

Poster Presentation

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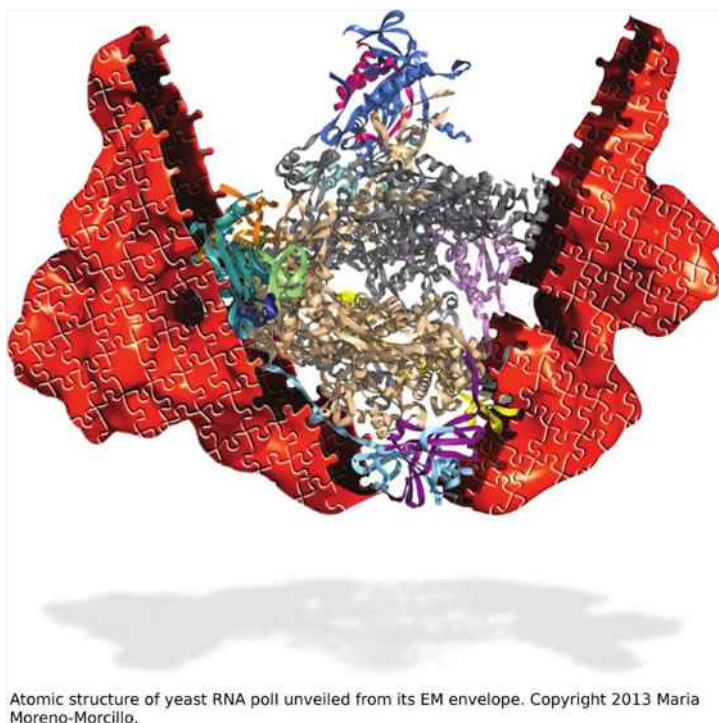
Backstage the RNA Polymerase I Structure: The Art of Crystallography

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Life relies on the accurate cascade of protein production from the genomic code, the DNA, via RNA. RNA polymerase I (Pol I) is one of three types responsible for the transcription of DNA to RNA. It is responsible for the production of rRNA incorporated into the Ribosome. Without the extremely low error rate of this synthesis process life would not have evolved beyond the status of bacteria and amoebae. The X-ray structures of the 14-subunit yeast RNA polymerase I [1,2] provide insight into one of the cornerstones in this process of life. Altogether four different crystal structures at about 3 resolution are now available. The biological impact of the beautiful structure will be presented by C. F.-T. at this meeting. Yet, not only biologically, but also crystallographically this work presents a real masterpiece. Before the structure could be published the limits of crystallographic expertise and technology had to be exploited. Interesting structures of large complexes seldomly diffract to a resolution where the convenience of automated methods can be used. Great care was required at every step. Some of the important ones will be explained in this presentation: In order to overcome the lack of non-crystallographic symmetry, multi-crystal averaging across several crystal forms was applied. A weak anomalous signal, not sufficient by itself to solve the structure, was crucial to climb out of a dead end sink directed by model bias when the structure was only 50 complete. The program mrtailor [3] was written to combine the information from multiple sequence alignment with structural data to minimise model bias from external restraints. Mrtailor is particularly well suited to work with multi-domain structures. The options available in refmac5 were tweaked in order to reveal the hidden feature in the lake of noise. This presentation gives insight into "high-end" crystallography beyond common textbook knowledge and how to deal with difficult cases.

[1] C. Fernández-Tornero, M. Moreno-Morcillo, U. J. Rashid, N. M. I. Taylor, F. M. Ruiz, T. Gruene, P. Legrand, U. Steuerwald, C. W. Müller, *Nature*, 2013, 502, 644–649., [2] C. Engel, S. Sainsbury, A. C. Cheung, D. Kostrewa, P. Cramer, *Nature*, 2013, 502, 650-655, [3] T. Gruene, *Acta Cryst. D*, 2013, 69, 1861-1863



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