

tRNA ligase complex ligates tRNA exons

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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. [↗](#)

Reactome database release: 88

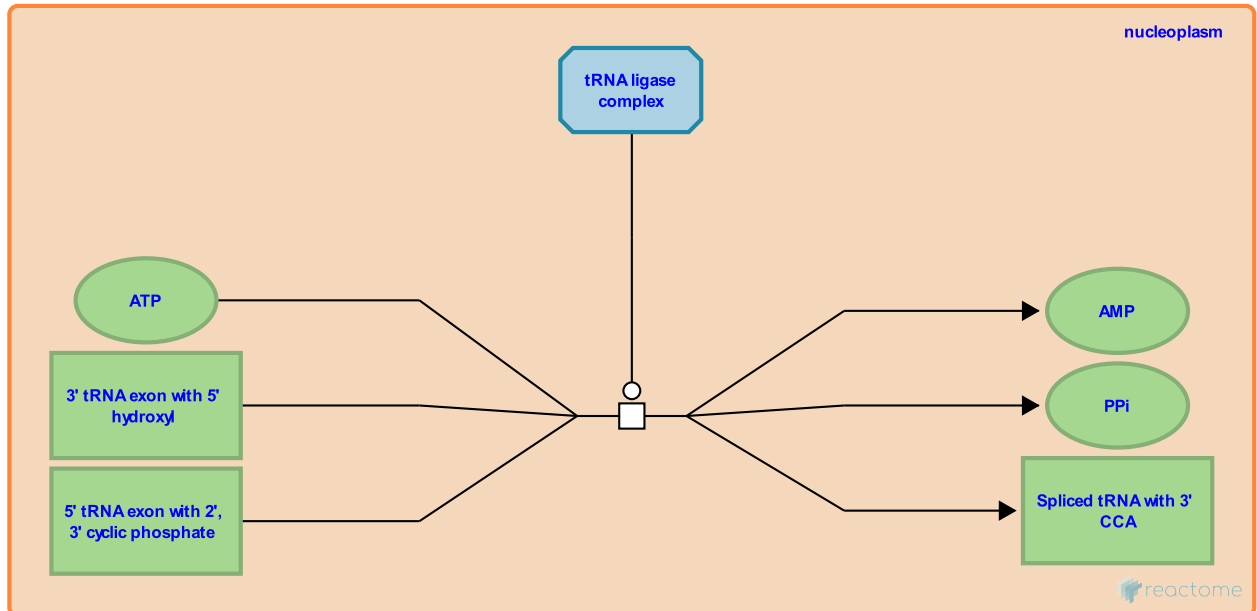
This document contains 1 reaction ([see Table of Contents](#))

tRNA ligase complex ligates tRNA exons [↗](#)

Stable identifier: R-HSA-5696816

Type: transition

Compartments: nucleoplasm



The RNA ligase complex ligates tRNA exons yielding intact, spliced tRNAs (Popow et al. 2011, Popow et al. 2014). The reaction apparently occurs in one step with no residual 2' phosphate that requires removal, as in yeast.

Literature references

Martinez, J., Will, CL., Lührmann, R., Trowitzsch, S., Mechtler, K., Schleiffer, A. et al. (2011). HSPC117 is the essential subunit of a human tRNA splicing ligase complex. *Science*, 331, 760-4. [↗](#)

Martinez, J., Jurkin, J., Schleiffer, A., Popow, J. (2014). Analysis of orthologous groups reveals archease and DDX1 as tRNA splicing factors. *Nature*, 511, 104-7. [↗](#)

Editions

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