Microsymposium

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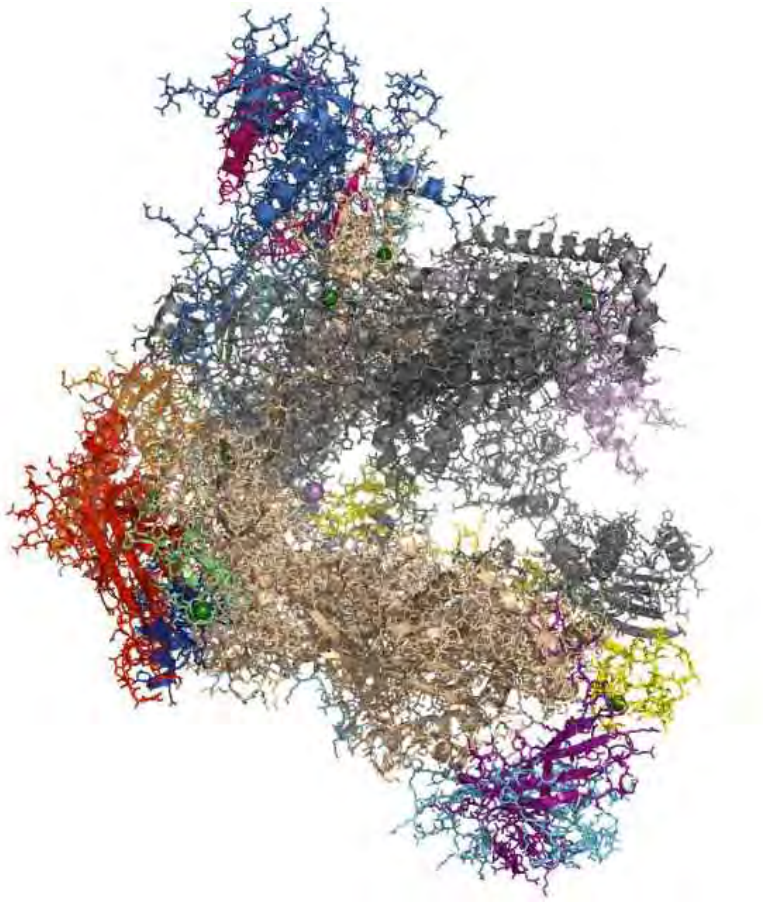
Crystal structure of RNA polymerase I

C. Fernández-Tornero[1]

[1]*Centro de Investigaciones Biológicas – CSIC, Madrid, Spain*

In eukaryotes ribosome biosynthesis starts with ribosomal RNA production by RNA polymerase I (Pol I), a process that is critical to regulate cell growth and proliferation. We were able to obtain the crystal structure of yeast Pol I, a 14-subunit complex with a total mass of 590 kDa, at 3.0 Å resolution [1]. The current communication deals with the functional implications of this beautiful structure, while details on structure determination will be presented by Tim Gruene at this meeting. The structure represents the latent state of the enzyme, characterized by three major features. First, it forms dimers that involve the C-terminal tail of the stalk subunit A43. Second, the two enzyme halves pivot along the DNA-binding cleft to produce an open cleft and an unfolded bridge helix. Third, an extended loop in subunit A190 mimics the DNA backbone along the cleft, hampering nucleic acid binding. All three features must be resolved during enzyme activation. The Pol I crystal structure also reveals intrinsic modules that only bind transiently in other RNA polymerases. Subunit A12.2 inserts a TFIIS-like zinc ribbon into the active site, providing insight into its role in RNA cleavage and Pol I insensitivity to α-amanitin. The A49-A34.5 heterodimer binds the outer side of subunit A135 through a TFIIF-like dimerization module, suggesting how it may function during transcriptional initiation and elongation.

[1] *Fernández-Tornero C, Moreno-Morcillo M, Rashid UJ, Taylor NMI, Ruiz FM, Gruene T, Legrand P, Steuerwald U, Müller CW (2013) Nature 502:644–649*



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