

# Cytosolic PHD2,3 hydroxylates proline residues on HIF3A

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10/05/2024

## 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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

## 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: 88

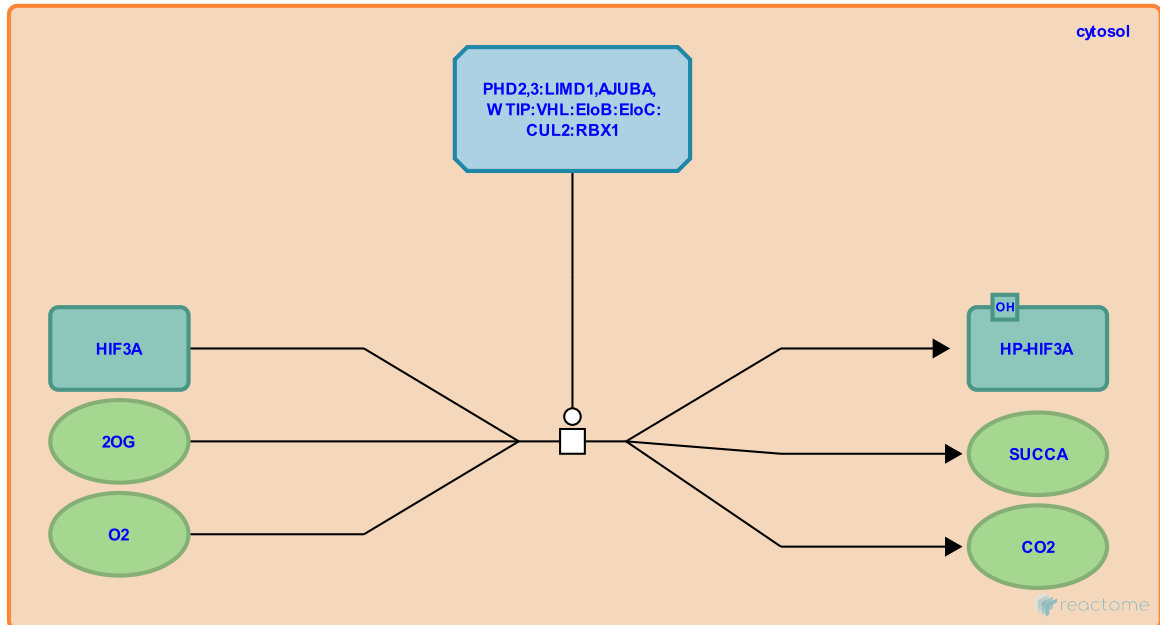
This document contains 1 reaction ([see Table of Contents](#))

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

**Stable identifier:** R-HSA-1234173

**Type:** transition

**Compartments:** cytosol



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

### Literature references

Lee, EH., Chung, J., Maynard, MA., Qi, H., Ohh, M., Conaway, JW. et al. (2003). Multiple splice variants of the human HIF-3 alpha locus are targets of the von Hippel-Lindau E3 ubiquitin ligase complex. *J Biol Chem*, 278, 11032-40. [↗](#)

Himanen, V., Metzen, E., Högel, H., Rantanen, K., Jaakkola, PM., Pursiheimo, J. (2008). Prolyl hydroxylase PHD3 activates oxygen-dependent protein aggregation. *Mol. Biol. Cell*, 19, 2231-40. [↗](#)

Stengel, P., Klinger, M., Acker, H., Hellwig-Bürgel, T., Fandrey, J., Wotzlaw, C. et al. (2003). Intracellular localisation of human HIF-1 alpha hydroxylases: implications for oxygen sensing. *J Cell Sci*, 116, 1319-26. [↗](#)

Hirsilä, M., Günzler, V., Koivunen, P., Myllyharju, J., Kivirikko, KI. (2003). Characterization of the human prolyl 4-hydroxylases that modify the hypoxia-inducible factor. *J Biol Chem*, 278, 30772-80. [↗](#)

### Editions

2011-03-09

Authored, Edited

May, B.

2012-05-19

Reviewed

Rantanen, K.