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

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

Awards and Honors

Stanford University

2026	Stanford Data Sciences Open Science Champion
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

Selected Professional Activities and Service

2024-present	Course director, Stanford Biochemistry Bootcamp graduate course
2011-present	Course director, Stanford's Biological Macromolecules graduate course
2009-present	Advisor, 14 Ph.D. students in Stanford Biophysics, Biochemistry, Bioengineering
2024	Stanford-HBCU Faculty Fellow, inaugural cohort
2022, 2024	Assessor, 15th and 16th Critical Assessment of Structure Prediction (CASP)
2021-22	Co-founder & CEO, Inceptive
2020	Stanford University COVID-19 research oversight committee
2019	Co-author, RNA Synthetic Biology Roadmap, Engineering Biology Research Consortium
2017-20	Editorial advisory board, *Biochemistry*
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

171. Townley, J. Kladwang, W. Baker, D. Blair, H.M. Choe, C.A. El Nesr, G. Favor, A. Fisker, E. Haack, D.B. He, S. Hingey, J. Huang, P.-S. Huang, R. Joshi, C.K. Karagianes, T. Kubaney, A. Liò, P. Mancino, A. Romano, J. Rudolfs, B. Spellmon, N. Toor, N. Verma, J. Wu, V. Yu, Z. Eterna Participants, & **Das, R.** (2026) "De novo design of RNA pseudoknots with deep learning" *Science* **393**, 931-937 (2026).

170. Balch, S. Franco-Echevarría, E. Ghanim, G.E. Kretsch, R.C. **Das, R.**, & Nguyen, T.H.D. (2026) "Structures of nucleotide-bound human telomerase at several steps of its telomeric DNA repeat addition cycle" *Nature Communications* **17**, 1847 (2026).

169. Kretsch, R.C., Posani, E., Baulin, E.F., Bujnicki, J.M. Bussi, G. Cheatham III, T.E., Chen, S.-J., Elofsson, A. Farsani, M.A., Fisher, O.N., Gromiha, M.M., Gupta, A., Hamada, M., Harini, K.., Hu, G., Huang, D., Iwakiri, J. Jain, A. Kagaya, Y., Kihara, D., Kmiecik, S. Krishnan, S.R., Kurisaki, I., Languin-Cattoën, O., Li, J., Li, S., Malekzadeh, K., Nakamura, T., Ni, W., Nithin, C., Palo, M.Z., Park, J.H., Pilla, S.P., Poblete, S., Pucci, F., Punuru, P., Saha, A., Sato, K., Srivastava, A., Terashi, G., Tugolukova, E., Verburgt, J., Wuyun, Q., Zerze, G.H., Zhang, K., Zhang, S., Zheng, W., Zhou, Y., Chiu, W.†, Case, D.A.†, & **Das, R.**† (2025) "Blind prediction of complex water and ion ensembles around RNA in CASP16." *Proteins: Structure, Function, and Bioinformatics* in press. https://doi.org/10.1002/prot.70079

168. Zhang J., Yuan R., Kryshtafovych A., Kretsch R.C., Schaeffer R.D., Zhou J., **Das R.**, Grishin N.V., & Cong Q. (2025) "Assessment of protein complex predictions in CASP16: Are we making progress?" *Proteins: Structure, Function, and Bioinformatics* in press. https://doi.org/10.1002/prot.70068

167. Kretsch R.C., Hummer, A.M., He, S., Yuan, R., Zhang, J., Karagianes, T., Cong, Q., Kryshtafovych, A., & **Das, R.** (2025) "Assessment of nucleic acid structure prediction in CASP16." *Proteins: Structure, Function, and Bioinformatics* in press. https://doi.org/10.1002/prot.70072

