

Cytosolic PHD2,3 hydroxylates proline residues on HIF3A

May, B., Rantanen, K.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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

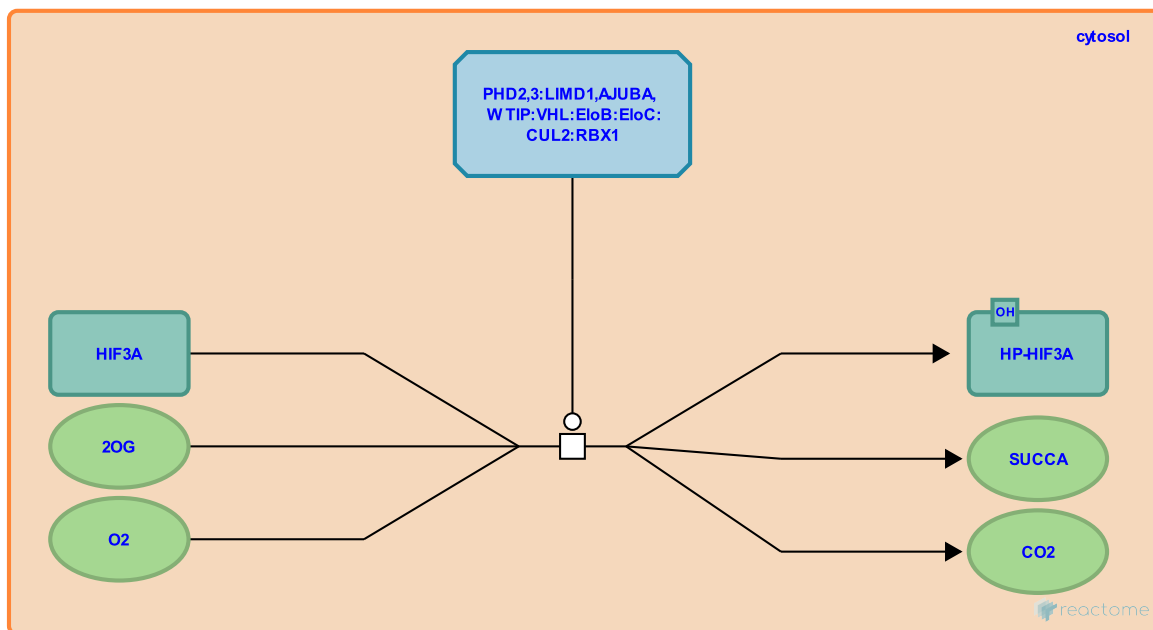
This document contains 1 reaction ([see Table of Contents](#))

Cytosolic PHD2,3 hydroxylates proline residues on HIF3A [↗](#)

Stable identifier: R-HSA-1234173

Type: transition

Compartments: cytosol



Proline hydroxylases PHD2 (EGLN1) and PHD3 (EGLN3) located in the cytosol (Metzen et al. 2003) hydroxylate HIF3A at proline-492 (Hirsila et al. 2003, Maynard et al. 2003). A portion of PHD3 (EGLN3) is also located in the nucleus (Rantanen et al. 2008).

Literature references

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Editions

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