NR2E1 associated with transcription repressors binds PTEN promoter

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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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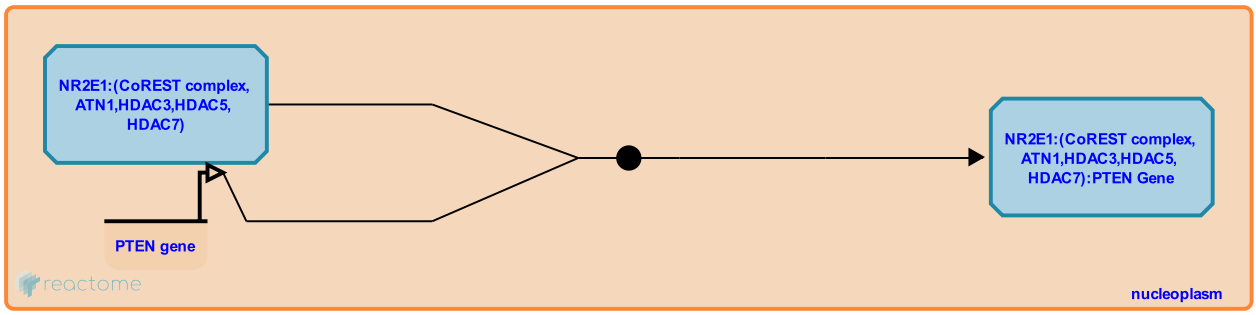
Stable identifier: R-HSA-6807077

Type: binding

Compartments: nucleoplasm

Inferred from: Nr2e1 binds Pten promoter (Mus musculus)



NR2E1 (TLX) associated with transcription repressors binds the evolutionarily conserved TLX consensus site in the PTEN promoter. NR2E1 inhibits PTEN transcription by associating with various transcriptional repressors, probably in a cell type or tissue specific manner. PTEN transcription is inhibited when NR2E1 forms a complex with ATN1 (atrophin-1) (Zhang et al. 2006, Yokoyama et al. 2008), KDM1A (LSD1) histone methyltransferase containing CoREST complex (Yokoyama et al. 2008), or histone deacetylases HDAC3, HDAC5 or HDAC7 (Sun et al. 2007).

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Editions

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