

*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  
(on partial leave beginning Sep. 2021)  
**2020-** Stanford Medicine Endowed Faculty Scholar (anonymous donor)

*Inceptive Nucleics, Inc.*

- 2021-** Chief Executive Officer

### **Awards and Honors**

*Oklahoma School of Science and Mathematics*

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

<b>2017, 2020</b>	Stanford School of Medicine Discovery Innovation Award
<b>2020</b>	Stanford Medicine Endowed Faculty Scholar (anonymous)
<b>2021</b>	Selected as Howard Hughes Medical Institute Investigator

### Invited Lectures (selected out of >100)

<b>2011</b>	Foundations of Nanotechnology (keynote)
<b>2013</b>	Design Research Conference, Chicago (keynote)
<b>2014</b>	Genentech Innovation Summit (keynote)
<b>2014</b>	Gordon Research Conference, Computational Chemistry
<b>2014</b>	DNA 20, Kyoto, Japan (keynote)
<b>2015</b>	U. Rochester, Cellular & Molecular Biology (student-invited)
<b>2015</b>	Oregon State University, Biochemistry (student invited)
<b>2016</b>	EMBO RNA structure meets function, Stockholm
<b>2016</b>	NIH Center for Excellence in Genomic Sciences (keynote)
<b>2017</b>	Gordon Research Conference, RNA Nanotechnology
<b>2018</b>	NIH/UCSF Crowdsourcing & Interactive Digital Media (opening keynote)
<b>2018</b>	J. James Woods Lecture in Science and Mathematics, Butler University
<b>2018</b>	Tsinghua International Symposium of Computational Structural Biology and Biophysics
<b>2018</b>	North Eastern Structure Symposium
<b>2019</b>	Gordon Research Conference, Computer-Aided Drug Design
<b>2019</b>	Harvard T.H. Chan School of Public Health
<b>2020</b>	Stanford University School of Medicine COVID-19 town hall
<b>2020</b>	Rustbelt RNA 2020 (plenary)
<b>2020</b>	Biophysical Society Symposium: “Biophysicists Address COVID-19 Challenges”
<b>2021</b>	Iowa State University, Biochemistry (student invited)

### Selected Professional Activities and Service

<b>2007-8</b>	Advisor, Foldit videogame
<b>2008-</b>	Principal investigator, RosettaCommons consortium
<b>2009-</b>	Co-founder and principal investigator, Eterna videogame
<b>2011</b>	Co-organizer, RosettaCon, Leavenworth WA
<b>2011-15</b>	Co-organizer, Stanford Frontiers in Quantitative Biology seminar series
<b>2013</b>	National Institutes of Health NIGMS RNA advisory meeting
<b>2015</b>	Advisor, NOVA RNA Lab
<b>2015-20</b>	Co-organizer, EternaCon, Stanford CA
<b>2017-2020</b>	Editorial advisory board, <i>Biochemistry</i>
<b>2019</b>	Co-author, RNA Synthetic Biology Roadmap, Engineering Biology Research Consortium
<b>2020</b>	Stanford University COVID-19 research oversight committee

### Peer-Reviewed and Preprint 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., Thiagarajan, 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., Baldissari, 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<sup>2+</sup> 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.  
<https://papers.nips.cc/paper/3173-feature-selection-methods-for-improving-protein-structure-prediction-with-rosetta>
  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. doi: 10.1038/nature05990.]
  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. doi: 10.1038/nchembio1208-725.]
  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. doi: 10.1038/nchem.1209. Highlight: (2011). "'Mutate-and-map' RNA structure characterization." *Nature Methods*, 8, 997. doi: 10.1038/nmeth.1794.]
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  $\beta$ -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. 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, 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. doi: 10.1126/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 <sup>1</sup>H 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.)
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Leppek, K.\*, Byeon, G.W.\* , Kladwang, W.\* , Wayment-Steele, H.K. \*, Kerr, C.\* , Xu, A.F., Kim, D.S., Topkar, V.V., Choe, C., Rothschild, D., Tiu, G.C., Wellington-Oguri, R., Fujii, K., Sharma, E., Watkins, A.M., Nicol, J.J., Romano, J., Tunguz, B., Eterna Participants, Barna, M.†, **Das, R.**†(2021) “Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics.” In *bioRxiv*.

<https://doi.org/10.1101/2021.03.29.437587>

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#### Patents (4)

1. **Das, R.**, Choe, C. A., Wayment-Steele, H. K., & Sharma, E. "Systems and Methods to Enhance RNA Stability and Translation and Uses Thereof" (U.S. Provisional Patent Application No. 63/051,269). Filed Jul 13, 2020.
2. **Das, R.**, Shih, K. Y., & Adrianowycz, M. A. "Systems and Methods for Ratiometric and Multiplexed Isothermal Amplification of Nucleic Acids" (PCT Patent Application No. PCT/US2020/031011). Filed May 01, 2020.
3. **Das, R.**, Yesselman, J., & Kappel, K. "Systems and Methods for Designing RNA Nanostructures and Uses Thereof" (PCT Patent Application No. PCT/US2020/029018). Filed Apr 20, 2020.
4. Pham, E. A., Glenn, J. S., Saluti, R. H., Elazar, M., **Das, R.**, Zheludev, I. N., Wayment-Steele, H. K., & Rangan, R. "Anti-Coronaviral Compositions and Methods of Using the Same" (U.S. Provisional Patent Application No. 62/992,659). Filed Mar 20, 2020.