166. Kretsch, R.C., Albrecht, R., Andersen, E.S., Chen, H., Chiu, W., **Das, R.,** Gezelle, J.G., Hartmann, M.D., Höbartner, C., Hu, Y., Jadhav, S., Johnson, P.E., Jones, P., Koirala, D., Kristoffersen, E.L., Largy, E., Lewicka, A., Mackereth, C.D., Marcia, M., Nigro, M., Ojha, M., Piccirilli, J.A., Rice, P.A., Shin, H., Steckelberg, A., Su, Z., Srivastava, Y., Wang, L., Wu, Y., Xie, J., Zwergius, N.H., Moult, J., & Kryshtafovych, A. (2025) "Functional relevance of CASP16 nucleic acid predictions as evaluated by structure providers." *Proteins: Structure, Function, and Bioinformatics* in press. https://doi.org/10.1002/prot.70043

165. Balch S., Sekne Z., Franco-Echevarría E., Ludzia P., Kretsch R.C., Sun W., Yu H., Ghanim G.E., Thorkelsson S., Ding Y., **Das R.,** & Nguyen T.H.D. (2025) "Cryo-EM structure of human telomerase dimer reveals H/ACA RNP-mediated dimerization." *Science* 389 (6757): eadr5817

164. Choe, C.A., Andreasson, J.O.L., Melaine, F., Kladwang, W., Wu, M.J., Portela, F., Wellington-Oguri, R., Nicol, J.J., Wayment-Steele, H.K., Gotrik, M., Eterna Participants, Khatri, P., Greenleaf, W.J.†, & **Das, R.**† (2025) "Compact RNA sensors for increasingly complex functions of multiple inputs." *Nature Chemistry*, *17*, 1839–1852.

163. Rangan, R., Huang, R. , Hunter O., Pham P., Ares, Jr., M., & **Das, R.** (2025) "Comprehensive analysis of *Saccharomyces cerevisiae* intron structures in vivo" *Nature Structure Molecular Biology*, *32*, 1488–1502.

162. Tse V., Guiterrez M., Townley J., Romano J., Pearl J., Chacaltana G., Eterna Players, **Das R.,** Sanford J.R., & Stone M.D. (2025) "OpenASO: RNA Rescue - designing splice-modulating antisense oligonucleotides through community science." *RNA*, *31,* 1091-1102.

161. Kretsch, R.C., Wu, Y., Shabalina, S.A., Lee, H. Nye, G., Koonin, E.V. , Gao, A., Chiu, W.†, & **Das, R.**† (2025) "Naturally ornate RNA-only complexes revealed by cryo-EM." *Nature*, *643*, 1135–1142 .

160. Kretsch, R.C.*, Li, S.*, Pintilie, G.*, Palo, M.Z., Case, D.A., **Das, R.**†, Zhang, K.†, & Chiu, W.† (2025) "Complex water networks visualized through 2.2-2.3 Angstrom cryogenic electron microscopy of RNA." *Nature, 642*, 250–259.

159. Bu, F., Adam, Y., Adamiak, R.W., Antczak, M., de Aquino, B.R.H., Badepally, N.G., Batey, R.T., Baulin, E.F., Boinski, P., Boniecki, M.J., Bujnicki, J.M., Carpenter, K.A., Chacon, J., Chen, S.J., Chiu, W., Cordero, P., Das, N.K., **Das, R.,** Dawson, W.K., DiMaio, F., Ding, F., Dock-Bregeon, A.C., Dokholyan, N.V., Dror, R.O., Dunin-Horkawicz, S., Eismann, S., Ennifar, E., Esmaeeli, R., Farsani, M.A., Ferré-D'Amaré, A.R., Geniesse, C., et.al. (2025) "RNA-Puzzles Round V: blind predictions of 23 RNA structures." *Nature Method*s *22*, 399 – 411.

158. Kretsch, R.C., Xu, L., Zheludev, I.N., Zhou, X., Huang, R., Nye, G., Li, S., Zhang, K., Chiu, W.,† & **Das, R.**† (2024) "Tertiary folds of the SL5 RNA from the 5' proximal region of SARS-CoV-2 and related coronaviruses." *Proceedings of the National Academy of Sciences of the United States of America*, *121* (10), e2320493121.

157. Tangpradabkul, T., Palo, M., Townley, J., Hsu, K.B., Eterna participants, Smaga, S., Das, R., & Schepartz, A. (2024) "Minimization of the *E. coli* ribosome, aided and optimized by community science." *Nucleic Acids Research*, *52* (3), 1027-1042.

