TTF-I binds to the Sal Box

Comai, L., Gillespie, ME., Iben, S., Shiao, YH.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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

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Reactome database release: 88
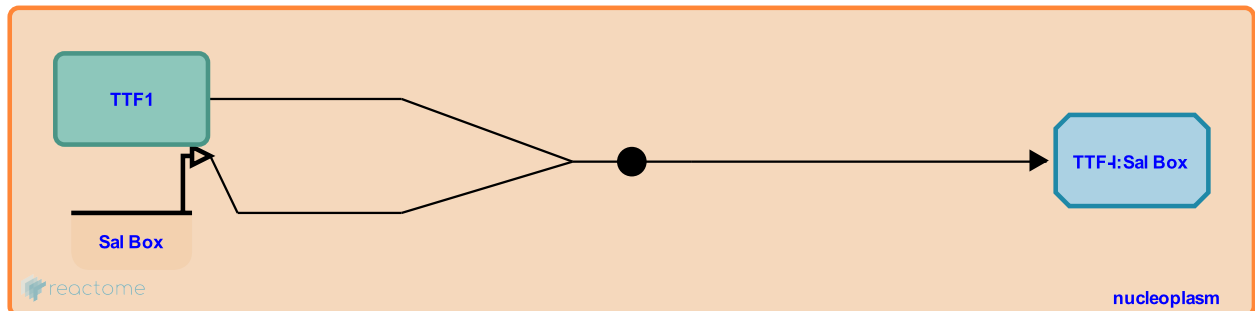
This document contains 1 reaction (see Table of Contents)

TTF-I binds to the Sal Box ↗

Stable identifier: R-HSA-74987

Type: binding

Compartments: nucleoplasm

Inferred from: Ttf-I binds the T0 region (Sal Box) of the rDNA (Mus musculus)

As inferred from mouse cell models, the Transcription termination factor (TTF1, also known as TTF-1 and TTF-I) binds an 18 base pair sequence element known as the Sal Box found in multiple copies in the nontranscribed spacer downstream of the 28S rRNA coding region. This element is the termination signal for ribosomal gene transcription. Binding of TTF1 mediates the pausing of the elongating transcription complex. TTF1 has a relatively low affinity for purified DNA but binds cooperatively to chromatin. Oligomers of TTF1 interact in trans to bind adjacent intergenic regions and form loops of the rDNA. Binding of TTF1 to the Sal Box is also influenced by interaction of TTF1 with TIP5 and possibly other proteins.

Literature references

Evers, R., Grummt, I. (1995). Molecular coevolution of mammalian ribosomal gene terminator sequences and the transcription termination factor TTF-I. *Proc Natl Acad Sci U S A, 92*, 5827-31. ↗

Editions

2003-07-03	Authored	Comai, L.
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