

# TIMM9:TIMM10 binds hydrophobic proteins

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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: 74

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

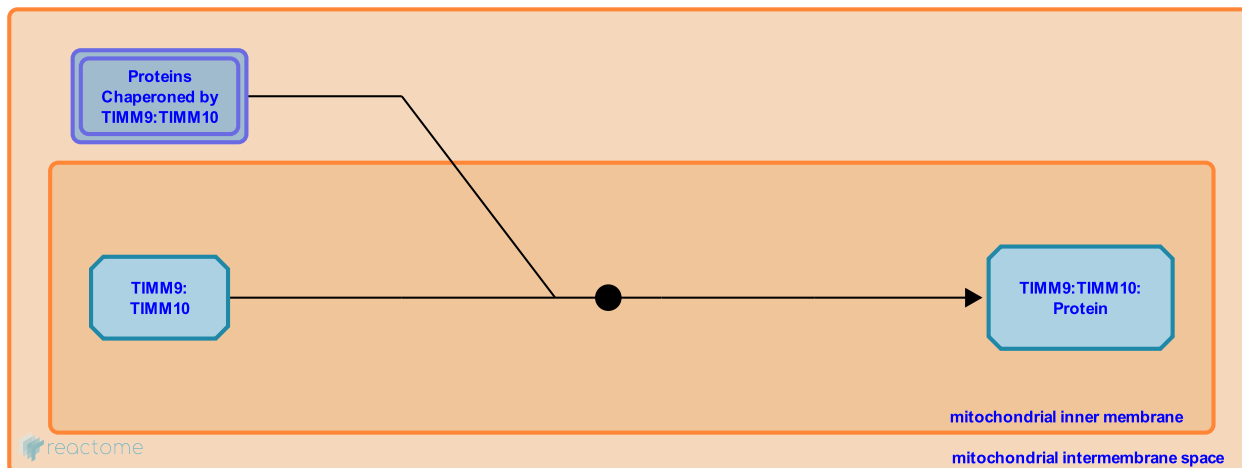
## TIMM9:TIMM10 binds hydrophobic proteins ↗

**Stable identifier:** R-HSA-1299481

**Type:** binding

**Compartments:** mitochondrial inner membrane, mitochondrial intermembrane space

**Inferred from:** [TIM9:TIM10 binds hydrophobic proteins \(Saccharomyces cerevisiae\)](#)



As inferred from the yeast TIM9:TIM10 complex, the human TIMM9:TIMM10:FXC1 complex chaperones hydrophobic membrane proteins in the intermembrane space until their insertion into the inner or outer membrane. Whereas the yeast TIM9:TIM10 complex is soluble in the intermembrane space, the human TIMM9:TIMM10 complex is associated with the outer surface of the inner membrane (Muhlebein et al. 2004).

Experimentally verified substrates of the yeast TIM9:TIM10 complex include AAC (ADP/ATP translocase 1, ANT, SLC25A4 in human), TIM17 (TIMM17 in human), TOM40 (TOMM40 in human), TIM23 (TIMM23 in human), TIM22 (TIMM22 in human), and Tafazzin (Tafazzin, TAZ in human). Many other mitochondrial proteins are anticipated to be chaperoned by the TIMM9:TIMM10 complex.

### Literature references

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### Editions

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