

Nuclear PHD1,3 hydroxylates proline residues on HIF1A

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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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Reactome database release: 77

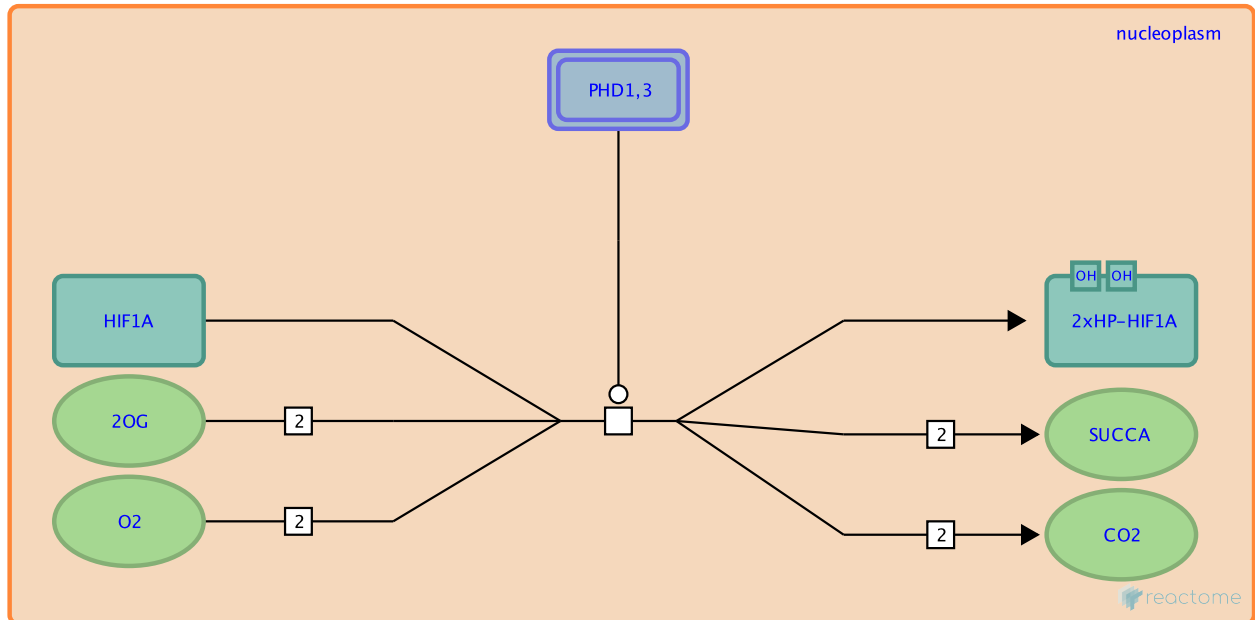
This document contains 1 reaction ([see Table of Contents](#))

Nuclear PHD1,3 hydroxylates proline residues on HIF1A ↗

Stable identifier: R-HSA-1234181

Type: transition

Compartments: nucleoplasm



Proline hydroxylases PHD1 (EGLN2) and PHD3 (EGLN3) located in the nucleus (Metzen et al. 2003) hydroxylate HIF1A at proline-402 and proline-564 (Buick and McKnight 2001, Jaakkola et al. 2001, Ivan et al. 2001, Ivan et al. 2002, Berra et al. 2003, Hirsila et al. 2003, Appelhoff et al. 2004, Tuckerman et al. 2004, Fedulova et al. 2007, Tian et al. 2011). The amount of hydroxylation occurring in the nucleus is controversial. Most hydroxylation is believed to occur in the cytosol.

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Editions

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