Defective CYP26B1 does not 4-hydroxylate atRA

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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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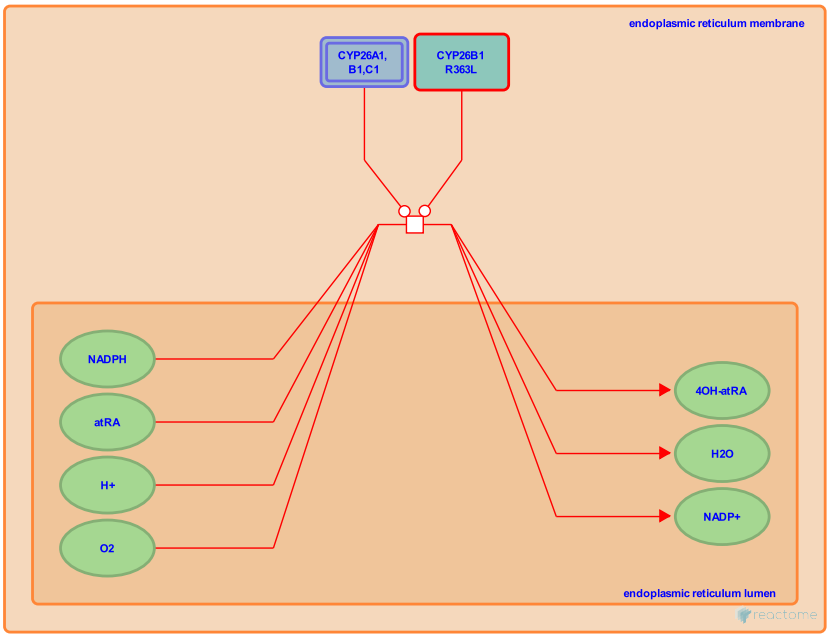
Stable identifier: R-HSA-5602063

Type: transition

Compartments: endoplasmic reticulum membrane, endoplasmic reticulum lumen

Diseases: craniosynostosis



Retinoic acid (RA) is a biologically active analogue of vitamin A (retinol). RA plays an important role in regulating cell growth and differentiation.CYP26A1 and B1 are involved in the metabolic breakdown of RA by 4-hydroxylation. High expression levels of CYP26B1 in the cerebellum and pons of human brain suggests a protective role of specific tissues against retinoid damage (White et al. 2000). Excess exogenous retinoic acid (RA) has teratogenic effects in the limb and craniofacial skeleton. Defects in CYP26B1 can cause radiohumeral fusions with other skeletal and craniofacial anomalies (RHFCA; MIM:614416), a disease characterised by craniofacial malformations and multiple skeletal anomalies. Laue et al. identified homozygosity for a 1088G-T transversion in the CYP26B1 gene, predicting an R363L substitution. The reduction of enzymatic activity for the mutant protein was comparable to that underlying a zebrafish cyp26b1 null allele, indicating that the human mutation constitutes a null allele (Laue et al. 2011).

Literature references

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Editions

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