

RNA

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Cover Illustration: Tetrahymena ribozyme (PDB id: 7EZ0; Su Z, Zhang K, Kappel K, Li S, Palo MZ, Pintilie GD, Rangan R, Luo B, Wei Y, Das R, Chiu W. 2021. Cryo-EM structures of full-length Tetrahymena ribozyme at 3.1 Å resolution. *Nature* **596**: 603–607). The Tetrahymena thermophila group I self-splicing intron is a prominent model system for the study of RNA catalysis. The full-length Tetrahymena ribozyme (apo state) was visualized for the first time using cryoelectron microscopy at a resolution of 3.1 Å. Previously unseen peripheral regions include two coaxially stacked helices interconnected by two kissing loop pseudoknots that wrap around the catalytic core. The ribozyme RNA backbone is displayed as a red ribbon; block bases use NDB colors: A—red, C—yellow, G—green, U—cyan. Cover image provided by the Nucleic Acid Database (NDB)/Nucleic Acid Knowledgebase (NAKB; nakb.org). Image generated using DSSR and PyMOL (Lu XJ. 2020. *Nucleic Acids Res* **48**: e74).

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