

# 39S subunit binds 28S subunit:mRNA:fMet-tRNA

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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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)

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

Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)

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: 88

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

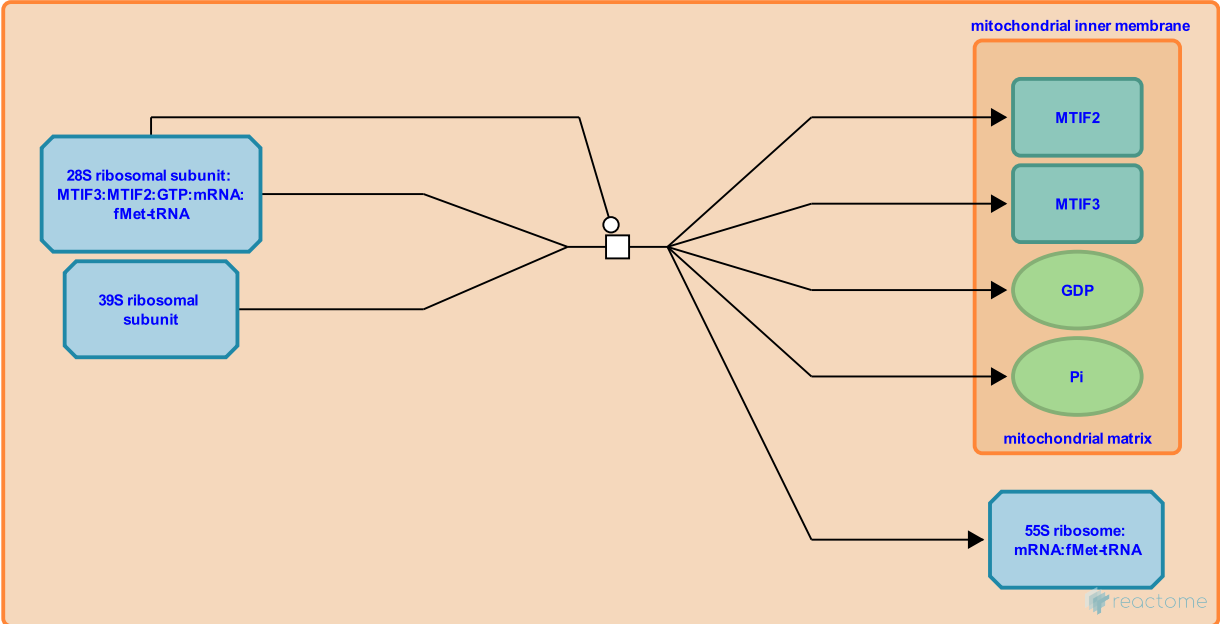
**39S subunit binds 28S subunit:mRNA:fMet-tRNA**

**Stable identifier:** R-HSA-5389839

**Type:** transition

**Compartments:** mitochondrial matrix, mitochondrial inner membrane

**Inferred from:** 39S subunit binds 28S subunit:mRNA:fMet-tRNA (Bos taurus)



As inferred from bovine homologs, the 39S ribosomal subunit binds the 28S subunit:mRNA:N-formylmethionyl-tRNA complex, MTIF2 hydrolyzes GTP, then MTIF2, GDP, and MTIF3 dissociate. (MTIF2 has a very low affinity for GDP so it is unclear whether MTIF2 and GDP remain associated after hydrolysis of GTP.) The 28S subunit, 39S subunit, and 55S holoribosome associate with the inner mitochondrial membrane during translation and in the absence of translation.

**Editions**

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