Loading of antigen peptide onto MHC class I molecule

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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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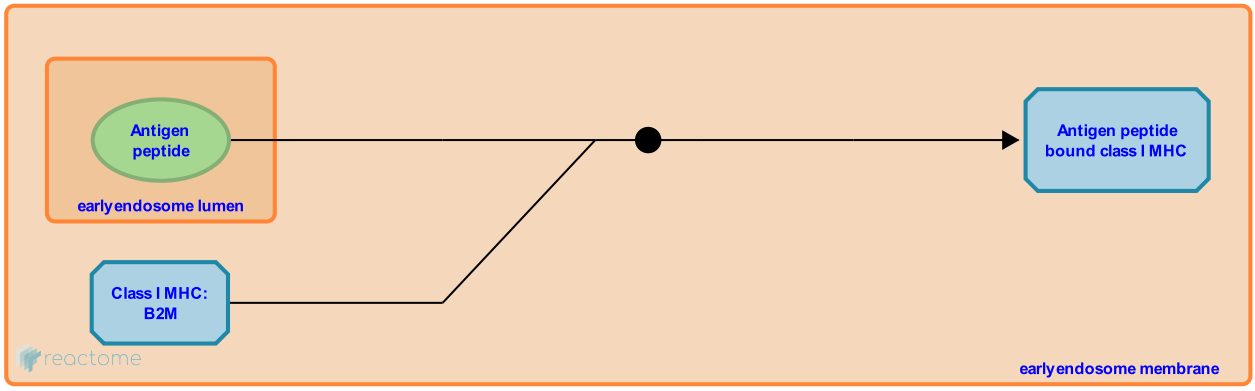
Stable identifier: R-HSA-1236943

Type: binding

Compartments: early endosome lumen, early endosome membrane



Peptides generated by Cathepsin S or IRAP-mediated proteolysis in the endosomes are loaded onto MHC class I molecules, which are internalized and transported to early and late endosomal compartments where antigenic peptides can be loaded. A fraction of the internalized cell surface class I molecules enter MHC class II compartments (MIICs) within endocytic vesicles (Gromme et al. 1999, Kleijmeer et al. 2001). Microscopic analysis has revealed that surface MHC-I molecules are internalized and transported to early and late endosomal compartments (Basha et al. 2008, Lizee et al. 2003). A tyrosine-based endocytic trafficking motif (YXXA) is required for the constitutive internalization of MHC-I molecules from the cell surface into early/late endosomes for peptide loading (Basha et al. 2008, Lizee et al. 2003). Upon entry in to these endosomal compartments the MHC class I complexes exchange their pre-bound peptides with exogenously derived antigenic peptides.

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Editions

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