Expression of Erythropoietin (EPO)

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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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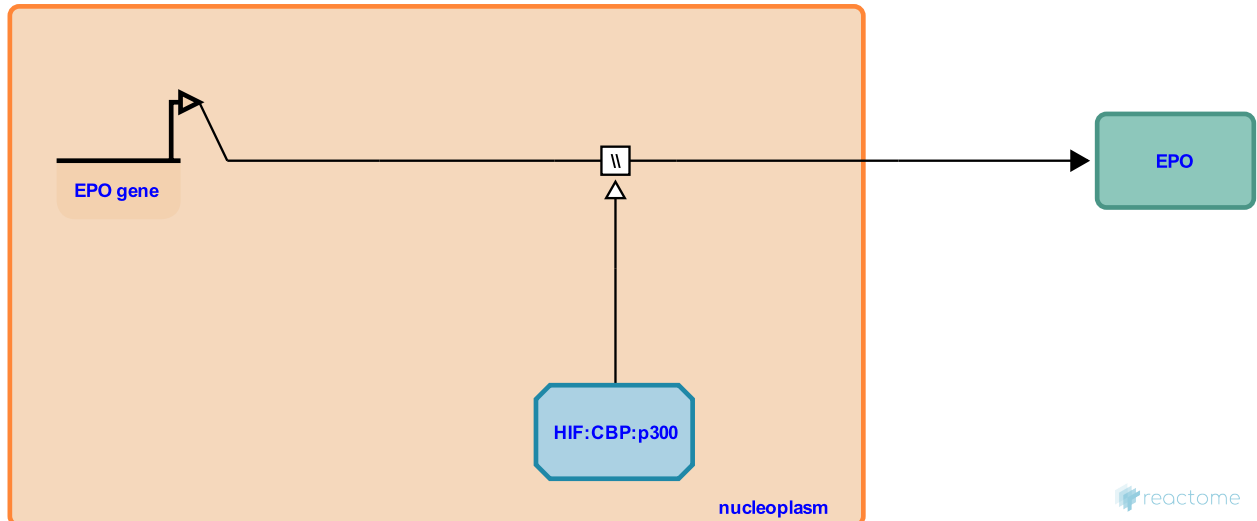
Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

Expression of Erythropoietin (EPO) ↗

Stable identifier: R-HSA-1235070

Type: omitted

Compartments: nucleoplasm, extracellular region

The EPO gene is transcribed to yield mRNA and the mRNA is translated to yield protein. Transcription of EPO is enhanced by Hypoxia-inducible factor, which binds to the EPO promoter.
The HIF heterodimer binds the promoter of the EPO gene and recruits p300 and CBP to enhance transcription of EPO.

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Editions

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