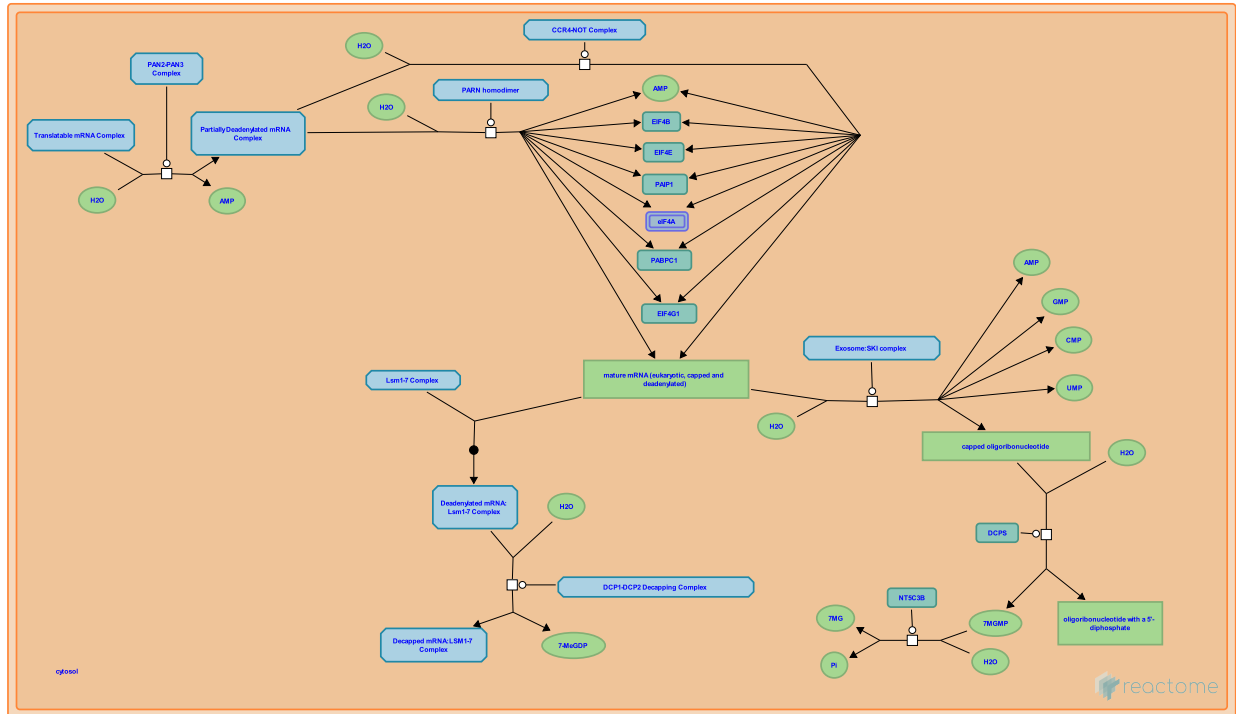


# Deadenylation-dependent mRNA decay



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This is just an excerpt of a full-length report for this pathway. To access the complete report, please download it at the [Reactome Textbook](#).

04/05/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## Literature references

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Reactome database release: 88

This document contains 4 pathways ([see Table of Contents](#))



