

TUFM:GDP dissociates from 55S ribosome

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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

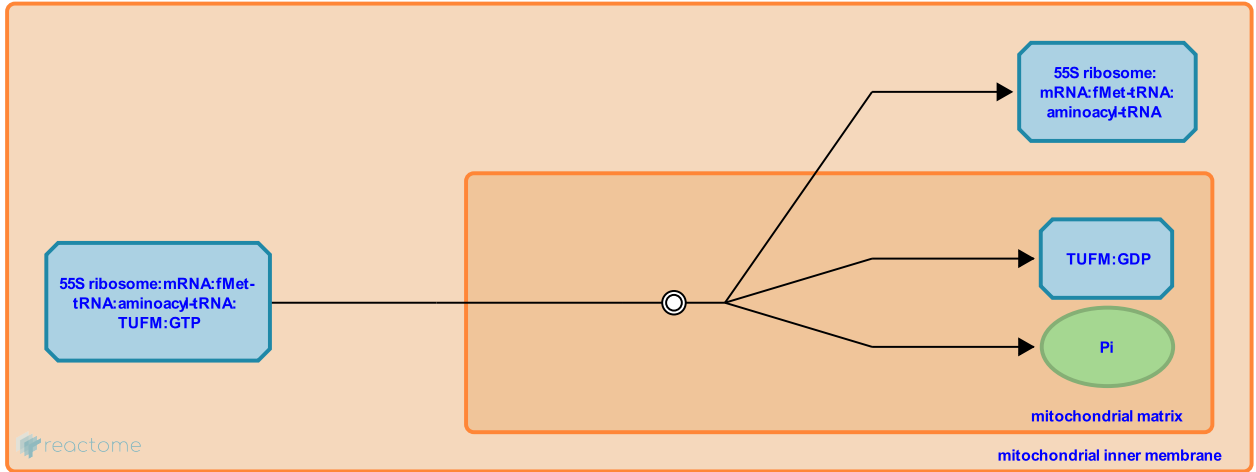
This document contains 1 reaction ([see Table of Contents](#))

TUFM:GDP dissociates from 55S ribosome

Stable identifier: R-BTA-5432388

Type: dissociation

Compartments: mitochondrial matrix



Interaction of the cognate aminoacyl-tRNA in the A-site with the codon in the mRNA causes hydrolysis of GTP by TUFM (EF-Tu) and dissociation of TUFM:GDP from the ribosome. (Kumazawa et al. 1991, Schwartzbach and Spremulli 1991, Woriat et al. 1997).

Literature references

Kaziyo, Y., Spremulli, LL., Kumazawa, Y., Watanabe, K., Miura, K., Mizumoto, K. et al. (1991). Interactions of bovine mitochondrial phenylalanyl-tRNA with ribosomes and elongation factors from mitochondria and bacteria. *Biochim. Biophys. Acta*, 1090, 167-72. [↗](#)

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Editions

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