reactome

Loading of antigenic peptides on to class I MHC

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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., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res, 46*, D649-D655. ↗

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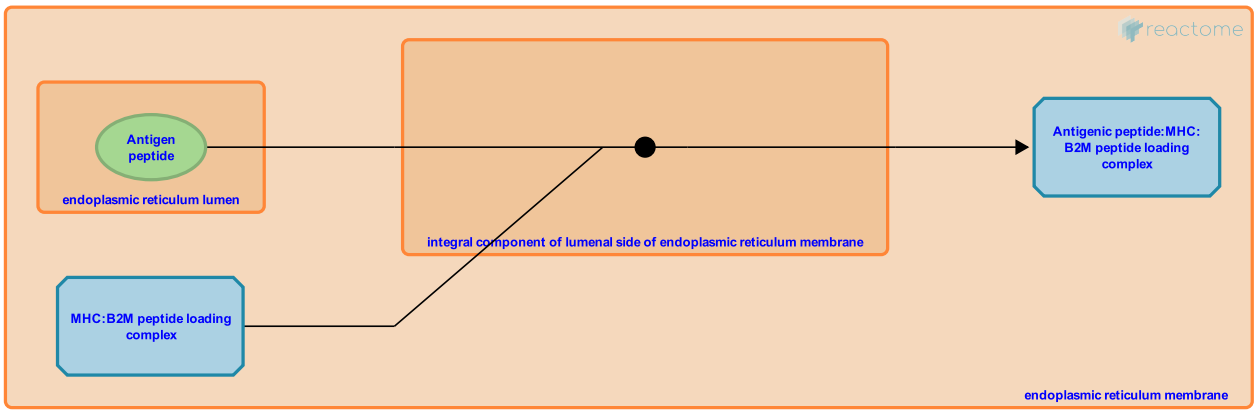
Stable identifier: R-HSA-8951499

Type: binding

Compartments: integral component of lumenal side of endoplasmic reticulum membrane, endoplasmic reticulum lumen, endoplasmic reticulum membrane



MHC class I heterodimers are only stable in peptide bound form and only as a trimer (with bound peptide) present on the cell surface. Class I MHC molecules prefer nonapeptides, and less frequently use octa- or deca-peptides. The peptide binding groove in MHC class I molecules is formed by the intimate association of the alpha1 and alpha2 domains of the heavy chain. Structural studies have revealed that the alpha1:alpha2 domains form a single peptide binding groove consisting of 2 parallel helices on a floor of 8 beta-strands. Hydrogen bonding networks are established in the binding groove with the antigenic peptide main chain and terminal atoms that enable largely sequence independent ligation. Upon peptide binding the class I MHC molecule releases from the peptide loading complex (PLC) and clusters at ER exit sites and is finally exported to the cell surface.

MHC I molecules bound to low-affinity peptides are not transferred to the cell surface and are instead cycled back to ER. They can proceed to the cell surface only when they become bound to high-affinity peptide (Howe et al, 2009; Garstka et al, 2007). Calreticulin binds to these low-affinity peptide bound class I molecules and mediate the retrieval from golgi apparatus to ER and for effcient presentation of a model antigen (Howe et al, 2009).

Literature references

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Editions

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