

METAP1/2 demethylates GNAT1

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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

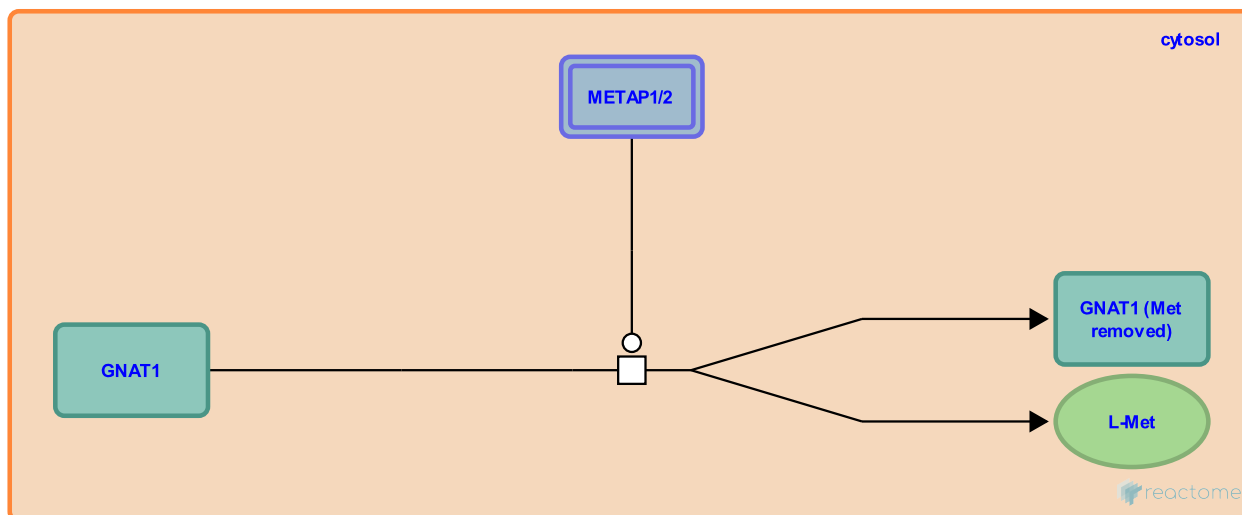
This document contains 1 reaction ([see Table of Contents](#))

METAP1/2 demethylates GNAT1 [↗](#)

Stable identifier: R-HSA-2534096

Type: transition

Compartments: cytosol



All eukaryotic proteins synthesized in the cytosol are initiated by methionine (Met). For the maturation of many proteins, the removal of N-terminal Met is essential and is mediated by methionine-aminopeptidases (METAPs). In human, there are two forms, METAP1 and 2 (Arfin et al. 1995). These enzymes utilise 2 cobalt ions (Co²⁺) as cofactors (Addlagatta et al. 2005, Hu et al. 2006, Marino et al. 2007).

Literature references

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Editions

2012-10-23	Authored, Edited	Jassal, B.
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