

Egress of internalized antigen into cytosol from early endosome

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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: 90

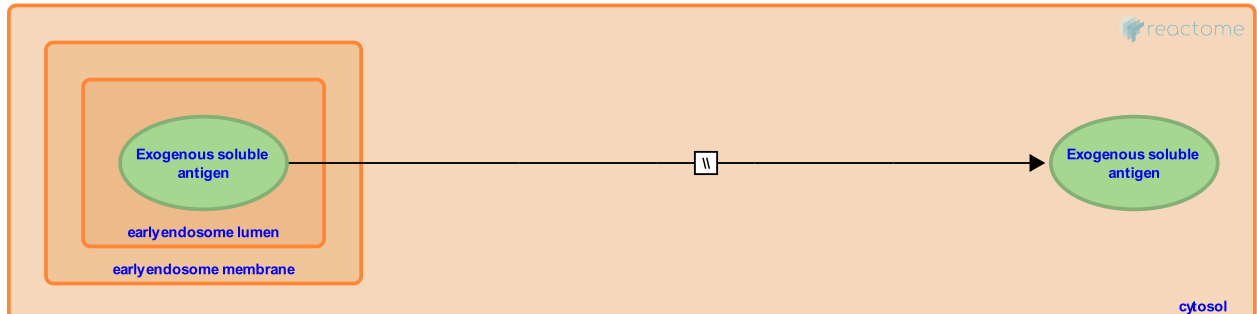
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Egress of internalized antigen into cytosol from early endosome [↗](#)

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Compartments: early endosome lumen, cytosol



Endocytosed antigens must leave the endocytic structure to enter into the MHC I pathway before exhaustive degradation within lysosomes. The canonical pathway is the transporter associated with antigen processing (TAP)-dependent cytosolic pathway, which involves the translocation of endocytosed antigens into the cytosol where they are degraded into antigenic peptides by the proteasome and transported to ER through TAP. This hypothesis comes from indirect evidence showing that proteasome inhibitors block cross-presentation of certain antigens (Amigorena et al. 2010, Burgdorf et al. 2008). According to this model antigens are translocated into the cytosol by an undefined mechanism.

There are less well-characterized mechanisms for the delivery of exogenous antigens into the cytosol. Certain peptides with highly positively charged sequences derived from HIV tat protein or the Antennapedia homeodomain (AntHD) protein seem to penetrate into the cytosol directly across the plasma membrane (Monu et al. 2007, Vendeville et al. 2004). It is also proposed that some exogenous antigens can be exchanged between neighboring cells through gap junctions, leading to cross presentation by the recipient cell (Monu et al. 2007, Neijssen et al. 2005).

Once internalized, antigens are routed into the cytosol, where they follow the conventional pathway of proteasome digestion and TAP-mediated transport of peptides into the ER lumen.

Literature references

- Zhuang, X., Rust, MJ., Lakadamyali, M. (2006). Ligands for clathrin-mediated endocytosis are differentially sorted into distinct populations of early endosomes. *Cell*, 124, 997-1009. [↗](#)
- Rodriguez, A., Regnault, A., Ricciardi-Castagnoli, P., Amigorena, S., Kleijmeer, M. (1999). Selective transport of internalized antigens to the cytosol for MHC class I presentation in dendritic cells. *Nat Cell Biol*, 1, 362-8. [↗](#)
- Nolan, GP., Kim, DT., Fathman, CG., Brockstedt, DG., Mitchell, DJ., Rothbard, JB. et al. (1997). Introduction of soluble proteins into the MHC class I pathway by conjugation to an HIV tat peptide. *J Immunol*, 159, 1666-8. [↗](#)
- Trombetta, ES., Pack, M., Mellman, I., Chang, H., Delamarre, L. (2005). Differential lysosomal proteolysis in antigen-presenting cells determines antigen fate. *Science*, 307, 1630-4. [↗](#)
- Rayne, F., Vendeville, A., Montcourrier, P., Beaumelle, B., Bonhoure, A., Bettache, N. (2004). HIV-1 Tat enters T cells using coated pits before translocating from acidified endosomes and eliciting biological responses. *Mol Biol Cell*, 15, 2347-60. [↗](#)

Editions

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