

# pGFAP binds GFAP in LAMP2a multimer

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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](#))

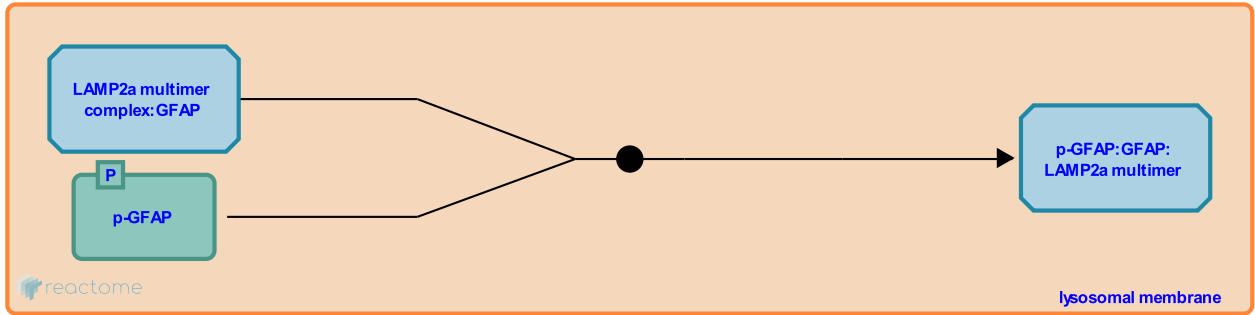
**pGFAP binds GFAP in LAMP2a multimer** ↗

**Stable identifier:** R-HSA-9626039

**Type:** binding

**Compartments:** lysosomal membrane

**Inferred from:** p-Gfap binds Gfap in Lamp2 multimer (Rattus norvegicus)



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 (LAMP2a). Subsequently, LAMP2a 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 $\alpha$  (EEF1A1). During autophagy, a phosphorylated version of GFAP remains bound to EEF1A1. When GTP becomes available, EEF1A1 dissociates from GFAP and binds with GTP in the cytosol. Subsequently, EEF1A1 is translocated from lysosomal membrane to cytosol. This makes p-GFAP available to bind with GFAP in the LAMP2a multimer complex (Bandyopadhyay U et al. 2010). Experiments confirming this binding were performed in rats.

**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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