RNA Polymerase I Transcription

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references


Reactome database release: 79

This document contains 3 pathways (see Table of Contents)
RNA polymerase (Pol) I (one of three eukaryotic nuclear RNA polymerases) is devoted to the transcription of the ribosomal DNA genes, which are found in multiple arrayed copies in every eukaryotic cell. These genes encode for the large ribosomal RNA precursor, which is then processed into the three largest subunits of the ribosomal RNA, the 18S, 28S, and 5.8S RNAs. In human cells the rDNA gene clusters are localized on the short arm of the five pairs of the acrocentric chromosomes. The rRNA promoter has two essential and specially spaced sequences: a CORE element and an upstream control element (UCE, also called UPE). The CORE element of the human promoter overlaps with the transcription start site, extending from 20 to 45, and is required for specific initiation of transcription.

The polymerase is a multisubunit complex, composed of two large subunits (the most conserved portions include the catalytic site that shares similarity with other eukaryotic and bacterial multisubunit RNA polymerases) and a number of smaller subunits. Under a number of experimental conditions the core is competent to mediate ribonucleic acid synthesis, in vivo however, it requires additional factors to select the appropriate template. In humans the RNA transcript (45S) is approximately 13,000 nucleotides long. Before leaving the nucleus as assembled ribosomal particles, the 45S rRNA is cleaved to give one copy each of the 28S rRNA, the 18S rRNA, and the 5.8S rRNA. Equal quantities of the three rRNAs are produced by initially transcribing them as one transcript.

**Literature references**


**Editions**

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RNA Polymerase I Promoter Clearance

Location: RNA Polymerase I Transcription

Stable identifier: R-HSA-73854

Compartments: nucleolus

Promoter clearance is one of the rate-limiting steps in Polymerase I transcription. This step is composed of three phases, promoter opening, transcription initiation and promoter escape.

Literature references


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RNA Polymerase I Transcription Termination

**Location:** RNA Polymerase I Transcription

**Stable identifier:** R-HSA-73863

**Compartments:** nucleolus

Termination of transcription by RNA polymerase I is a 4 step process. Initially TTF-1 binds the template rDNA. This complex pauses polymerase I allowing PTRF to interact with the quaternary complex releasing both pre-rRNA and Pol I from the template and TTF-1.

**Literature references**


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