Ttf-I binds the T0 region (Sal Box) of the rDNA

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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: 82

This document contains 1 reaction (see Table of Contents)

[https://reactome.org](https://reactome.org)
Ttf-I binds the T0 region (Sal Box) of the rDNA

**Stable identifier:** R-MMU-573369

**Type:** binding

**Compartments:** nucleoplasm

The Transcription termination factor (Ttf1, also known as Ttf-1 and Ttf-I) binds the Sal box element in the intergenic regions of rRNA genes (Grummt et al. 1986, Evers and Grummt 1995). Affinity of Ttf1 for Sal box DNA is about 0.1X the affinity of other transcription factors, such as the A and B isoforms of human MAX, for their binding sites (Diermeier et al. 2013). Ttf1 cooperatively binds Sal box chromatin and forms oligomers that organize rDNA repeats into loops (Diermeier et al. 2013). Ttf1 participates in pausing transcription and in epigenetic regulation of rRNA transcription (Diermeier et al. 2013). Interactions with other proteins such as Tip5 influence the DNA-binding activity of Ttf1 (Nemeth et al. 2004).

**Literature references**


**Editions**

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