MET binds LRIG1

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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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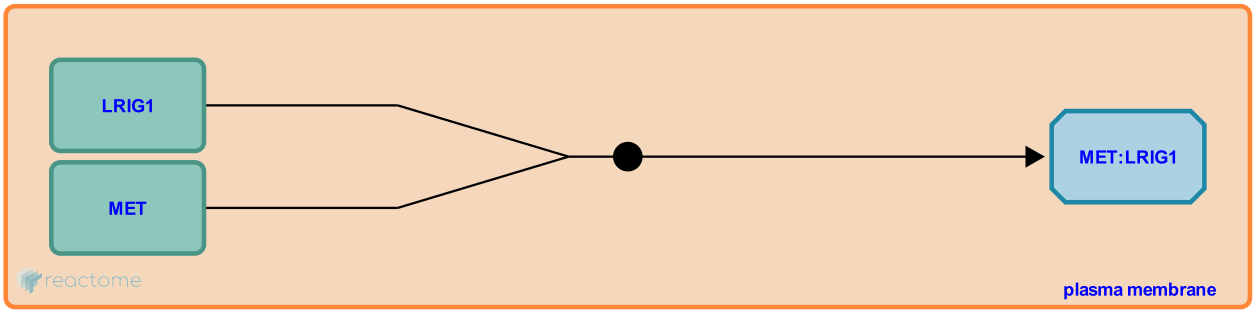
MET binds LRIG1

Stable identifier: R-HSA-8875374

Type: binding

Compartments: plasma membrane



LRIG1 can bind the MET receptor in the absence of HGF-mediated MET activation and trigger MET downregulation in a CBL-independent manner (Shattuck et al. 2007). MET targeting by the therapeutic antibody SAIT301 leads to LRIG1-mediated MET degradation through the lysosomal route. LRIG1-mediated MET downregulation requires ubiquitination of LRIG1 by an unknown ubiquitin ligase and can be inhibited by the ubiqitin hydrolase USP8, which deubiquitinates LRIG1 (Oh et al. 2014, Lee et al. 2014). Ubiquitinated LRIG1 binds to HGS (Hrs), a protein involved in clathrin-mediated endocytosis, and LRIG1 and MET co-localize with the lysosomal marker LAMP1 (Oh et al. 2014).

Literature references

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Editions

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