

# **HSPA8** binds substrate

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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: 89

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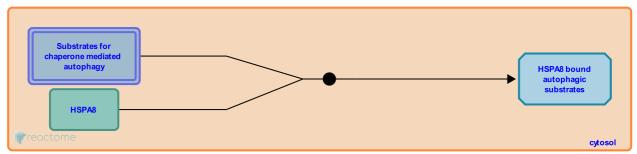
### **HSPA8** binds substrate **孝**

Stable identifier: R-HSA-9615721

Type: binding

**Compartments:** cytosol

Inferred from: Hspa8 binds Rnase1 (Rattus norvegicus)



Intracellular proteins are targeted for proteolytic degradation in the lysosome with the aid of chaperones. Heat shock cognate 71 kDa protein (HSPA8) acts as the constitutive chaperone that binds substrate proteins in the cytosol. HSPA8 recognizes a motif based on the charge of the amino acids (Chiang H et al. 1989, Dice JF et al. 1990). This allows the motif to have multiple sequence possibilities and also create a motif through post-translational modifications such as phosphorylation and acetylation. Once bound with HSPA8, the substrates are targeted to the lysosome or endosome.

### Literature references

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Cuervo, AM., Kaushik, S. (2015). Degradation of lipid droplet-associated proteins by chaperone-mediated autophagy facilitates lipolysis. *Nat. Cell Biol.*, 17, 759-70.

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### **Editions**

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