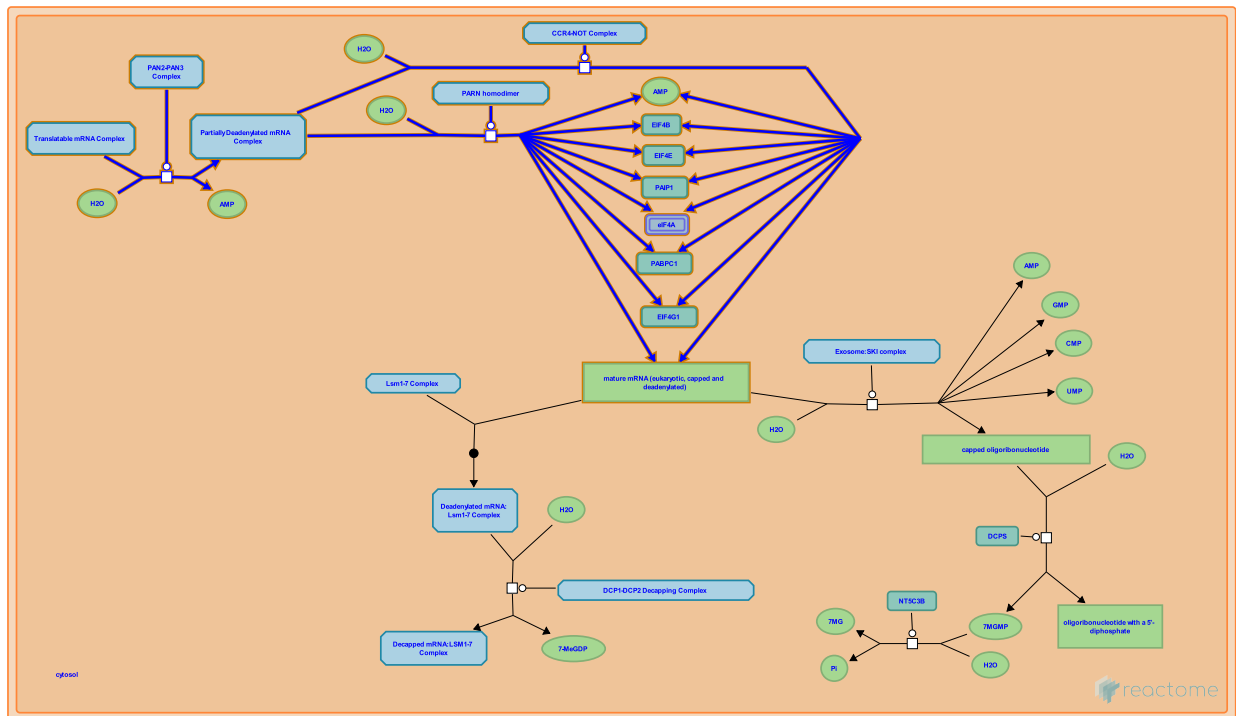
## Deadenylation of mRNA ↗

**Location:** Deadenylation-dependent mRNA decay

**Stable identifier:** R-GGA-429947

**Compartments:** cytosol

**Inferred from:** Deadenylation of mRNA (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

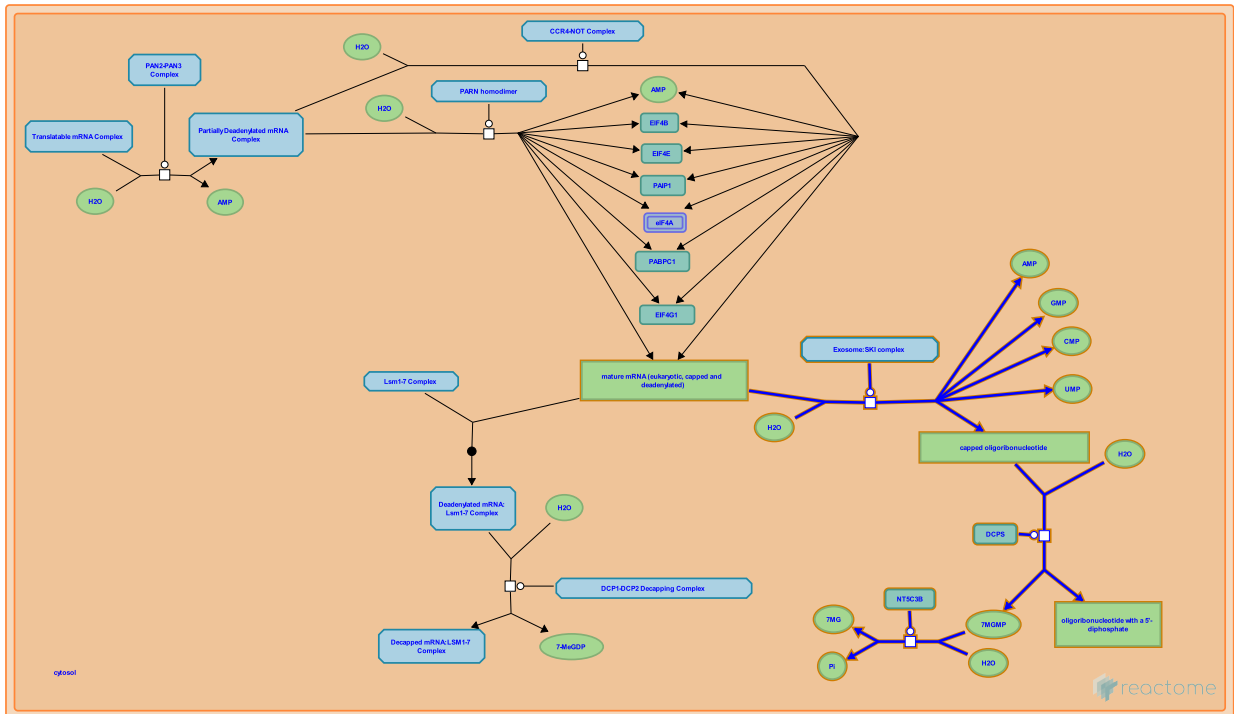
## mRNA decay by 3' to 5' exoribonuclease ↗

