

IPAF binds procaspase-1

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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

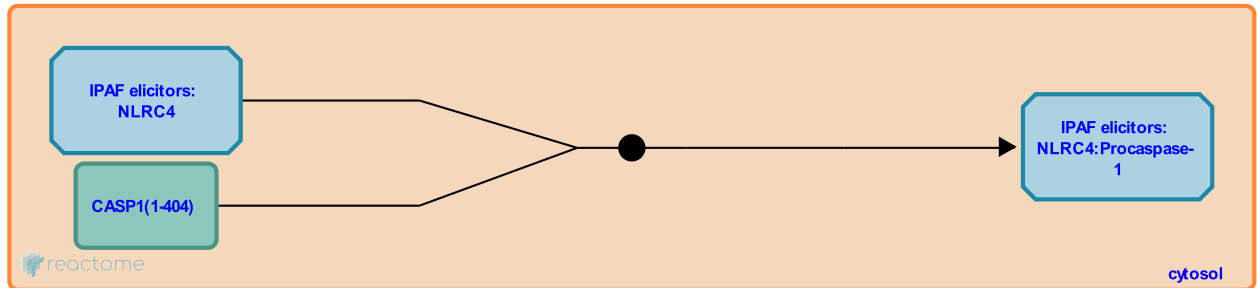
This document contains 1 reaction ([see Table of Contents](#))

IPAF binds procaspase-1 [↗](#)

Stable identifier: R-HSA-844617

Type: binding

Compartments: cytosol



IPAF contains an N-terminal CARD domain, a central nucleotide-binding domain, and a C-terminal regulatory leucine-rich repeat domain. IPAF associates with the CARD domain of procaspase-1 through a CARD-CARD interaction.

Literature references

Srinivasula, SM., Tnani, M., Razmara, M., Poyet, JL., Alnemri, ES., Fernandes-Alnemri, T. (2001). Identification of Ipaf, a human caspase-1-activating protein related to Apaf-1. *J Biol Chem*, 276, 28309-13. [↗](#)

Editions

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