MIR132 gene expression is stimulated by p-S133-CREB1

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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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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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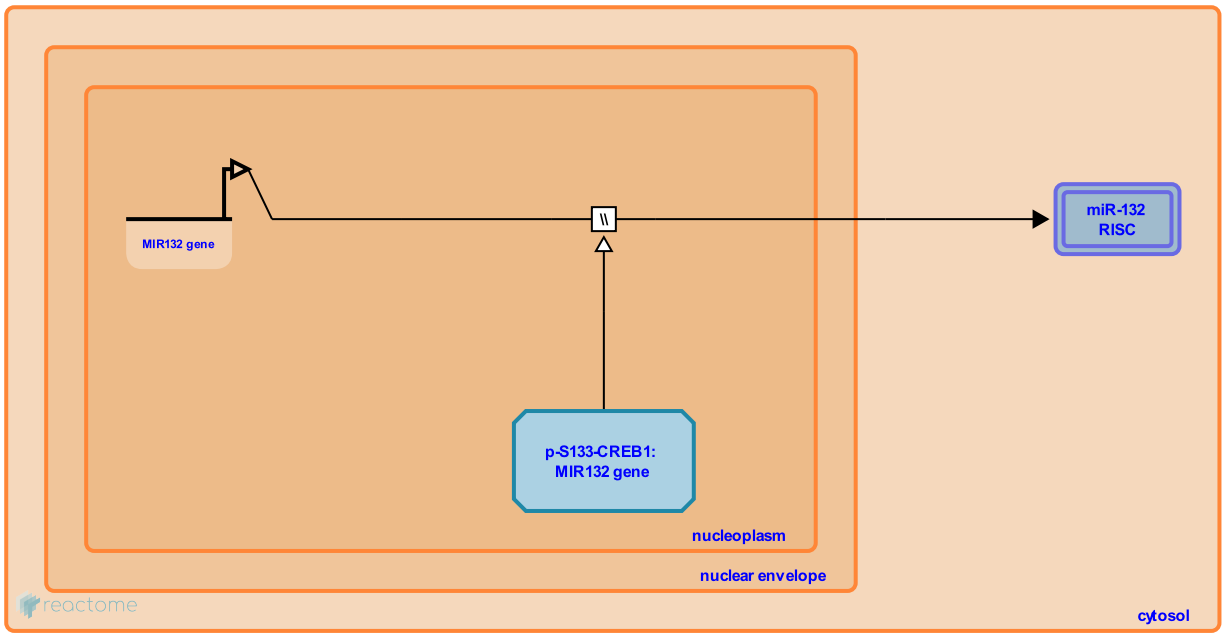
Stable identifier: R-HSA-9615501

Type: omitted

Compartments: nucleoplasm, cytosol

Inferred from: Mir132 gene expression is stimulated by p-S133-Creb1 (Rattus norvegicus)



Based on studies in rat and mouse cells, CREB1 induces transcription of the MIR132 gene, encoding miR-132 microRNA (Vo et al. 2005, Lyu et al. 2016). Activation of CREB1 by phosphorylation at serine residue S133 in response to PTEN knockdown results in increased levels of miR-132 (Lyu et al. 2016).

Editions

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