**Location:** Deadenylation-dependent mRNA decay

**Stable identifier:** R-GGA-429958

**Compartments:** cytosol

**Inferred from:** mRNA decay by 3' to 5' exoribonuclease (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

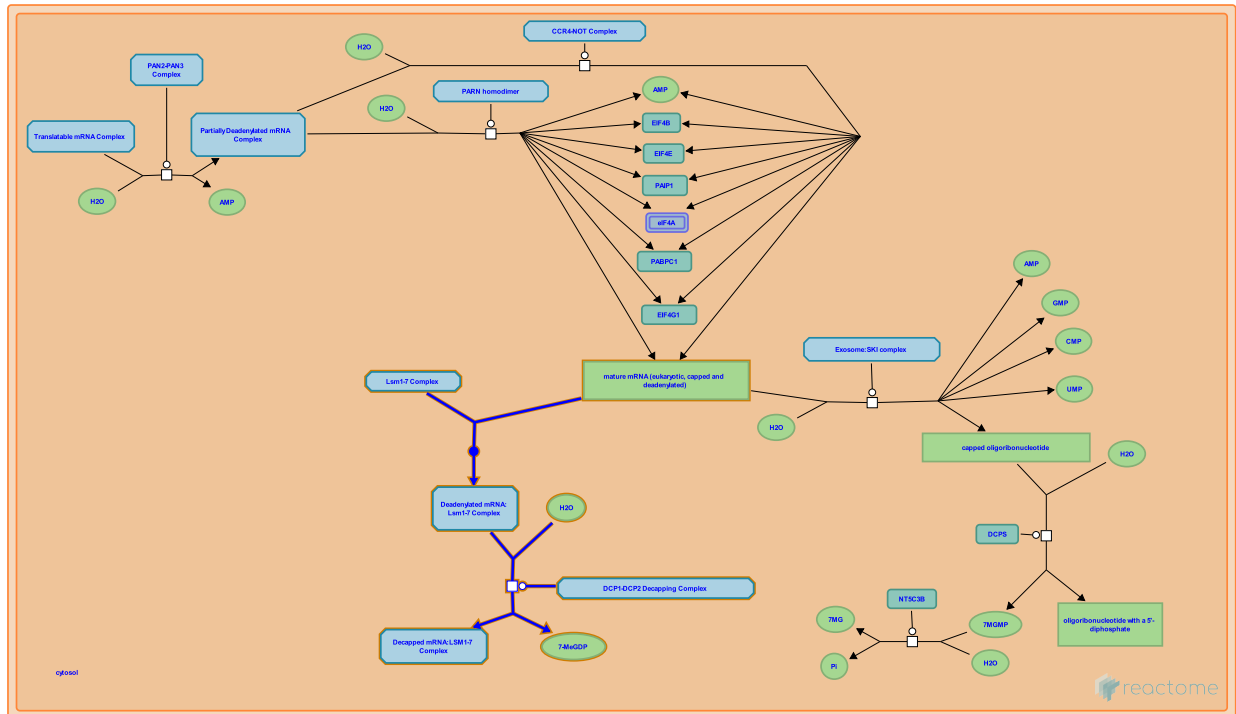
## mRNA decay by 5' to 3' exoribonuclease ↗

**Location:** Deadenylation-dependent mRNA decay

**Stable identifier:** R-GGA-430039

**Compartments:** cytosol

**Inferred from:** mRNA decay by 5' to 3' exoribonuclease (Homo sapiens)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping from PANTHER. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 75% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

[More details and caveats of the event inference in Reactome.](https://www.reactome.org) For details on PANTHER see also: <http://www.pantherdb.org/about.jsp>

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