Structural basis of RNA polymerase I activation

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Biosynthesis of the eukaryotic ribosome starts with ribosomal RNA production by RNA polymerase I (Pol I), a process that is critical to regulate cell growth and proliferation. Binding of initiation factor Rrn3 activates Pol I, fostering recruitment to ribosomal DNA promoters. In the past, we determined the crystal structure of yeast Pol I, a 14-subunit complex composed of more than 80,000 atoms with a total mass of 590,000 Da, at 3.0 Å resolution [1]. The structure represents the latent state of the enzyme, which is dimeric and exhibits an open DNA-binding cleft with an extended loop blocking the active site. We now obtained the electron cryomicroscopy structures of monomeric Pol I and of the Pol I-Rrn3 complex at 4.9 and 7.7 Å resolution, respectively [2]. As expected, monomeric Pol I presents a partially-closed DNA-binding cleft and an accessible active site. Rrn3 binds on the enzyme stalk and restrains its conformation, thus generating a surface for the interaction with promoter-bound initiation factors. Our structural studies shed light on how the Pol I enzyme is activated to transcribe ribosomal DNA.

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[2] E. Torreira, J.A. Louro, I. Pazos, N. González-Polo, D. Gil-Carton, A.G. Duran, S. Tosi, O. Gallego, O. Calvo, C. Fernández-Tornero. *eLife* 2017, doi: 10.7554/eLife.20832.