

Dissociation of the Antigenic peptide:MHC:B2M peptide loading com- plex

Elliott, T., Garapati, P V.

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

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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: 75

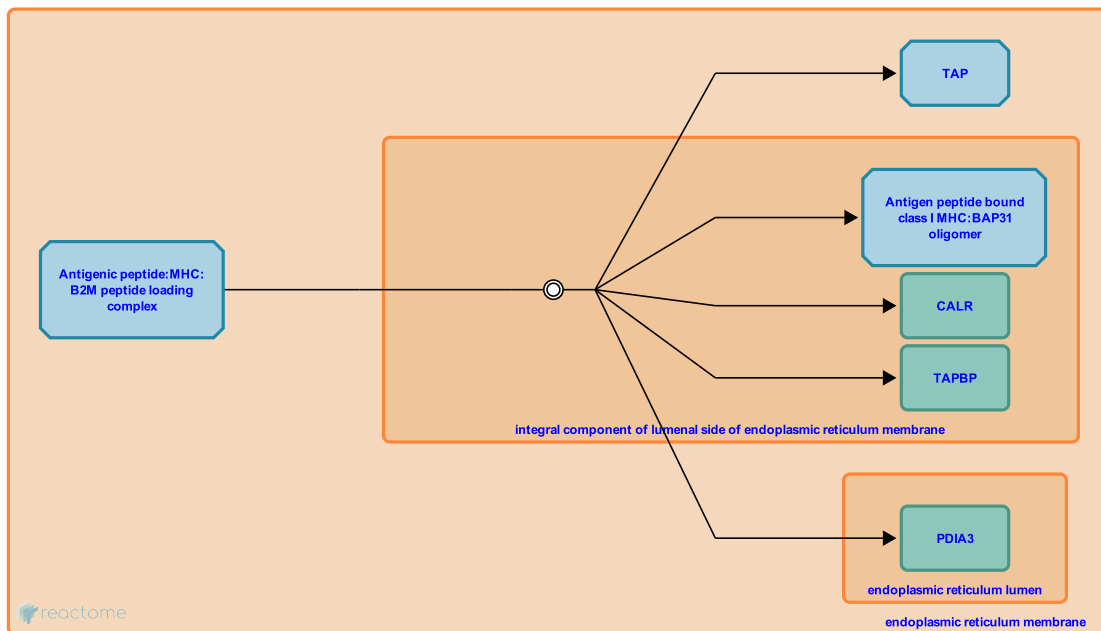
This document contains 1 reaction ([see Table of Contents](#))

Dissociation of the Antigenic peptide:MHC:B2M peptide loading complex ↗

Stable identifier: R-HSA-983161

Type: dissociation

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



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 efficient presentation of a model antigen (Howe et al. 2009).

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Editions

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