

# MPP hydrolyzes presequence of matrix precursors

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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: 75

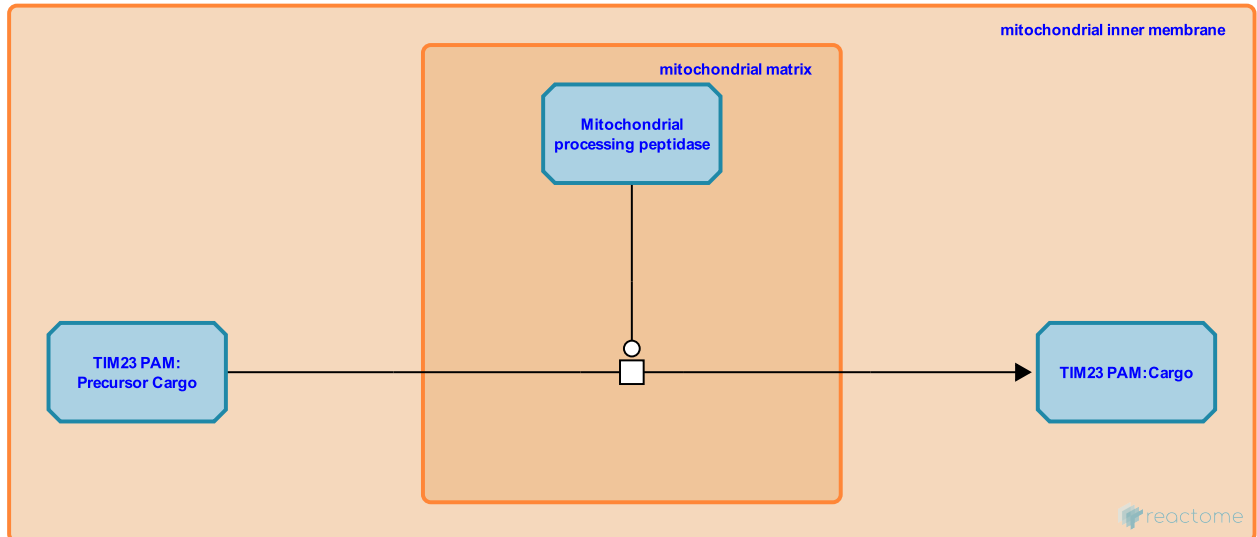
This document contains 1 reaction ([see Table of Contents](#))

## MPP hydrolyzes presequence of matrix precursors ↗

**Stable identifier:** R-SCE-1268017

**Type:** transition

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



The alpha subunit (MAS2, Alpha-MPP) of the mitochondrial processing peptidase (MPP) binds presequences of mitochondrial precursors and the beta subunit (MAS1, Beta-MPP) cleaves the presequence (Yang et al. 1991, Géli 1993, Luciano et al. 1997, Luciano et al. 1998, Taylor et al. 2001, Dvorakova-Hola et al. 2010). After cleavage, proteins destined for the matrix are drawn into the matrix by ATP-dependent interaction with mtHSP70 (SSC1) of the PAM complex.

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### Editions

2011-04-27	Authored, Edited	May, B.
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