

# NDUF subunits bind to form the IP sub- complex

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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: 76

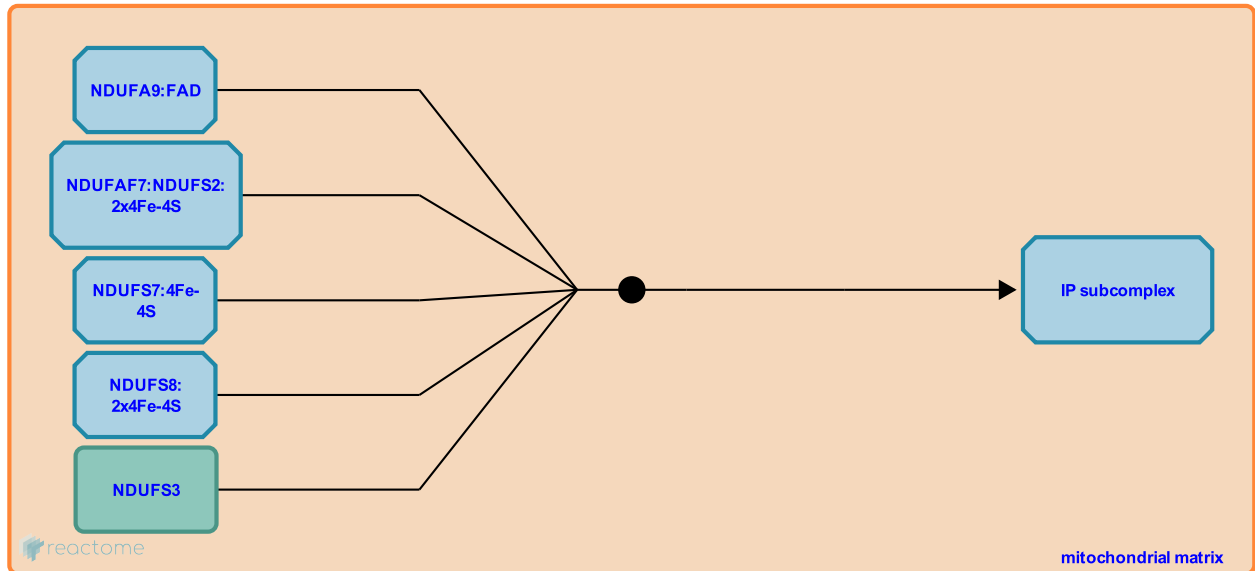
This document contains 1 reaction ([see Table of Contents](#))

## NDUF subunits bind to form the IP subcomplex ↗

**Stable identifier:** R-HSA-6800868

**Type:** binding

**Compartments:** mitochondrial matrix



The subunits NDUFS7, S8 and A9, together with NDUFS2 and S3, form an evolutionarily conserved hydrogenase module as part of the Iron-Sulfur protein fraction (IP) subcomplex (Mckenzie & Ryan 2010, Andrews et al. 2013).

### Literature references

McKenzie, M., Ryan, MT. (2010). Assembly factors of human mitochondrial complex I and their defects in disease. *IUBMB Life*, 62, 497-502. ↗

Andrews, B., Carroll, J., Ding, S., Fearnley, IM., Walker, JE. (2013). Assembly factors for the membrane arm of human complex I. *Proc. Natl. Acad. Sci. U.S.A.*, 110, 18934-9. ↗

### Editions

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