156. **Das, R.**,*,† Kretsch, R.*, Simpkin, A., Mulvaney, T., Pham, P., Rangan, R., Bu, F., Keegan, R., Topf, M., Rigden, D., Miao, Z.†, & Westhof, E.† (2023) "Assessment of three-dimensional RNA structure prediction in CASP15." *Proteins: Structure, Function, and Bioinformatics*, *91* (12), 1747 – 1770.

155. Mulvaney, T., Kretsch, R., Elliott, L., Beton, J., Kryshtafovych, A., Rigden, D.J., **Das, R.,** & Topf, M. (2023) "CASP15 cryoEM protein and RNA targets: refinement and analysis using experimental maps" *Proteins: Structure, Function, and Bioinformatics*, *91* (12), 1935-1951.

154. Kretsch, R., Andersen, E., Bujnicki, J., Chiu, W., **Das, R.**, Luo, B., Masquida, B., McRae, E., Schroeder, G., Su, Z., Wedekind, J., Xu, L., Zhang, K., Zheludev, I., Moult, J., & Kryshtafovych, A. (2023) "RNA target highlights in CASP15: Evaluation of predicted models by structure providers." *Proteins: Structure, Function, and Bioinformatics*, *91* (12), 1600-1615. (reverse cover image)

153. Kryshtafovych, A., Antczak, M., Szachniuk, M., Zok, T., Kretsch, R., Rangan, R., Pham, P., **Das, R.**, Robin, X., Studer, G., Durairaj, J., Eberhardt, J., Sweeney, A., Topf, M., Schwede, T., Fidelis, K., & Moult, J. (2023) "New prediction categories in CASP15." *Proteins: Structure, Function, and Bioinformatics*, *91* (12), 1550-1557.

152. Ma, H., Pham, P., Luo, B., Rangan, R., Kappel, K., Su, Z., & **Das, R.** (2023) "Auto-DRRAFTER: automated RNA modeling based on cryo-EM density." *Methods Mol Biol.*, 2568, 193 – 211. (invited book chapter)

151. Krüger, A, Watkins A.M., Wellington-Oguri R., Romano, J., Kofman, C., DeFoe, A., Kim, Y., Anderson-Lee, J., Fisker, E., Townley J., Eterna Participants, d'Aquino, A.E., Das, R.†, & Jewett, M.C.† (2023) "Community science designed ribosomes with beneficial phenotypes." *Nature Communications*, *14*, 961.

150. Watkins, A.M. and **Das, R.** (2023) "RNA 3D Modeling with FARFAR2, Online." *Methods Mol Biol*, *2586,* 233 – 249. (invited book chapter)

149. Kofman, C., Watkins, A., Kim, D., Willi, J., Wooldredge, A., Karim, A., **Das, R.,** & Jewett, M. (2022) "Computationally-guided design and selection of high performing ribosomal active site mutants." *Nucleic Acids Research*, *50* (22), 13143-13154

148. Wayment-Steele, H.K.,* Kladwang, W.,* Watkins, A.M.,* Kim, D.S.,* Tunguz, B.,* Reade, W., Demkin, M., Romano, J., Wellington-Oguri, R., Nicol, J.J., Gao, J., Onodera, K., Fujikawa, K., Mao, H., Vandewiele, G., Tinti, M., Steenwinckel, B., Ito, T., Noumi, T., He, S., Ishi, K., Lee, Y., Öztürk, F., Chiu, K.Y., Öztürk, E., Amer, K., Fares, M., Eterna Participants & **Das, R.** (2022). "Deep learning models for predicting RNA degradation via dual crowdsourcing." *Nature Machine Intelligence*, *4*, 1174-1184.

147. Ma, H., Pham, P., Luo, B., Rangan, R., Kappel, K., Su, Z.,† & **Das, R.**† (2022) "Auto-DRRAFTER: automated RNA modeling based on cryo-EM density." *Methods Mol Biol.*, *2568*, 193-211. (invited book chapter)

146. Wayment-Steele, H. K., Kladwang, W., Eterna Participants, & **Das, R.** (2022). "RNA secondary structure packages ranked and improved by high-throughput experiments." *Nature Methods*, *19*, 1234-1242.

