference”, *Biochemistry* **51**: 7037-7039.
55. Molski, M.A., Goodman, J.L., Baker, D.[†], **Das, R.**[†], and Schepartz, A.[†] (2012) “Rational remodeling of a β -peptide bundle protein”, *Chemical Science* **4**: 319-324.
56. Cordero, P., Lucks, J., and **Das, R.** (2012) “The RNA Mapping Database for sharing and visualizing RNA structure mapping experiments”, *Bioinformatics* **28**: 3006-3008.
57. Chou F.-C., Sripakdeevong, P., and **Das, R.** (2013) “Correcting pervasive errors in RNA crystallography through enumerative structure prediction”, *Nature Methods* **10**: 74-76.
58. 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).
59. Lyskov, S., Chou, F.-C., Ó Conchúir, S., 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* **e8**(5): e63906.
60. Kim, H., Cordero, P., **Das, R.**[†], and Yoon, S.[†] (2013) “HiTRACE-Web: an online tool for robust analysis of high-throughput capillary electrophoresis”, *Nucleic Acids Research* **41**(Web Server issue): W492-8.
61. Drew, K., Renfrew, P.D., Craven, T., Butterfoss, G.L., Chou, F.-C., Lyskov, S., Bullock, B.N., Watkins, A., 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 and foldamer design”, *PLOS One* **8**(7): e67051.
62. **Das, R.** (2013) “Atomic-accuracy prediction of protein loop structures through an RNA-inspired ansatz”, *PLOS One* **8**(10): e74830.
63. Cordero, P., Kladwang, W., VanLang, C.C., and **Das, R.** (2014) “A mutate-and-map protocol for inferring base pairs in structured RNA”, *Methods in Molecular Biology, RNA folding*, ed. C. Waldsich, **1086**:53-77 (invited book chapter).
64. Seetin, M., Kladwang, W., Bida, J.P., and **Das, R.** (2014) “Massively parallel RNA chemical mapping with a reduced bias MAP-seq protocol”, *Methods in Molecular Biology, RNA folding*, ed. C. Waldsich, **1086**:95-117 (invited book chapter).

65. Kryshafaovych, A., Moulton, J., Bales, P., Bazan, J.F., 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., van Raaij, M.J., Rohwer, F., Segall, A., Seguritan, V., Zeth, K., 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* **83**:26-42.
66. Sripakdeevong, P., Cevcec, 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. and **Das, R.** (2014) “High-resolution structure determination of noncanonical RNA motifs guided by ¹H NMR chemical shift data”, *Nature Methods* **11**: 413–41.
67. Lee, J., Kladwang, W., Lee, M., Cantu, D., Azizyan, M., Kim, H., Limpaecher, A., Gaikwad, S., Yoon, S., Treuille, A.†, **Das, R.†**, and EteRNA players (2014) “RNA design rules from a massive open laboratory”, *Proc. Natl. Acad. Sci. U.S.A.* **111**(6):2122-2127. **Highlight:** Bohannon, J. (2014) “Online video game plugs players into remote-controlled biochemistry lab”, *Science* **343**(6170): 475.
68. Treuille, A. & **Das, R.** (2014) “Scientific rigor through videogames”, *Trends in Biochemical Sciences* **39**: 507-509 (invited perspective).
69. Beauchamp, K., Pande, V.†, and **Das, R.†** (2014) “Bayesian energy landscape tilting: towards concordant models of molecular ensembles”, *Biophys. J.* **106**(6): 1381-1390.
70. Kladwang, W., Mann, T.H., Becka, E., Tian, S., Kim, H., Yoon, S., and **Das, R.** (2014) “Standardization of RNA chemical mapping experiments”, *Biochemistry* **53**: 3063-3065.
71. Chou, F.-C., Lipfert, J., and **Das, R.** (2014) “Blind predictions of DNA and RNA tweezers experiments with force and torque”, *PLoS Comp. Bio.* **10**(8): e1003756.
72. Tian, S., Cordero, P., Kladwang, W., and **Das, R.** (2014) “High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states”, *RNA* **20**: 1815-1826
73. Lipfert, J., Skinner, G.M., Keegstra, J.M., Hensgens, T., Jager, T., Dulin, D., Donkers, S.P., Chou, F.-C., **Das, R.**, and Dekker N.H. (2014) “Double-stranded RNA under force and torque: Similarities to and striking differences from double-stranded DNA”, *Proc. Natl. Acad. Sci. U.S.A.* **111**(43):15408-13.
74. Cheng, C.Y., Chou, F.-C., and **Das, R.** (2015) “Modeling complex RNA tertiary folds with Rosetta”, *Methods in Enzymology, Computational methods for RNA structure*, ed. Chen, S.-J. and Burke, D. **553**: 35–64 (invited book chapter).
75. Xue, S., Tian, S., **Das, R.**, Barna, M. (2015) “RNA regulons in Hox 5′ UTRs confer ribosome specificity to gene regulation and body plan formation”, *Nature* **517**:33-38.
76. Miao, Z., Adamiak, R.W., Blanchet, M-F., Boniecki, M., Bujnicki, J.M., Chen, S.-J., Cheng, C., Chojnowski, G., Chou, F.-C., Cordero, P., Cruz, J.A., Ferré-D’Amaré, A, **Das, R.**, Ding, F., Dokholyan, N.V., Dunin-Horkawicz, S., Kladwang, W., Krokhotin, A., Lach, G., Magnus, M., Major, F., Mann, T.H., Masquida, B., Matelska, D., Meyer, M., Peselis, A., Popena, M., Purzycka, K.J., Serganov, A., Stasiewicz, J., Szachniuk, M., Tandon, A., Tian, S., Wang, J., Xiao, Y., Xu, X., Zhang, J., Zhao, P., Zok, T. and Westhof, E., (2015) “RNA-Puzzles Round II: Assessment of RNA structure prediction programs applied to three large RNA structures”, *RNA* **21** (6): 1066-1084.
77. Lee, S., Kim, H., Tian, S., Lee, T., Yoon, S.†, **Das, R.†** (2015), “Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles”, *Bioinformatics* **31** (17): 2808 – 2815.
78. Chou, F.-C., Echols, N., Terwilliger, T.C., and **Das, R.** (2015) “RNA structure refinement using the ERRASER-Phenix pipeline”, *Methods in Molecular Biology, Nucleic Acid Crystallography*, ed. E. Ennifar, **1320**: 269 – 282 (invited book chapter)
79. Tian, S., Yesselman, J.D., Cordero, P. and **Das, R.** (2015) “Primerize: automated primer assembly for transcribing non-coding RNA domains”, *Nucleic Acids Research* (Web Server issue) **43** (W1): W522 – W526.
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