SMG6 hydrolyzes mRNA with premature termination codon

May, B., Neu-Yilik, G.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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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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

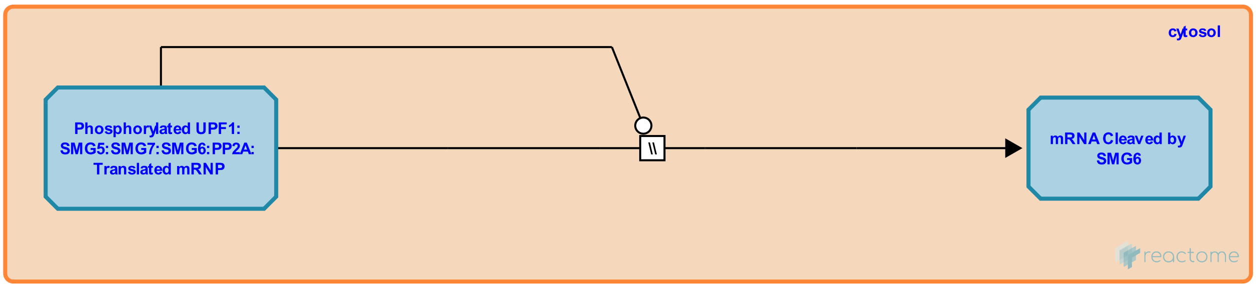
This document contains 1 reaction (see Table of Contents)

SMG6 hydrolyzes mRNA with premature termination codon ↗

Stable identifier: R-HSA-927836

Type: omitted

Compartments: cytosol


cytosol
Phosphorylated UPF1:SMG5:SMG7:SMG6:PP2A:Translated mRNP
mRNA Cleaved by SMG6
\\
reactome

SMG6 is an endoribonuclease which cleaves the mRNA bound by UPF1 near the premature termination codon (Glavan et al. 2006, Eberle et al. 2009).

Literature references

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Editions

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