HSPA8:Substrate binds LAMP2a

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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. ↗

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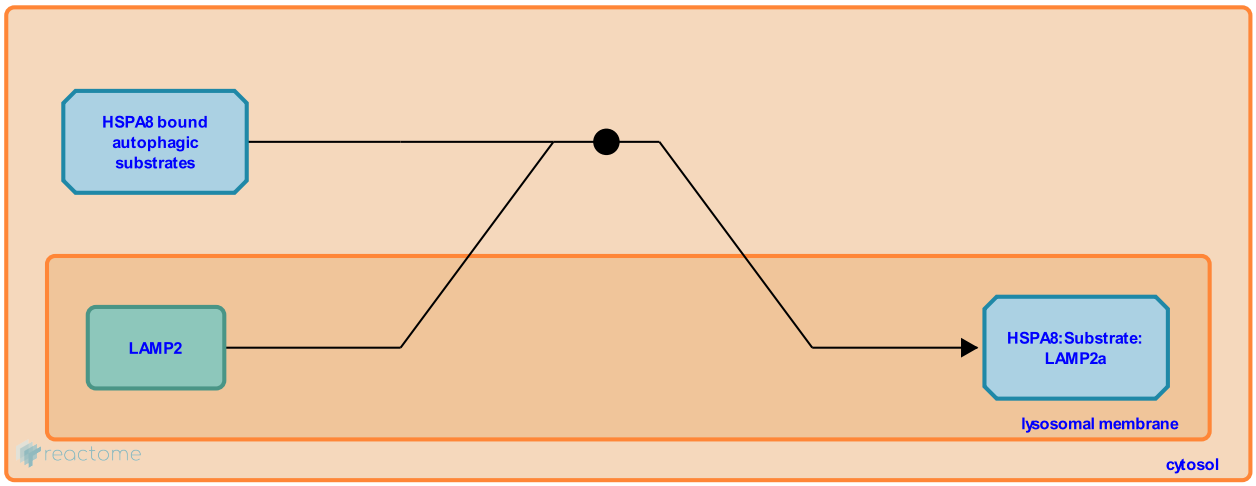
Stable identifier: R-HSA-9620197

Type: binding

Compartments: lysosomal membrane, cytosol

Inferred from: Hspa8:Rnase1 binds Lamp2a (Rattus norvegicus)



Intracellular proteins are targeted for proteolytic degradation in lysosome with the aid of chaperones. Heat shock cognate 71 kDa protein (HSPA8) acts as the constitutive chaperone that binds substrates in the cytosol. Consequently, the Hspa8:Substrate complex translocates from cytosol to lysosomal membrane where it binds to Lysosome-associated membrane glycoprotein 2 (LAMP2a) (Cuervo AM and Dice JF. 1996). Four positively charged amino acids in the cytosolic tail of the LAMP2a isoform is known to regulate the binding mechanism (Cuervo AM and Dice JF. 2000). Experiments confirming this binding were performed on rat models.

Literature references

Dice, JF., Cuervo, AM. (1996). A receptor for the selective uptake and degradation of proteins by lysosomes. *Science, 273*, 501-3. ↗

Dice, JF., Cuervo, AM. (2000). Unique properties of lamp2a compared to other lamp2 isoforms. *J. Cell. Sci., 113*, 4441-50. ↗

Editions

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