145. Li, S., Palo, M.Z., Pintilie, G., Zhang, X., Su, Z., Kappel, K., Chiu, W.,† Zhang, K.,† & **Das, R**.† (2022) "Topological crossing in the misfolded Tetrahymena ribozyme resolved by cryo-EM." *Proceedings of the National Academy of Sciences 119* (37), e2209146119.

144. Hagey, R.J., Elazar, M., Pham, E.A., Tian, S., Ben-Avi, L., Bernardin-Souibgui, C., Yee, M.F., Moreira, F.R., Rabinovitch, M.V., Meganck, R.M., Fram, B., Beck, A., Gibson, S.A., Lam, G., Devera, J., Kladwang, W., Nguyen, K., Xiong, A., Schaffert, S., Avisar, T., Liu, P., Rustagi, A., Fichtenbaum, C.J., Pang, P.S., Khatri, P., Tseng, C., Taubenberger, J.K., Blish, C.A., Hurst, B.L., Sheahan, T.P., Das, R., & Glenn, J.S. (2022) "Programmable antivirals targeting critical conserved viral RNA secondary structures from influenza A virus and SARS-CoV-2." *Nature Medicine*, *28*, 1944-1955.

143. Kim, D.S.*, Watkins, A.*, Bidstrup, E., Lee, J., Topkar, V., Kofman, C., Schwarz, K.J., Liu, Y., Pintilie, G., Roney, E., **Das, R.**, & Jewett, M.C. (2022) "Three-dimensional structure-guided evolution of a ribosome with tethered subunits." *Nature Chemical Biology*, *18* (9), 990-998.

142. Andreasson, J.O.L., Gotrik, M.R., Wu, M.J., Wayment-Steele, H.K., Kladwang, W., Portela, F., Wellington-Oguri, R., **Das, R.**†, & Greenleaf, W.J.† (2022) "Crowdsourced RNA design discovers diverse, reversible, efficient, self-contained molecular sensors." *Proceedings of the National Academy of Sciences of the United States of America*, *119* (18) e211297919.

141. 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., Diaz F., Cai, H., Guo, P., Wu, J., Meng, F., Shi, S., Eterna Participants, Dormitzer, P.R., Solórzano, A., Barna, M.†, & **Das, R.**† (2022) "Combinatorial optimization of mRNA structure, stability, and translation for RNA-based therapeutics." *Nature Communications 13*, 1536.

140. **Das, R**† & Watkins, A.M. (2021) "RiboDraw: semiautomated two-dimensional drawing of RNA tertiary structure diagrams." *NAR Genomics and Bioinformatics. 3*(4).

139. Wayment-Steele, H. K., Kim, D.S., Choe, C. A., Nicol, J. J., Wellington-Oguri, R., Parra Sperberg, R.A., Huang, P.S., Eterna Participants, & **Das, R.** (2021). "Theoretical basis for stabilizing messenger RNA through secondary structure design." *Nucleic Acids Research, 49* (18), 10604 – 10617.

138. **Das, R.**† & Russell, R.† (2021) "How to kinetically dissect an RNA machine." *Biochemistry 60* (46), 3485–3490. (invited perspective)

137. Zhang, K.*, Zheludev, I. N.*, Hagey, R. J., Wu, M. T.-P., Haslecker, R., Hou, Y. J., Kretsch, R., Pintilie, G. D., Rangan, R., Kladwang, W., Li, S., Pham, E. A., Bernardin-Souibgui, C., Baric, R. S., Sheahan, T. P., D Souza, V., Glenn, J. S.†, Chiu, W.†, & Das, R.† (2021). "Cryo-electron microscopy and antisense targeting of the 28-kDa frameshift stimulation element from the SARS-CoV-2 RNA genome." *Nature Structure and Molecular Biology*, 28, 747–754.

