

p-S MAPK6 phosphorylates NCOA3

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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

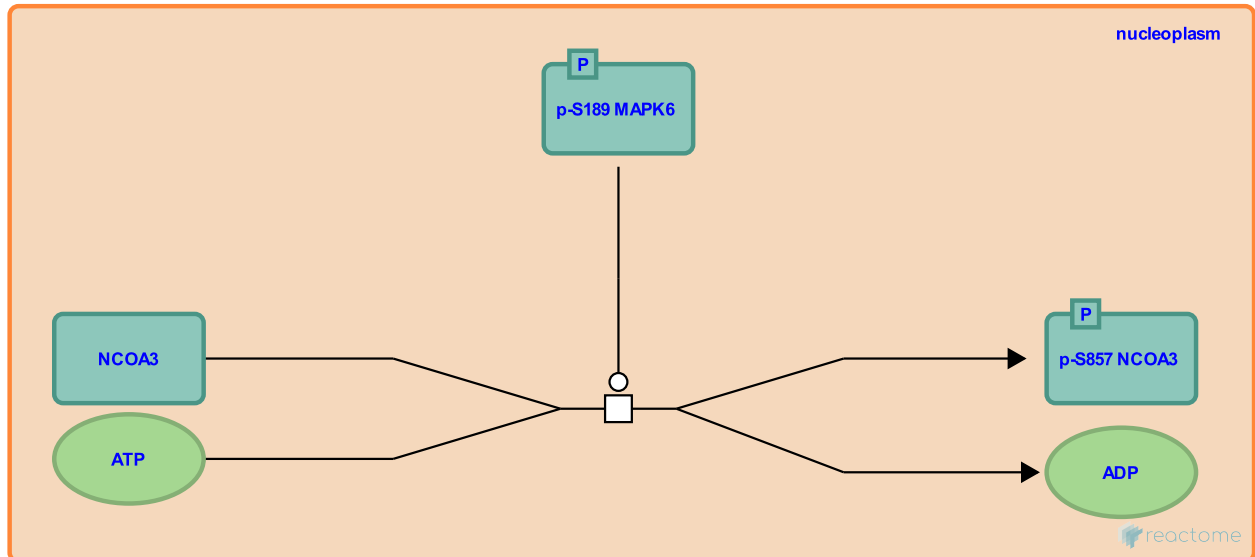
This document contains 1 reaction ([see Table of Contents](#))

p-S MAPK6 phosphorylates NCOA3 [↗](#)

Stable identifier: R-HSA-5687090

Type: transition

Compartments: nucleoplasm



MAPK6 is proposed to phosphorylate NCOA3 at serine 857. This phosphorylation is required for NCOA3 to interact with the transcription factor ETV4 (also known as PEA3). Together, ETV4 and NCOA3 bind to the promoters and regulate the expression of metalloprotease genes such as MMP2 and MMP10 and in this way contribute to cell motility and invasiveness in lung cancer (Long et al, 2012; Qin et al, 2008; Yan et al, 2008; Li et al, 2008; reviewed in Kostenko et al, 2012).

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Editions

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