

Cleavage of PAK-2 at 212

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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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- 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. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

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

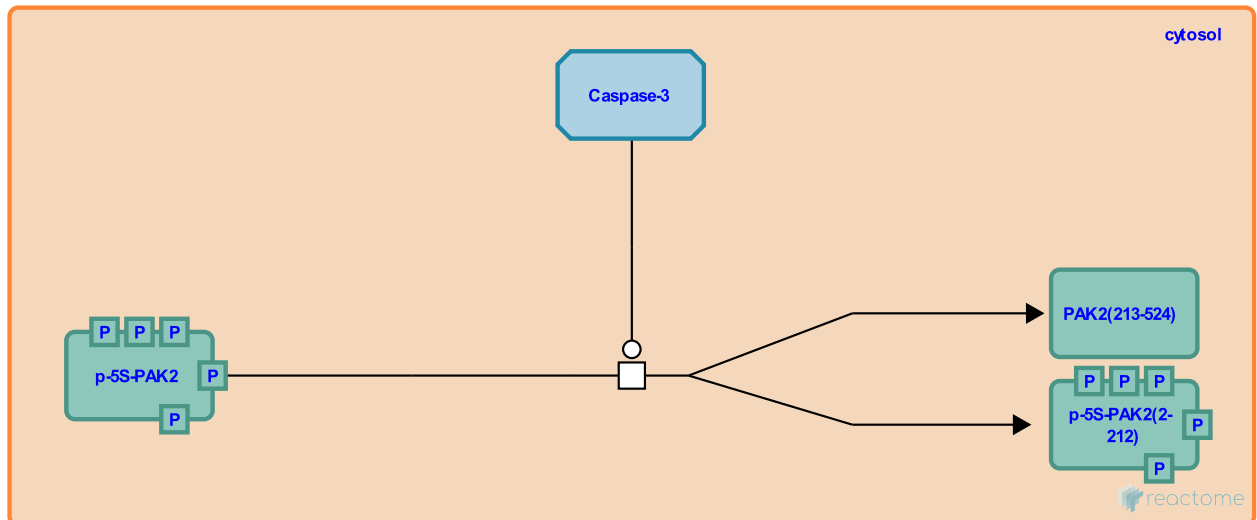
Cleavage of PAK-2 at 212 ↗

Stable identifier: R-HSA-211651

Type: transition

Compartments: cytosol

Inferred from: [Cleavage of PAK-2 at 212 \(Oryctolagus cuniculus\)](#)



p21-activated protein kinase (PAK-2), also known as gamma-PAK, is cleaved by caspase-3 during apoptosis and plays a role in regulating cell death. Cleavage produces two peptides; 1-212 containing most of the regulatory domain and 213-524 containing 34 amino acids of the regulatory domain as well as the catalytic domain (Walter et al., 1998). Proteolytic cleavage of PAK by caspase-3 creates the constitutively active PAK-2p34 fragment (Jakobi et al., 2003). Evidence for this reaction comes from experiments using both human and rabbit proteins.

Editions

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