

Eef1a1 dissociates from p-Gfap

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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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Reactome database release: 88

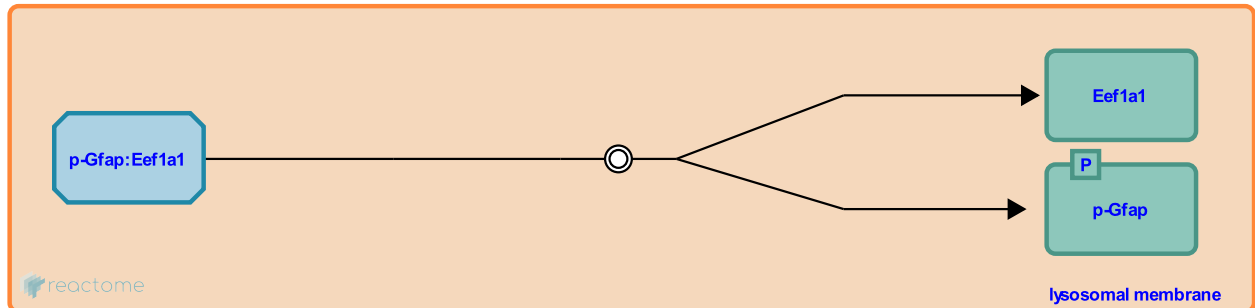
This document contains 1 reaction ([see Table of Contents](#))

Eef1a1 dissociates from p-Gfap ↗

Stable identifier: R-RNO-9626032

Type: dissociation

Compartments: lysosomal membrane



Intracellular proteins are targeted for proteolytic degradation in lysosome with the aid of chaperones. Heat shock cognate 71 kDa protein (Hspa8) transports substrates from the cytosol to the lysosomal membrane where it binds to Lysosome-associated membrane glycoprotein 2 (Lamp2). Subsequently, Lamp2 forms a multimeric complex stabilized with the aid of Hsp90 and glial fibrillary acidic protein (Gfap). This multimer allows the transfer of substrate into the lumen. The stability of this complex is regulated by the dynamics of Gfap and elongation factor 1 α (Eef1a1). During autophagy, a phosphorylated version of Gfap remains bound to Eef1a1. When GTP becomes available, Eef1a1 dissociates from Gfap (Bandyopadhyay U et al. 2010).

Literature references

Cuervo, AM., Kiffin, R., Sridhar, S., Kaushik, S., Bandyopadhyay, U. (2010). Identification of regulators of chaperone-mediated autophagy. *Mol. Cell*, 39, 535-47. ↗

Editions

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