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Centro Singular de Investigación en Química Biolóxica e Materiais Moleculares

Conferencia:

The structure of RNA polymerase I reveals essential aspects of enzyme activation

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CIB-CSIC –Madrid - España

3/11/16

Aula de Seminarios do CIQUS

17:00h

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Carlos Fernández Tornero

Degrees

2002 PhD in Molecular Biology, University Autónoma of Madrid
Thesis: "A Novel Solenoid Fold in the Cell Wall Anchoring Domain of the Pneumococcal virulence Factor LytA"
1997 Bachelor in Biochemistry, University of Granada

Research Positions

Since 2016 Senior group leader at CIB-CSIC, Madrid
2009-2016 Junior group leader at CIB-CSIC, Madrid
2007-2009 Staff scientist at EMBL-Heidelberg (Germany)
2002-2007 Post-doctoral fellow at EMBL-Grenoble (France)
1998-2002 PhD student at CIB-CSIC, Madrid

Grants and awards

2015 Best Research Bets in Madrid Award, Comunidad de Madrid-CSIC
2015 Research Grant of the Ramón Areces Foundation (PI)
2013 Research Grant of the Spanish National R&D Program, Ministry of Economy (PI)
2010 Research Grant of the Spanish National R&D Program, Ministry of Science (PI)
2008 Ramón y Cajal Fellow, Spanish Ministry of Science
2002 Long-Term EMBO Fellowship, EMBO

Carlos Fernández Tornero leads the group of "Structure of Macromolecular Assemblies" at CIB-CSIC since 2011. He is co-author of more than twenty research papers plus several dissemination articles, and has been invited to more than a dozen international conferences and seminars at different research institutions.

"The structure of RNA polymerase I reveals essential aspects of enzyme activation"

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. We were able to obtain the crystal structure of yeast Pol I, a 14-subunit complex composed of more than 80,000 atoms with a total mass of 590 kDa, at 3.0 Å resolution [1, 2]. 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. The Pol I crystal structure also reveals intrinsic modules that only bind transiently in other RNA polymerases, such as a TFIIS-like zinc ribbon in subunit A12.2 and a TFIIF-like dimerization module in the A49/A34.5 heterodimer.

[1] Moreno-Morcillo M, Taylor NM, Gruene T, Legrand P, Rashid UJ, Ruiz FM, Steuerwald U, Müller CW & Fernández-Tornero C* (2014) Solving the RNA polymerase I structural puzzle. *Acta Cryst*. *D*70(10):2570-2582
[2] Fernández-Tornero C*, Moreno-Morcillo M, Rashid UJ, Taylor NM, Ruiz FM, Gruene T, Legrand P, Steuerwald U, Müller CW* (2013) Crystal structure of the 14-subunit RNA polymerase I. *Nature* 502(7473):644-649