

APP gene expression

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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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Reactome database release: 88

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

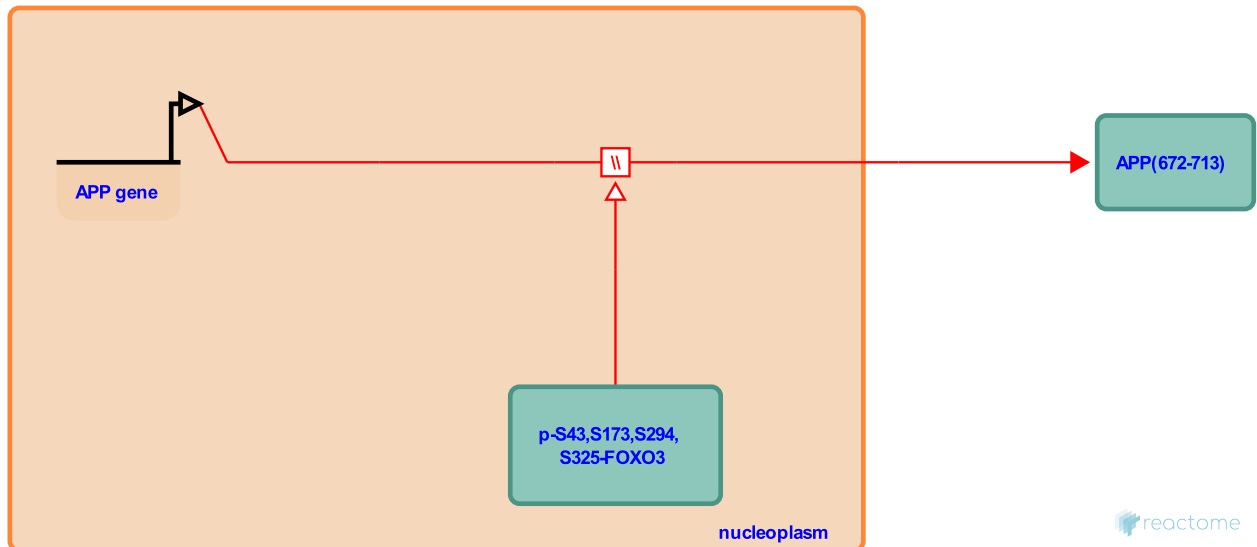
APP gene expression [↗](#)

Stable identifier: R-HSA-8870710

Type: omitted

Compartments: extracellular region, nucleoplasm

Diseases: Alzheimer's disease



Transcription of the APP gene is increased by FOXO3, downstream of FOXO3 phosphorylation by aberrantly activated CDK5 (Shi et al. 2016).

Literature references

Viccaro, K., Shi, C., Lee, HG., Shah, K. (2016). Cdk5-FOXO3a axis: initially neuroprotective, eventually neurodegenerative in Alzheimer's disease models. *J. Cell. Sci.* [↗](#)

Editions

2016-02-23	Authored	Shah, K.
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