

TFAM binds to mitochondrial promoters

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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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- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
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Reactome database release: 88

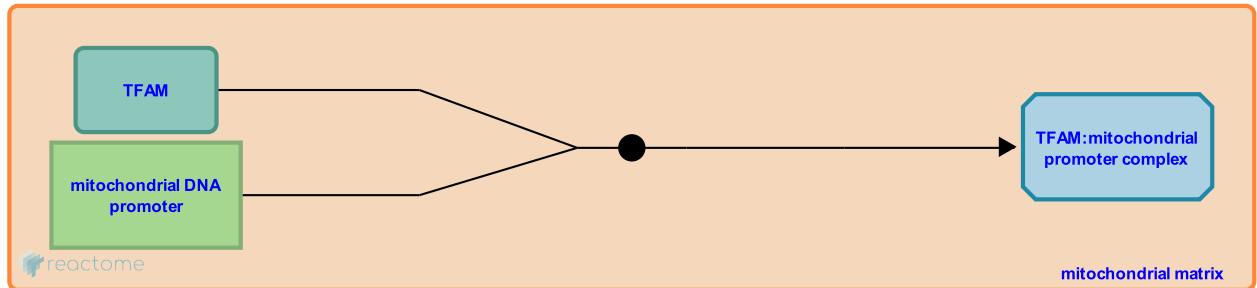
This document contains 1 reaction ([see Table of Contents](#))

TFAM binds to mitochondrial promoters [↗](#)

Stable identifier: R-HSA-163310

Type: binding

Compartments: mitochondrial matrix



Studies of human LSP have revealed that a minimal DNA fragment corresponding to position -28 to +16 relative to the transcription initiation site is able to support transcription initiation in a mitochondrial extract (Chang and Clayton, 1984). TFAM interacts directly with nucleotides between positions -35 and -17 (Fisher et al., 1987), and the exact distance between the TFAM-binding site and the transcription start site is essential for promoter activity (Dairaghi et al., 1995).

Literature references

Topper, JN., Fisher, RP. (1987). Promoter selection in human mitochondria involves binding of a transcription factor to orientation-independent upstream regulatory elements. *Cell*, 50, 247-58. [↗](#)

Editions

2005-04-26	Authored	Gustafsson, CM.
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