PUS1 isoform 2 transforms uridine residues to pseudouridine in the anticodon stems of tRNAs

Jarrous, N., Levinger, L., May, B., Motorin, Y.

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

29/04/2024

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

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. ↗

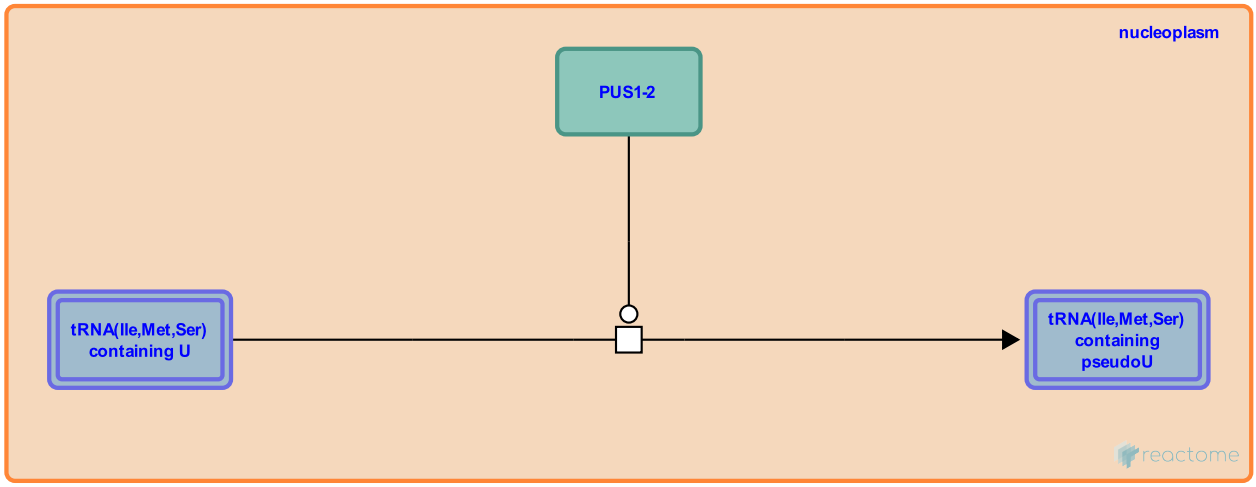
PUS1 isoform 2 transforms uridine residues to pseudouridine in the anticodon stems of tRNAs

Stable identifier: R-HSA-6782381

Type: transition

Compartments: nucleoplasm

Inferred from: PUS1 transforms uridine residues to pseudouridine in unspliced tRNA(Ile,Tyr) (Saccharomyces cerevisiae)



The shorter isoform of PUS1, PUS1-2, converts uridine to pseudouridine in the anticodon stem of tRNAs in the nucleus (Fernandez-Vizarra et al. 2007, Sibert et al. 2008). The longer isoform of PUS1 (PUS1-1) is present in mitochondria; a shorter isoform of PUS1 (PUS1-2) possessing a different N-terminus is present in the nucleus (Fernandez-Vizarra et al. 2007). In contrast, the yeast Saccharomyces cerevisiae has 2 genes: PUS1 which encodes the nuclear enzyme and PUS2 which encodes the mitochodrial enzyme. PUS1 and its substrates are conserved from yeast to humans. Like the yeast homologue, Pus1p, human PUS1 may also act on additional tRNAs, pre-tRNAs, and U2 snRNA. Mutations in PUS1 cause mitochondrial myopathy and sideroblastic anemia (MLASA) (Bykhovskaya et al. 2004, Fernandez-Vizarra et al. 2007).

Literature references

Bykhovskaya, Y., Casas, K., Inbal, A., Fischel-Ghodsian, N., Mengesha, E. (2004). Missense mutation in pseudouridine synthase 1 (PUS1) causes mitochondrial myopathy and sideroblastic anemia (MLASA). *Am. J. Hum. Genet., 74*, 1303-8.

Sibert, BS., Patton, JR., Fischel-Ghodsian, N. (2008). Partial activity is seen with many substitutions of highly conserved active site residues in human Pseudouridine synthase 1. *RNA, 14*, 1895-906.

Valente, L., Fernandez-Vizarra, E., Berardinelli, A., Zeviani, M., Tiranti, V. (2007). Nonsense mutation in pseudouridylate synthase 1 (PUS1) in two brothers affected by myopathy, lactic acidosis and sideroblastic anaemia (MLASA). *J. Med. Genet., 44*, 173-80.

Editions

2015-06-06	Authored, Edited	May, B.
2015-08-11	Reviewed	Levinger, L.
2015-08-25	Reviewed	Motorin, Y.
2015-10-24	Reviewed	Jarrous, N.