136. Su, Z.†,*, Zhang, K.*, Kappel, K.*, Li, S., Palo, M., Pintilie, G., Rangan, R., Luo, B., Wei, Y., **Das, R.**†, & Chiu, W.† (2021). "Cryo-EM Structures of the full-length *Tetrahymena* ribozyme at 3.1 Å resolution.", *Nature*, 596, 603–607.

135. Townshend, R.*, Watkins, A.M.*, Eismann, S.*, Rangan, R., **Das, R.**†, & Dror R.† (2021) "Geometric deep learning of RNA structure." *Science*, 373(6558), 1047–1051. [Highlight: Weeks, K.M. (2021) "Piercing the fog of the RNA structure-ome." *Science*, 373(6558),964-965.]

134. **Das R.** (2021) "RNA structure: a renaissance begins?" *Nature Methods,* 18,439. (invited perspective)

133. Ghanim, G.E., Fountain, A.J., van Roon, A.M., **Das, R.**, Collins, K., & Nguyen, T.H.D. (2021), "Structure of human telomerase holoenzyme with bound telomeric DNA." *Nature*, 593(7859), 449–453.

132. Rangan, R., Watkins, A.M, Chacon, J, Kretsch, R., Kladwang, W., Zheludev, I.N., Townley, J., Rynge, M., Thain, G., & **Das, R.** (2021) "De novo 3D models of SARS-CoV-2 RNA elements and small- molecule-binding RNAs to aid drug discovery." *Nucleic Acids Research*, 49(6), 3092–3108.

131. Liu, X., Sun, T., Shcherbina, A., Li, Q., Kappel, K., Jarmoskaite, I., Ramaswami, G., **Das, R.,** Kundaje, A., & Li, J. (2021) "Learning cis-regulatory principles of ADAR-based RNA editing from CRISPR- mediated mutagenesis." *Nature Communications*, Apr 12;12(1),2165.

130. Byeon, G. W., Cenik, E. S., Jiang, L., Tang, H., **Das, R.**, & Barna, M. (2021). "Functional and structural basis of extreme conservation in vertebrate 5' untranslated regions." *Nature Genetics*, 53**,** 729–741.

129. Le, K., Adolf-Bryfogle, J., Klima, J., Lyskov, S., Labonte, J., Bertolani, S., Roy Burman, S., Leaver-Fay, A., Weitzner, B., Maguire, J., Rangan, R., Adrianowycz, M., Alford, R., Adal, A., Nance, M., Das, R., Dunbrack, R., Schief, W., Kuhlman, B., Siegel, J., & Gray, J. (2021) "PyRosetta jupyter notebooks teach biomolecular structure prediction and design." *The Biophysicist*, 2 (1), 108 – 122.

128. Palka, C., Forino, N., Hentschel, J., **Das, R.**, & Stone, M. D. (2020). "Folding heterogeneity in the essential human telomerase RNA three-way junction." *RNA,* 26(12), 1787–1800.

127. Watkins, A. M., Rangan, R., & **Das, R.** (2020). "FARFAR2: Improved de novo Rosetta prediction of complex global RNA folds." *Structure*, 28(8), 963–976.e6.

126. Rangan, R., Zheludev, I. N., Hagey, R. J., Pham, E. A., Wayment-Steele, H. K., Glenn, J. S.†, & **Das, R.**† (2020). "RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: A first look." *RNA*, *26*(8), 937–959.

125. Miao, Z., Adamiak, R. W., Antczak, M., Boniecki, M. J., Bujnicki, J., Chen, S.-J., Cheng, C. Y., Cheng, Y., Chou, F.-C., **Das, R.,** Dokholyan, N. V., Ding, F., Geniesse, C., Jiang, Y., Joshi, A., Krokhotin, A., Magnus, M., … Westhof, E. (2020). "RNA-Puzzles Round IV: 3D structure predictions of four ribozymes and two aptamers." RNA, 26(8), 982–995.

