

GPAM gene expression is stimulated by RUNX1 and ESR1

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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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Reactome database release: 70

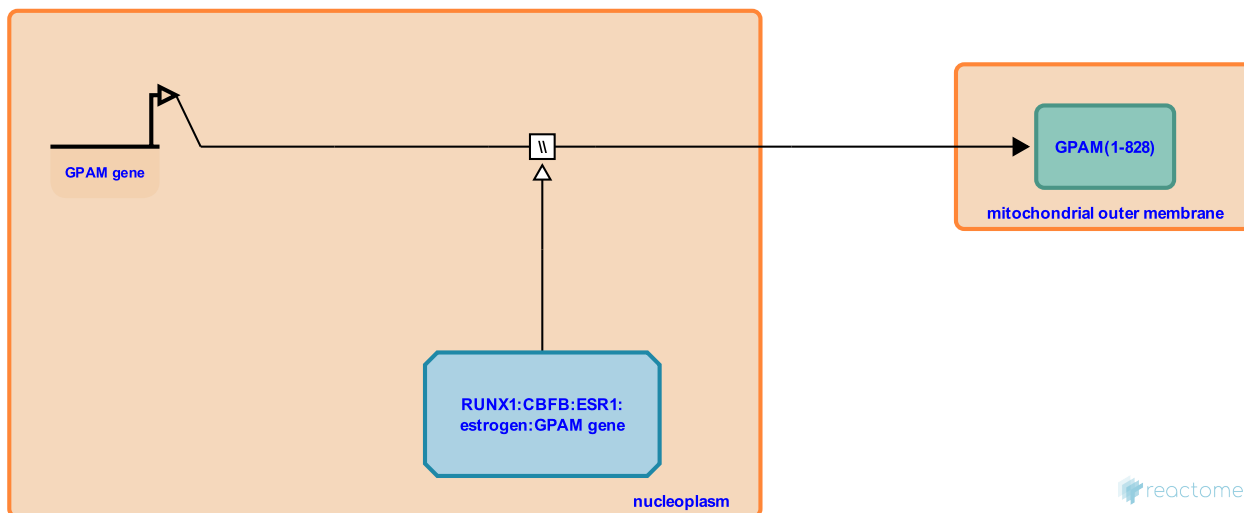
This document contains 1 reaction ([see Table of Contents](#))

GPAM gene expression is stimulated by RUNX1 and ESR1 [↗](#)

Stable identifier: R-HSA-8932020

Type: omitted

Compartments: nucleoplasm, mitochondrial outer membrane



GPAM gene expression is cooperatively stimulated by RUNX1 and ESR1, which form a complex and bind the GPAM gene enhancer (Stender et al. 2010). GPAM encodes a glycerol-3-phosphate acyltransferase whose high expression correlates with better overall survival in breast cancer (Brockmoller et al. 2012).

Literature references

Stender, JD., Kim, K., Charn, TH., Komm, B., Chang, KC., Kraus, WL. et al. (2010). Genome-wide analysis of estrogen receptor alpha DNA binding and tethering mechanisms identifies Runx1 as a novel tethering factor in receptor-mediated transcriptional activation. *Mol. Cell. Biol.*, 30, 3943-55. [↗](#)

Editions

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