TUT4,TUT7 oligouridylate 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

Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18*, 142. ↗

Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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. ↗

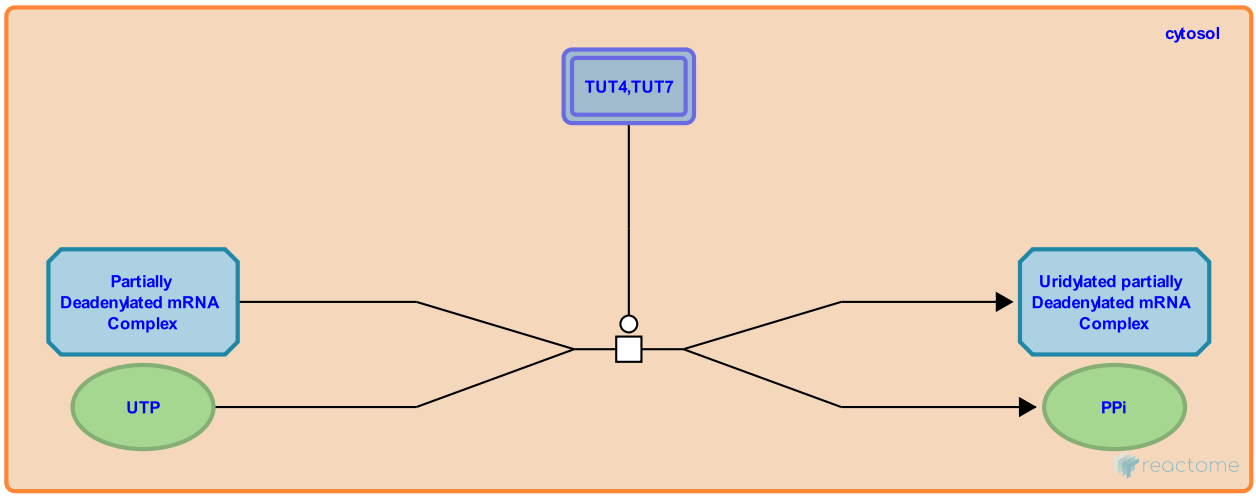
TUT4,TUT7 oligouridylate mRNA ↗

Stable identifier: R-HSA-8941312

Type: transition

Compartments: cytosol

Inferred from: Tut4,Tut7 oligouridylate mRNA (Mus musculus)



Uridylyltransferases mediate the terminal uridylation of mRNAs, RISC-cleaved transcripts and of various non-coding RNAs including miRNAs and their precursors mRNAs (Scott and Norbury 2013, Lee et al. 2014, Munoz-Tello et al. 2015, Scheer et al. 2016).
TUT4 and TUT7 (ZCCHC11, ZCCHC6) are mRNA uridylation enzymes that can act on the majority of mammalian mRNAs (Lim et al. 2014). More than 85% of mRNAs are uridylated at a frequency of higher than 1% in NIH 3T3 and HeLa cells (Chang et al. 2014). Uridylated tails were found mainly on mRNAs with polyA tails of less than 25 nucleotides, suggesting that uridylation may occur after deadenylation. There was a negative correlation between uridylation frequency and mRNA half-life, suggesting a role of uridylation in general mRNA decay (Lim et al. 2014). TUT4 and TUT7 (ZCCHC11, ZCCHC6) also uridylate replication-dependent histone mRNAs, which are not polyadenylated, to facilitate their degradation (Lackey et al 2016, Schmidt et al. 2011, Mullen & Marzluff 2008, Hoefig et al. 2013, Slevin et al. 2014). TUT4 and TUT7 also uridylate miRNAs and their precursors (Thornton et al. 2014, Lee et al. 2014, Ha & Kim 2014). Mono-uridylation of pre-miRNA facilitates miRNA processing, while polyuridylation of pre-miRNA triggers their degradation (Heo et al. 2012).
TUT4 and TUT7 are expressed during zygotic genome activation and uridylate the 3' ends of specific maternal mRNAs thereby targeting those mRNAs for degradation (inferred from mouse zygotes in Zhao et al. 2022). PABPN1L binds the terminal oligouridylate and recruits DIS3L2, a 3'-5' exoribonuclease (inferred from mouse zygotes in Zhao et al. 2022).

Literature references

Kwon, SC., Ha, M., Patel, DJ., Lim, J., Kim, VN., Simanshu, DK. et al. (2014). Uridylation by TUT4 and TUT7 marks mRNA for degradation. *Cell, 159*, 1365-76. ↗

Editions

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