Proteolytic PAK-2p34 fragment translocates to the nucleus

Chang, E., Jakobi, R., Matthews, L.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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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. ↗

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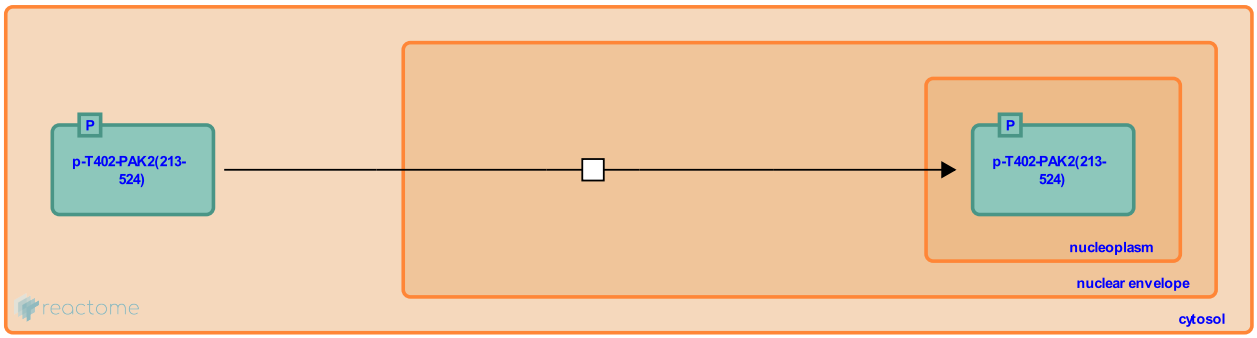
Stable identifier: R-HSA-211712

Type: transition

Compartments: nuclear envelope

Inferred from: Proteolytic PAK-2p34 fragment translocates to the nucleus (Oryctolagus cuniculus)



The subcellular localization of PAK-2 is controlled by nuclear localization and nuclear export signal motifs (Jakobi et al.,2003). The regulatory domain contains a nuclear export signal motif that prevents the nuclear accumulation of full-length PAK-2. The activating proteolytic cleavage disrupts the nuclear export signal in PAK-2 and removes most its regulatory domain. The resulting activated PAK-2p34 fragment contains a nuclear localization signal and translocates to and is retained in the nucleus (Jakobi et al.,2003).

Editions

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