

RDH11,14,DHRS3,DRHS4 reduce atRAL to atROL

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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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Reactome database release: 88

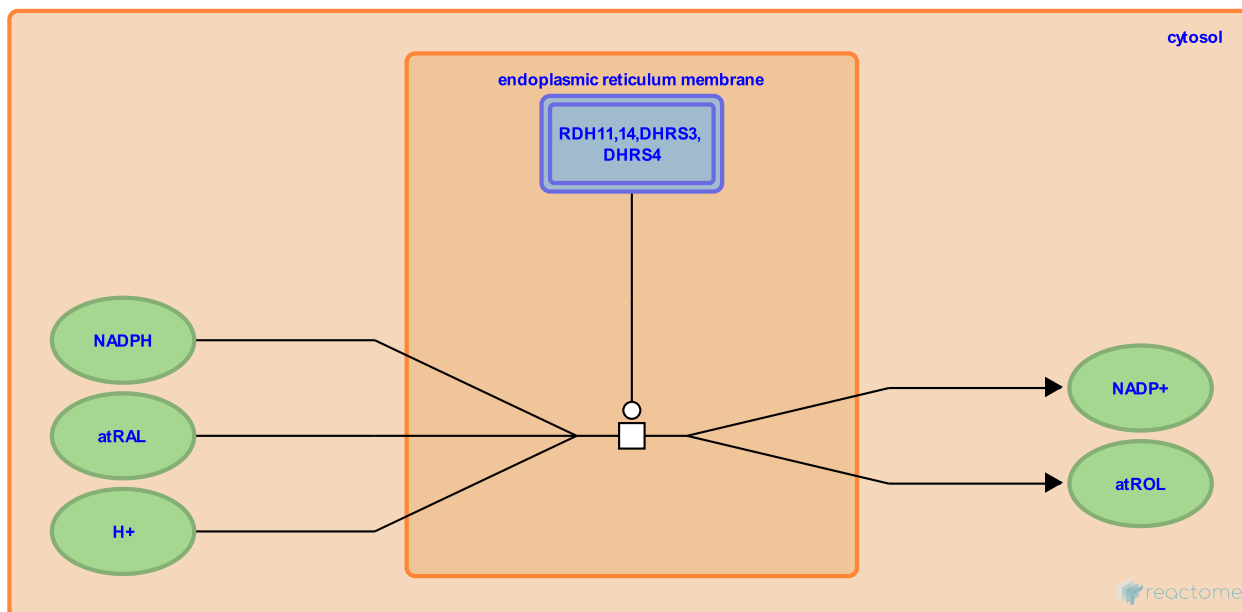
This document contains 1 reaction ([see Table of Contents](#))

RDH11,14,DHRS3,DRHS4 reduce atRAL to atROL [↗](#)

Stable identifier: R-HSA-5419165

Type: transition

Compartments: cytosol, endoplasmic reticulum membrane



Multiple reductases may contribute to the reduction of all-trans-retinal (atRAL) to all-trans-retinol (atROL), including RDH11 (aka PSDR1, RalR1), RDH14, DHRS3 (aka retSDR1, RDH17) and DHRS4 (aka RRD, SCAD-SRL) (Haeseleer et al. 1998, Haeseleer et al. 2002, Kedishvili et al. 2002, Lin et al. 2001, Zhen et al. 2003, Belyaeva et al. 2008).

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Editions

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