124. Kappel, K.*, Zhang, K.*, Su, Z.*, Watkins, A. M., Kladwang, W., Li, S., Pintilie, G., Topkar, V. V., Rangan, R., Zheludev, I. N., Yesselman, J., Chiu, W.†, & **Das, R.†** (2020). "Accelerated cryo-EM-guided determination of three-dimensional RNA-only structures." *Nature Methods*, *17*(7), 699–707. [Highlight: Richardson, J. S. (2020). "A new way to see RNAs." *Nature Methods*, *17*(7), 663–664.]

123. Leman, J. K., Weitzner, B. D., Lewis, S. M., Adolf-Bryfogle, J., Alam, N., Alford, R. F., Aprahamian, M., Baker, D., Barlow, K. A., Barth, P., Basanta, B., Bender, B. J., Blacklock, K., Bonet, J., Boyken, S. E., Bradley, P., Bystroff, C., Conway, P., Cooper, S., Correia, B.E., Coventry, B., **Das, R.**, … Bonneau, R. (2020). "Macromolecular modeling and design in Rosetta: Recent methods and frameworks." *Nature Methods*, *17*(7), 665–680.

122. Kladwang, W., Topkar, V. V., Liu, B., Rangan, R., Hodges, T. L., Keane, S. C., Al-Hashimi, H., & **Das, R.** (2020). "Anomalous reverse transcription through chemical modifications in polyadenosine stretches." *Biochemistry*, 59(23), 2154–2170.

121. Jain, N., Blauch, L. R., Szymanski, M. R., **Das, R.**, Tang, S. K. Y., Yin, Y. W., & Fire, A. Z. (2020). "Transcription polymerase-catalyzed emergence of novel RNA replicons." *Science*, *368*(6487).

120. Watkins, A. M., Rangan, R., & **Das, R.** (2019). "Using Rosetta for RNA homology modeling." *Methods in Enzymology*, *623*, 177–207. (Invited book chapter.)

119. Wayment-Steele, H., Wu, M., Gotrik, M., & **Das, R.** (2019). "Evaluating riboswitch optimality." *Methods in Enzymology*, *623*, 417–450. (Invited book chapter.)

118. **Das, R.**†, Keep, B., Washington, P., & Riedel-Kruse, I. H.† (2019). "Scientific discovery games for biomedical research." *Annual Review of Biomedical Data Science*, *2*(1), 253–279. (Invited review.)

117. Zhang, K.*, Li, S.*, Kappel, K.*, Pintilie, G., Su, Z., Mou, T.-C., Schmid, M. F., **Das, R.**†, & Chiu, W.† (2019). "Cryo-EM structure of a 40 kDa SAM-IV riboswitch RNA at 3.7 Å resolution." *Nature Communications*, *10*(1), 5511.

116. Magnus, M.†, Kappel, K., **Das, R.**†, & Bujnicki, J. M. (2019). "RNA 3D structure prediction guided by independent folding of homologous sequences." *BMC Bioinformatics*, *20*(1), 512.

115. 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, R. (2019). "A unified mechanism for intron and exon definition and back-splicing." *Nature*, *573*(7774), 375–380.

114. 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, M. C., Kieft, J. S., & Das, R. (2019). "Computational design of three-dimensional RNA structure and function." *Nature Nanotechnology*, 14(9), 866–873.

113. Huang, L., Wang, J., Watkins, A. M., **Das, R.**, & Lilley, D. M. J. (2019). "Structure and ligand binding of the glutamine-II riboswitch." *Nucleic Acids Research*, *47*(14), 7666–7675.

112. Yesselman, J., Denny, S. K., Bisaria, N., Herschlag, D.†, Greenleaf, W. J.†, & **Das, R.**† (2019). "Sequence-dependent RNA helix conformational preferences predictably impact tertiary structure formation." *Proceedings of the National Academy of Sciences of the United States of America*, 116(34), 16847–16855.

111. Wu, M. J., Andreasson, J. O. L., Kladwang, W., Greenleaf, W., & **Das, R.** (2019). "Automated design of diverse stand-alone riboswitches." *ACS Synthetic Biology*, *8*(8), 1838–1846.

110. 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). "A conserved RNA structural motif for organizing topology within picornaviral internal ribosome entry sites." *Nature Communications*, *10*(1), 3629.

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