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Nature：RNA 聚合酶-I的结构被确定

浏览次数：33 来源：Nature中文网 作者：Nature中文网 发布时间：2013-11-25 返回

RNA 聚合酶-I (Pol I) 转录核糖体RNA（后者是核糖体组装必不可少的），因此这种酶是蛋白生物合成和细胞生长的主要决定因子。

Pol I的误调控已被与几种类型的癌症联系了起来，而且Pol I也在成为抗癌药物的一个目标。

在本期Nature上，独立工作的两个小组发表了分别以3.0 A 和 2.8 A分辨率确定的由14个亚单元组成的酵母完整Pol I的线晶体结构。

Pol I的基本结构与Pol II 和 Pol III的基本结构相似，但其DNA结合槽有一个比在其他RNA聚合酶中所见到的更宽的构同时其他特点也让我们对其不同组成部分的功能角色有所认识。（生物谷Bioon.com）

生物谷推荐的英文摘要

Nature doi:10.1038/nature12636

Crystal structure of the 14-subunit RNA polymerase I

Carlos Fernandez-Tornero，Maria Moreno-Morcillo，Umar J. Rashid，Nicholas M. I. Taylor，Federico M. Ruiz，Tim Gru
Pierre Legrand，Ulrich Steuerwald& Christoph W. Müller

Protein biosynthesis depends on the availability of ribosomes， which in turn relies on ribosomal RNA production. In eukaryotes， this process is carried out by RNA polymerase I (Pol I)， a 14-subunit enzyme， the activity of which is a n determinant of cell growth. Here we present the crystal structure of Pol I from Saccharomyces cerevisiae at 3.0 resolution. Pol I structure shows a compact core with a wide DNA-binding cleft and a tightly anchored stalk. An extended loop mimics DNA backbone in the cleft and may be involved in regulating Pol I transcription. Subunit A12.2 extends from the A190 jaw t active site and inserts a transcription elongation factor TFIIS-like zinc ribbon into the nucleotide triphosphate entry pore， providing insight into the role of A12.2 in RNA cleavage and Pol I insensitivity to α-amanitin. The A49 – A34.5 heterodimer embraces subunit A135 through extended arms， thereby contacting and potentially regulating subunit A12.2.

doi:10.1038/nature12712

RNA polymerase I structure and transcription regulation

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Transcription of ribosomal RNA by RNA polymerase (Pol) I initiates ribosome biogenesis and regulates eukaryotic cell grow
The crystal structure of Pol I from the yeast Saccharomyces cerevisiae at 2.8 resolution reveals all 14subunits of the 590-
kilodalton enzyme， and shows differences to Pol II. An ‘expander’ element occupies the DNA template site and stabiliz
expanded active centre cleft with an unwound bridge helix. A ‘connector’ element invades the cleft of an adjacent polyme
and stabilizes an inactive polymerase dimer. The connector and expander must detach during Pol I activation to enable transc
initiation and cleft contraction by convergent movement of the polymerase ‘core’ and ‘shelf’ modules. Conversion bet
an inactive expanded and an active contracted polymerase state may generally underlie transcription. Regulatory factors can
modulate the core–shelf interface that includes a ‘composite’ active site for RNA chain initiation， elongation， proofre
and termination.