APAF1:CYCS binds APIP

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29/04/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

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Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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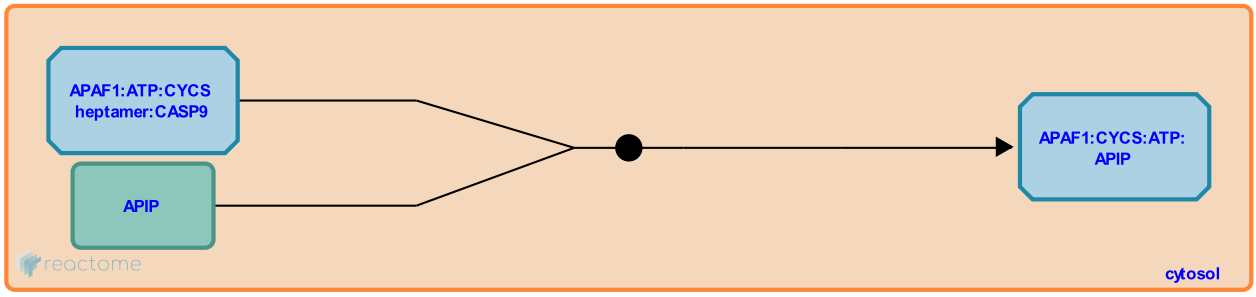
Stable identifier: R-HSA-6804596

Type: binding

Compartments: cytosol



The APAF1 interacting protein (APIP) is an endogenous regulators of the apoptosome apparatus. APIP is thought to bind to the CARD domain of APAF1 preventing procaspase-9 recruitment to the apoptosome (Cho DH et al., 2004; Cao G et al., 2004; Kang W et al. 2014). Moreover, during hypoxic conditions, APIP may also induce sustained activation of AKT and ERK1/2 kinases, which directly phosphorylate procaspase-9 to inhibit its activation in the apoptosome (Cho DH et al., 2007).

Literature references

Kim, TY., Yang, JK., Kim, HC., Ashida, H., Yokota, A., Le, le TM. et al. (2014). Structural and biochemical basis for the inhibition of cell death by APIP, a methionine salvage enzyme. *Proc. Natl. Acad. Sci. U.S.A., 111*, E54-61. ↗

Editions

2017-07-26	Authored	Shamovsky, V.
2018-11-02	Edited	Shamovsky, V.
2018-11-05	Reviewed	Matthews, L.