HSPA8 transports unfolded substrate to lysosomal lumen for degradation

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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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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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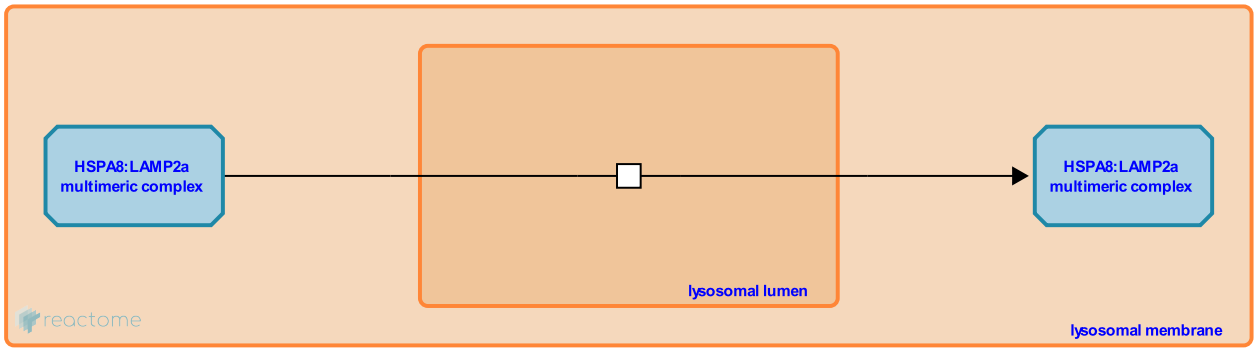
Stable identifier: R-HSA-9625188

Type: transition

Compartments: lysosomal lumen, lysosomal membrane

Inferred from: Hspa8 transports unfolded substrate to lysosomal lumen for degradation (Rattus norvegicus)



Heat shock cognate 71 kDa protein (HSPA8) translocates substrates from the cytosol to the lysosomal membrane. Subsequently, the substrate unfolds and binds to HSPA8 in the lysosomal lumen. HSPA8 facilitates the transport of the unfolded substrate to the lumen where it is then degraded (Agarraberes FA et al. 1997, Cuervo AM et al. 1997).

Literature references

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Editions

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