Transfer of GMP from the capping enzyme GT site to 5'-end of mRNA

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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. ↗

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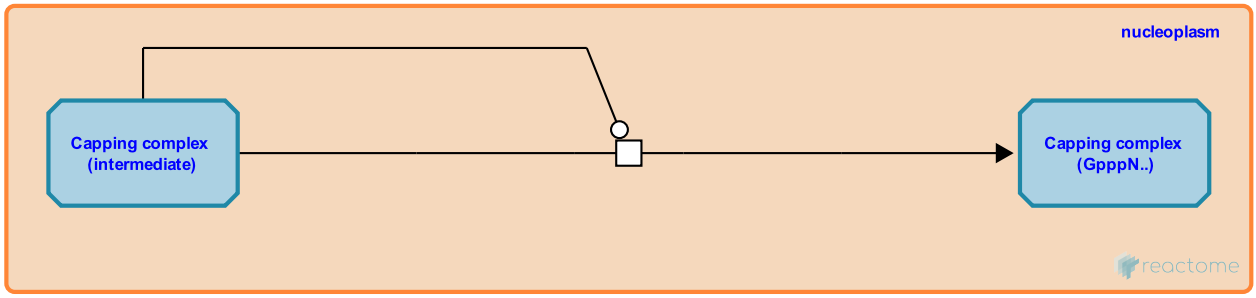
Stable identifier: R-HSA-77083

Type: transition

Compartments: nucleoplasm



The diphosphate 5'-end of the mRNA is joined to the GMP, releasing it from the enzyme. At this time, it is unclear how the RNA diphosphate end is transferred from the active site of the triphosphatase to the guanylyltransferase site. The covalent enzyme-GMP complex can form in the absence of RNA.
Guanylyltransferase (GT) catalyzed second reaction can be represented as:ppN(pN)n + GTP -> GpppN(pN)n + PPi

(Yamada-Okabe et al. 1998).

Literature references

Yamada-Okabe, H., Shimmi, O., Arisawa, M., Yamada-Okabe, T., Doi, R. (1998). Isolation and characterization of a human cDNA for mRNA 5'-capping enzyme. *Nucleic Acids Res, 26*, 1700-6. ↗

Editions

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