KTN1 binds Kinesin-1

Orlic-Milacic, M., Rivero Crespo, F.

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

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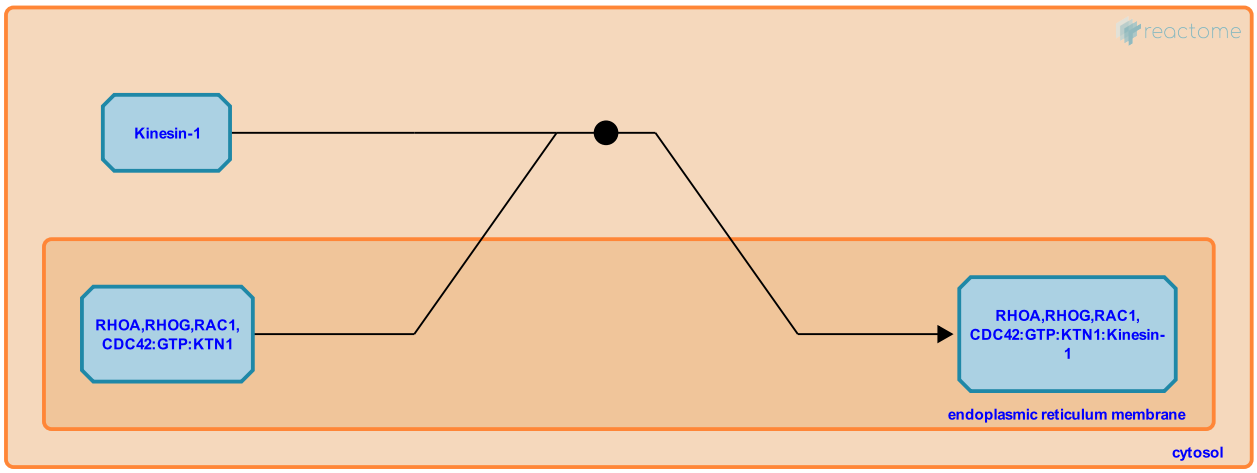
Stable identifier: R-HSA-5672083

Type: binding

Compartments: cytosol, endoplasmic reticulum membrane



The C-terminal region of KTN1 (kinectin) binds the cargo-binding tail of the kinesin heavy chain KIF5A and enhances microtubule-stimulated ATPase activity of KIF5A. KIF5A is a part of the conventional kinesin complex, kinesin-1. RHO GTPases, KTN1 and kinesin-1 colocalize on endoplasmic reticulum (ER) membranes and ER-derived vesicles and are thought to be involved in organelle/vesicle motility (Ong et al. 2000, Vignal et al. 2001)

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Editions

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