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## Structure watch

### SELF-REPLICATING RIBOZYME

Following the discovery of catalytic RNAs (or ribozymes) in the 1980s, it was postulated that life originated from self-replicating ribozymes that catalyse the synthesis of copies of themselves. RNA synthesis by RNA polymerases is mediated by the formation of a 5'→3'-phosphodiester bond between the 5'-triphosphate and the 3'-hydroxyl termini of two RNA fragments. Although no known ribozyme has this enzymatic activity, artificial ribozymes that catalyse a template-dependent 5'→3'-phosphodiester bond ligation reaction have been created by *in vitro* evolution, which provides a proof of principle that RNAs can catalyse their own replication. L1 RNA ligase is one such *in vitro* evolved ribozyme. Robertson and Scott crystallized the product of an autoligation reaction in which L1 RNA ligase was configured to join its own 3'-hydroxyl to its own 5'-triphosphate. The L1 RNA ligase reaction product appears in two conformational states in the crystal — a relaxed, undocked conformation and a docked conformation, which the authors interpreted as the catalytically active form. In the crystal of the docked enzyme, two ligase molecules form an asymmetrical unit, each consisting of stems A, B and C that form a three-helix junction. The ionic interactions between a single Mg<sup>2+</sup> ion and three phosphate groups as well as tertiary contacts that involve certain invariant residues stabilize the docking of stems A and C in the enzyme. These findings represent the first glimpse of what an RNA replicase might have looked like.

**ORIGINAL RESEARCH PAPER** Robertson, M. P. & Scott, W. G. The structural basis of ribozyme-catalyzed RNA assembly. *Science* **315**, 1549–1553 (2007)

### SLIDE AND EXPAND

Nucleoporins are the building blocks of the nuclear pore complex (NPC). The central channel of the NPC is lined by the Nup62 complex, which consists of Nup62, Nup58, Nup54 and Nup45. The minimal core domains of Nup58 and Nup45 are identical  $\alpha$ -helical regions (referred to as Nup58/45) and are sufficient for Nup62 complex assembly. Crystallization of Nup58/45 yielded tetramers in two independent crystal forms: each tetramer consists of two antiparallel hairpin dimers. Analysis of the different crystal forms revealed different tetramer conformations. Superposition of the different tetramer configuration states indicated lateral displacement of up to 11 Å between different tetramer conformations. This intermolecular sliding mechanism is thought to result from alternative hydrogen-bond networks between interaction residues in the tetramerization interface. Given that the central channel can change its diameter and the  $\alpha$ -helices of the Nup62 complex are thought to form the perimeter of the channel, the authors propose that circumferential sliding of Nup58/45 might adjust the diameter of the central transport channel.

**ORIGINAL RESEARCH PAPER** Melčák, I. *et al.* Structure of Nup58/45 suggests flexible nuclear pore diameter by intermolecular sliding. *Science* **315**, 1729–1732