

Expression of EPAS1 (HIF2A)

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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

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

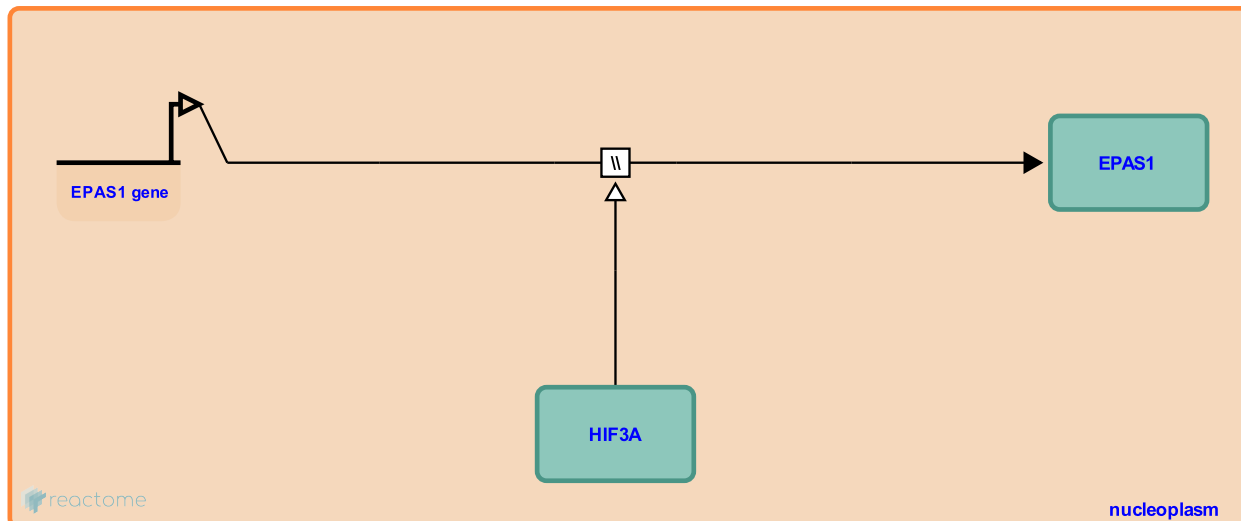
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Expression of EPAS1 (HIF2A) ↗

Stable identifier: R-HSA-480301

Type: omitted

Compartments: nucleoplasm



Hypoxia causes an increase in the level of HIF3A which in turn enhances expression of EPAS1 (HIF2A). The mechanism is unknown.

The EPAS1 (HIF2A) gene is transcribed to yield mRNA and the mRNA is translated to yield protein. EPAS1 is expressed in most adult tissues, but not in peripheral blood leukocytes (Tian et al. 1997). Normoxia causes constitutive oxygen-dependent hydroxylation of EPAS1 on asparagine and proline residues, resulting in degradation of EPAS1 via ubiquitinylation. Hypoxia therefore inhibits degradation of EPAS1 and also causes an increase in EPAS1 expression via HIF3A in embryonic stem cells, which experience hypoxic conditions in the reproductive tract prior to implantation (Forristal et al. 2010).

Literature references

Russell, DW., Tian, H., McKnight, SL. (1997). Endothelial PAS domain protein 1 (EPAS1), a transcription factor selectively expressed in endothelial cells. *Genes Dev*, 11, 72-82. ↗

Houghton, FD., Forristal, CE., Oreffo, RO., Wright, KL., Hanley, NA. (2010). Hypoxia inducible factors regulate pluripotency and proliferation in human embryonic stem cells cultured at reduced oxygen tensions. *Reproduction*, 139, 85-97. ↗

Editions

2010-11-12	Authored, Edited	May, B.
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