

# Expression of mTERF

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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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- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 70

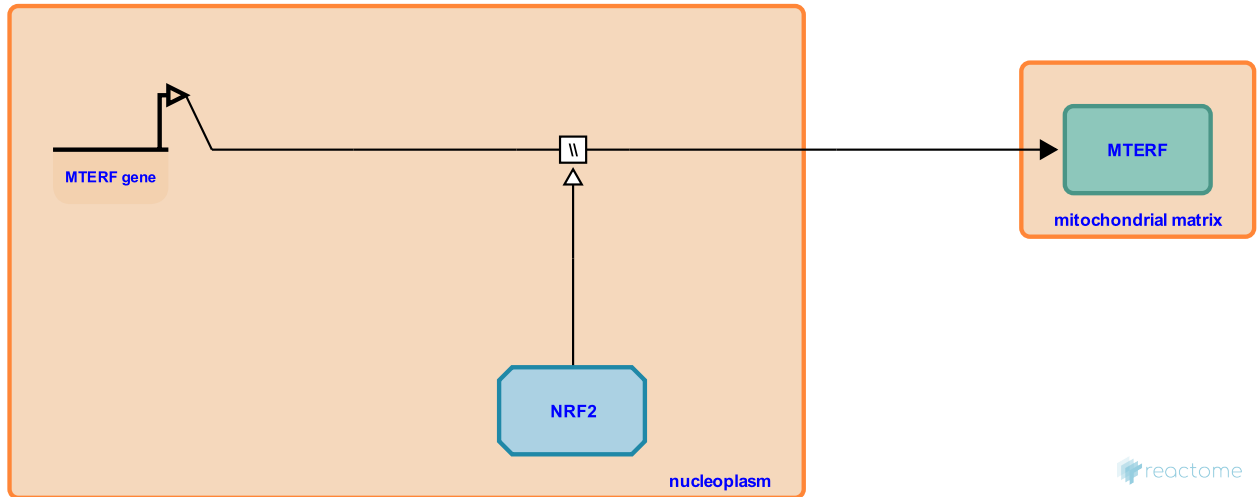
This document contains 1 reaction ([see Table of Contents](#))

## Expression of mTERF [↗](#)

**Stable identifier:** R-HSA-1592251

**Type:** omitted

**Compartments:** nucleoplasm, mitochondrial matrix



The mTERF gene is transcribed in the nucleus to yield mRNA and the mRNA is translated in the cytosol to yield precursor protein. mTERF is imported into the mitochondrial matrix where it plays a role in terminating transcription.

## Literature references

Bruni, F., Polosa, PL., Gadaleta, MN., Cantatore, P., Roberti, M. (2010). Nuclear respiratory factor 2 induces the expression of many but not all human proteins acting in mitochondrial DNA transcription and replication. *J Biol Chem*, 285, 3939-48. [↗](#)

## Editions

2011-08-20	Authored, Edited	May, B.
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