

Substrate:LAMP2a binds HSP90

Metzakopian, E., Varusai, TM.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u>
<u>License</u>. For more information see our <u>license</u>.

17/05/2024

https://reactome.org

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

https://reactome.org Page 2

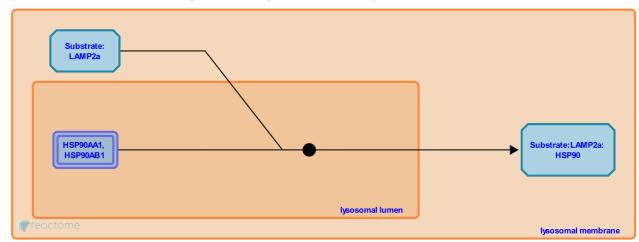
Substrate:LAMP2a binds HSP90 **对**

Stable identifier: R-HSA-9622831

Type: binding

Compartments: lysosomal lumen, lysosomal membrane

Inferred from: Substrate:Lamp2a binds Hsp90 (Rattus norvegicus)



Heat shock cognate 71 kDa protein (HSPA8) translocates substrates from cytosol to lysosomal membrane where it binds to Lysosome-associated membrane glycoprotein 2 (LAMP2a). HSPA8 is then released from this complex. Subsequently, Heat shock protein HSP 90 binds to the lysosomal luminal end of LAMP2a (Bandyopadhyay U et al. 2008). This facilitates the multimerization of LAMP2a and internalization of substrate into the lumen. Experiments confirming this binding were performed on rat models.

Literature references

Cuervo, AM., Kaushik, S., Bandyopadhyay, U., Varticovski, L. (2008). The chaperone-mediated autophagy receptor organizes in dynamic protein complexes at the lysosomal membrane. *Mol. Cell. Biol.*, 28, 5747-63.

Cuervo, AM., Kaushik, S. (2018). The coming of age of chaperone-mediated autophagy. *Nat. Rev. Mol. Cell Biol.*, 19, 365-381.

Editions

2019-02-21	Authored	Varusai, TM.
2019-02-22	Reviewed	Metzakopian, E.
2019-11-08	Edited	Varusai, TM.