Expression of PTGS2

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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. ↗

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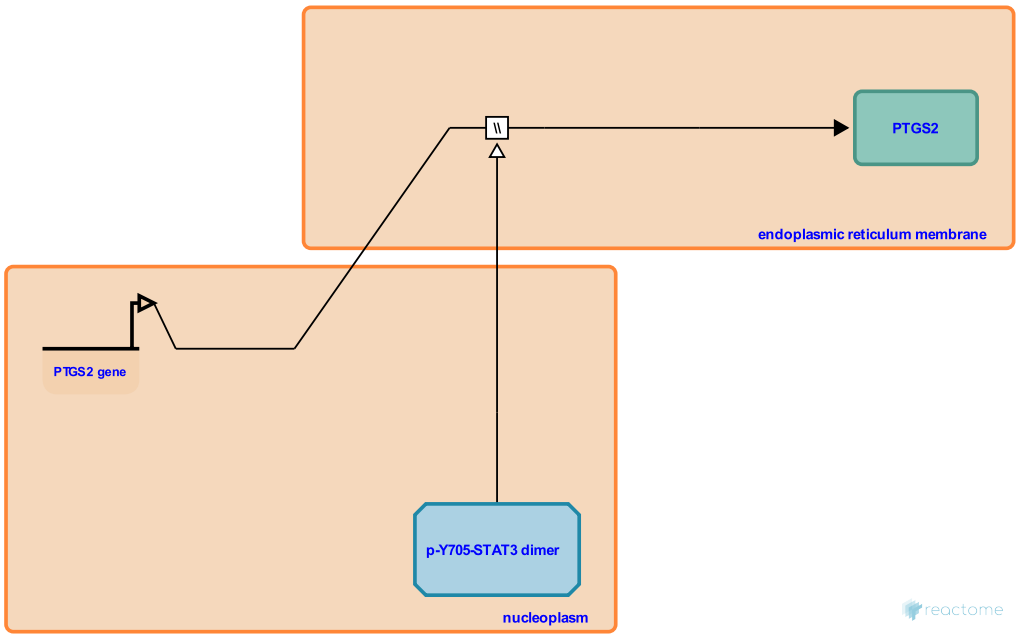
Stable identifier: R-HSA-6790029

Type: omitted

Compartments: endoplasmic reticulum membrane, nucleoplasm



Signal transducer and activator of transcription 3 (STAT3) is a key regulator of gene expression in response to signaling of many cytokines including interleukin-6 (IL6), Oncostatin M, and leukemia inhibitory factor. Using microarray techniques, hundreds of genes have been reported as potential STAT3 target genes (Dauer et al. 2005, Hsieh et al. 2005). Some of these genes have been proven to be direct STAT3 targets using genome-wide chromatin immunoprecipitation screening (Snyder et al. 2008, Carpenter & Lo 2014), including the gene which encodes the endoplasmic reticulum membrane protein Prostaglandin G/H synthase 2 (PTGS2, COX2) (Lo et al. 2010).

Literature references

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Editions

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